

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 30, 2007, 16:57:50 ; Search time 132 Seconds
(without alignments)
1140.491 Million cell updates/sec

Perfect score: 1824

Sequence: 1 MGRVAGSCAPGLLLVCLH.....SSWNIPAGFPNPPSPRLQMG 325

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1824	100.0	325	3	US-09-741-711-2
492	1824	100.0	325	4	US-10-174-587-238
556	1824	100.0	325	4	US-10-063-742-64
657	1824	100.0	325	4	US-10-276-162-10
671	1824	100.0	325	5	US-10-972-317-64
680	1824	100.0	325	6	US-11-002-844-10
681	1824	100.0	325	6	US-11-102-240-64
682	1824	100.0	325	6	US-11-103-195-64
683	1810	99.2	325	3	US-09-826-001-22
684	1810	99.2	325	3	US-09-994-365-6
685	1810	99.2	325	5	US-10-756-149-5496
686	1474	80.8	267	4	US-10-029-386-32252
687	724	39.7	388	3	US-09-361-630-1
688	724	39.7	388	6	US-11-130-821-1
689	693	38.0	131	4	US-10-029-386-30906
690	675.5	37.0	349	3	US-09-361-630-2
691	675.5	37.0	349	6	US-11-130-821-2
692	356.5	19.5	141	4	US-10-425-115-237300
693	194.5	10.7	1047	6	US-11-097-143-39414
694	174	9.5	1613	5	US-10-732-923-8153
695	174	9.5	1617	5	US-10-732-923-8154
696	173	9.5	1617	5	US-10-732-923-8077
697	168	9.2	371	5	US-10-450-763-35559
698	166.5	9.1	265	5	US-10-450-763-49597
699	165.5	9.1	2703	6	US-11-097-143-16689
700	163	8.9	1492	5	US-10-491-472-58
701	163	8.9	1647	3	US-09-824-574-4
702	163	8.9	1647	5	US-10-370-715B-356

Antibody
Allowed
method
ATL
new

703	163	8.9	1647	5	US-10-732-923-8821	Sequence 8821, Ap
704	163	8.9	1647	5	US-10-732-923-8822	Sequence 8822, Ap
705	163	8.9	1679	5	US-10-732-923-8823	Sequence 8823, Ap
706	159.5	8.7	266	4	US-10-087-192-570	Sequence 570, App
707	159	8.7	900	5	US-10-450-763-33892	Sequence 33892, A
708	156.5	8.6	1613	5	US-10-732-923-8824	Sequence 8824, Ap
709	156.5	8.6	1613	5	US-10-732-923-8825	Sequence 8825, Ap
710	154	8.4	244	4	US-10-767-701-35771	Sequence 35771, A
711	153.5	8.4	245	4	US-10-153-668-92	Sequence 92, Appl
712	153.5	8.4	259	4	US-10-029-386-31968	Sequence 31968, A
713	153.5	8.4	300	4	US-10-282-122A-49860	Sequence 49860, A
714	153.5	8.4	464	6	US-11-232-440-19	Sequence 19, Appl
715	153.5	8.4	464	6	US-11-232-440-67	Sequence 67, Appl
716	152	8.3	437	4	US-10-425-115-215389	Sequence 215389, A
717	151	8.3	1366	4	US-10-058-124-19	Sequence 19, Appl
718	151	8.3	1366	4	US-10-257-021-76	Sequence 76, Appl
719	151	8.3	1366	5	US-10-852-335A-158	Sequence 158, App
720	150	8.2	680	4	US-10-177-293-59	Sequence 59, Appl
721	150	8.2	680	4	US-10-295-027-110	Sequence 110, App
722	150	8.2	680	4	US-10-058-270A-80	Sequence 80, Appl
723	150	8.2	680	5	US-10-643-795A-118	Sequence 118, App
724	150	8.2	680	5	US-10-948-518-118	Sequence 118, App
725	150	8.2	680	5	US-10-936-626-83	Sequence 83, Appl
726	150	8.2	680	5	US-10-938-061-83	Sequence 83, Appl
727	150	8.2	903	4	US-10-156-761-11093	Sequence 11093, A
728	149	8.2	566	4	US-10-017-161-1040	Sequence 1040, Ap
729	148.5	8.1	566	4	US-10-425-115-336849	Sequence 336849, A
730	148.5	8.1	737	4	US-10-017-161-1350	Sequence 1350, Ap
731	148.5	8.1	737	4	US-10-292-798-1110	Sequence 1110, Ap
732	148	8.1	587	4	US-10-424-599-240882	Sequence 240882, A
733	148	8.1	1630	5	US-10-732-923-8792	Sequence 8792, Ap
734	147.5	8.1	926	6	US-11-097-143-22197	Sequence 22197, A
735	147	8.1	812	4	US-10-126-103-116	Sequence 116, App
736	147	8.1	812	4	US-10-108-260A-3673	Sequence 3673, Ap
737	147	8.1	812	4	US-10-431-096-116	Sequence 116, App
738	146.5	8.0	1046	5	US-10-156-761-10088	Sequence 10088, A
739	146	8.0	333	5	US-10-450-763-49596	Sequence 49596, A
740	146	8.0	1040	4	US-10-104-889-30	Sequence 30, Appl
741	146	8.0	1040	4	US-10-104-889-32	Sequence 32, Appl
742	146	8.0	1040	5	US-10-104-793-30	Sequence 30, Appl
743	146	8.0	1040	5	US-10-104-793-32	Sequence 32, Appl
744	146	8.0	1366	3	US-09-918-715-214	Sequence 214, App
745	146	8.0	1366	3	US-09-918-715-234	Sequence 234, App
746	146	8.0	1366	4	US-09-918-715-265	Sequence 265, App
747	146	8.0	1366	4	US-10-171-311-38	Sequence 38, Appl
748	146	8.0	1366	4	US-10-301-822-31	Sequence 31, Appl
749	146	8.0	1366	4	US-10-610-049-24	Sequence 24, Appl
750	146	8.0	1366	4	US-10-734-564-95	Sequence 95, Appl
751	146	8.0	1366	4	US-10-474-794-214	Sequence 214, App
752	146	8.0	1366	4	US-10-474-794-234	Sequence 234, App
753	146	8.0	1366	5	US-10-979-159-214	Sequence 214, App
754	146	8.0	1366	5	US-10-979-159-234	Sequence 234, App
755	146	8.0	1366	5	US-10-979-159-265	Sequence 265, App
756	146	8.0	1366	6	US-10-821-234-1431	Sequence 1431, Ap
757	146	8.0	1366	6	US-11-186-284-31	Sequence 31, Appl
758	146	8.0	1366	4	US-10-402-089-12	Sequence 12, Appl
759	146	8.0	1466	4	US-10-402-072A-12	Sequence 12, Appl
760	146	8.0	1466	5	US-10-719-993-784	Sequence 784, App
761	145.5	8.0	481	5	US-10-719-993-784	Sequence 784, App
762	145.5	8.0	533	4	US-10-087-192-1458	Sequence 1458, A
763	145.5	8.0	950	6	US-11-097-143-41331	Sequence 41331, A
764	145.5	8.0	1000	5	US-10-719-993-778	Sequence 778, App
765	145.5	8.0	1000	5	US-10-719-993-779	Sequence 779, App
766	145.5	8.0	1000	5	US-10-719-993-781	Sequence 781, App
767	145.5	8.0	1388	5	US-10-719-993-780	Sequence 780, App
768	145.5	8.0	1388	5	US-10-719-993-783	Sequence 783, App
769	145.5	8.0	1684	4	US-10-276-774-2398	Sequence 2398, Ap
770	145	7.9	209	4	US-10-424-599-241847	Sequence 241847, A
771	145	7.9	1717	6	US-11-182-016-20	Sequence 20, Appl
772	144.5	7.9	540	4	US-10-024-298A-170	Sequence 170, App
773	144.5	7.9	540	4	US-10-042-211A-170	Sequence 170, App
774	144.5	7.9	540	4	US-10-617-217A-170	Sequence 170, App
775	144.5	7.9	540	4	US-10-024-298A-170	Sequence 170, App

776	142.5	7.8	1735	4	US-10-333-680-1	Sequence 1, Appli	134	7.3	1767	5	US-10-995-561-914	Sequence 914, App
777	142	7.8	840	4	US-10-367-094-82	Sequence 82, Appl	134	7.3	1806	3	US-09-919-497-56	Sequence 56, Appl
778	142	7.8	1190	6	US-11-097-143-8340	Sequence 8340, Ap	134	7.3	1806	4	US-10-058-270A-122	Sequence 122, App
779	141.5	7.8	1189	4	US-10-408-765A-2272	Sequence 2272, Ap	134	7.3	1806	5	US-10-741-600-1478	Sequence 1478, Ap
780	141	7.7	362	6	US-11-097-143-15438	Sequence 15438, A	134	7.3	1806	5	US-10-741-600-1479	Sequence 1479, Ap
781	141	7.7	815	4	US-10-472-385-6	Sequence 6, Appli	134	7.3	1806	5	US-10-287-436A-498	Sequence 498, App
782	141	7.7	815	6	US-11-097-143-38289	Sequence 38289, A	134	7.3	1806	5	US-10-287-436A-1192	Sequence 1192, Ap
783	141	7.7	1309	5	US-10-461-862-27	Sequence 27, Appl	134	7.3	1806	5	US-10-995-561-912	Sequence 912, App
784	141	7.7	1366	4	US-10-357-851-2	Sequence 119, App	134	7.3	1806	5	US-10-995-561-915	Sequence 915, App
785	141	7.7	1366	4	US-10-357-851-2	Sequence 2, Appli	134	7.3	1806	6	US-11-051-720-1446	Sequence 1446, Ap
786	141	7.7	1366	4	US-10-358-024-2	Sequence 2, Appli	134	7.3	1806	6	US-11-051-720-1447	Sequence 1447, Ap
787	141	7.7	1366	4	US-10-788-792-153	Sequence 153, App	134	7.3	1818	5	US-10-741-600-1475	Sequence 1475, Ap
788	141	7.7	1319	5	US-10-461-862-25	Sequence 25, Appl	134	7.3	1818	5	US-10-741-600-1477	Sequence 1477, Ap
789	140.5	7.7	2060	4	US-10-408-765A-1674	Sequence 1674, Ap	134	7.3	1818	5	US-10-995-561-910	Sequence 910, App
790	140.5	7.7	448	4	US-10-244-596-14	Sequence 14, Appl	134	7.3	1818	5	US-10-995-561-913	Sequence 913, App
791	140.5	7.7	960	4	US-10-342-331-5	Sequence 5, Appli	134	7.3	1818	5	US-10-408-765A-1773	Sequence 1773, Ap
792	140.5	7.7	1727	4	US-10-408-765A-1813	Sequence 1813, Ap	134	7.3	1818	5	US-09-738-626-5676	Sequence 5676, Ap
793	139.5	7.6	472	4	US-10-437-963-136000	Sequence 136000, Ap	133	7.3	1818	5	US-10-094-749-3089	Sequence 3089, Ap
794	139.5	7.6	688	4	US-10-437-963-134726	Sequence 134726, Ap	133	7.3	1818	5	US-10-450-763-44644	Sequence 44644, A
795	139	7.6	500	4	US-10-437-963-139732	Sequence 139732, Ap	133	7.3	1818	5	US-10-450-763-44470	Sequence 44470, A
796	139	7.6	1823	5	US-10-741-600-1612	Sequence 1612, Ap	133	7.3	1818	5	US-10-051-874-166	Sequence 166, App
797	139	7.6	1823	5	US-10-995-561-988	Sequence 988, App	133	7.3	1818	5	US-10-240-154-18	Sequence 18, Appl
798	139	7.6	2102	5	US-10-741-600-1614	Sequence 1614, Ap	132	7.2	1818	5	US-11-097-143-42069	Sequence 42069, A
799	139	7.6	2102	5	US-10-995-561-990	Sequence 990, App	132	7.2	1818	5	US-10-648-593-233	Sequence 233, App
800	139	7.6	2108	5	US-10-741-600-1613	Sequence 1613, Ap	132	7.2	1818	5	US-10-723-860-4186	Sequence 4186, Ap
801	139	7.6	2108	5	US-10-995-561-989	Sequence 989, App	132	7.2	1818	5	US-10-756-149-5734	Sequence 5734, Ap
802	139	7.6	2157	5	US-10-741-600-1615	Sequence 1615, Ap	132	7.2	1818	5	US-11-072-175-233	Sequence 233, App
803	138.5	7.6	2157	5	US-10-995-561-991	Sequence 991, App	132	7.2	1818	5	US-10-411-120-78	Sequence 78, Appl
804	138.5	7.6	361	5	US-10-871-385-10	Sequence 10, Appl	132	7.2	1818	5	US-10-104-047-3364	Sequence 3364, Ap
805	138.5	7.6	1003	5	US-10-805-684-99	Sequence 99, Appl	132	7.2	1818	5	US-11-072-512-3364	Sequence 3364, Ap
806	138.5	7.6	2289	5	US-10-773-446-101	Sequence 101, App	132	7.2	1818	5	US-10-437-963-123652	Sequence 123652, A
807	138	7.6	639	4	US-10-369-493-3962	Sequence 3962, Ap	132	7.2	1818	5	US-10-437-963-123654	Sequence 123654, A
808	137.5	7.5	260	4	US-10-425-115-226835	Sequence 226835, Ap	132	7.2	1818	5	US-10-408-765A-1283	Sequence 1283, Ap
809	137.5	7.5	360	4	US-10-437-963-118547	Sequence 118547, Ap	132	7.2	1818	5	US-10-450-763-35199	Sequence 35199, A
810	137.5	7.5	826	5	US-10-719-993-782	Sequence 782, App	131	7.2	1818	5	US-11-097-143-13485	Sequence 13485, A
811	137	7.5	368	4	US-10-231-956A-446	Sequence 446, App	131	7.2	1818	5	US-10-375-592A-3	Sequence 3, Appli
812	137	7.5	670	4	US-10-437-963-137707	Sequence 137707, Ap	131	7.2	1818	5	US-11-035-623-16	Sequence 16, Appl
813	136	7.5	296	4	US-10-437-963-194347	Sequence 194347, Ap	131	7.2	1818	5	US-10-516-705-2	Sequence 2, Appli
814	136	7.5	498	4	US-10-437-963-123690	Sequence 123690, Ap	131	7.2	1818	5	US-10-901-816A-12	Sequence 12, Appl
815	136	7.5	510	4	US-10-425-114-72837	Sequence 72837, A	131	7.2	1818	5	US-10-259-165-302	Sequence 302, App
816	136	7.5	684	5	US-10-450-763-44485	Sequence 44485, A	131	7.2	1818	5	US-10-205-823-36	Sequence 36, Appl
817	136	7.5	1466	4	US-10-402-089-4	Sequence 4, Appli	130	7.2	1818	5	US-10-058-270A-94	Sequence 94, Appl
818	136	7.5	1466	4	US-10-402-089-6	Sequence 6, Appli	130	7.2	1818	5	US-10-333-894A-21	Sequence 21, Appl
819	136	7.5	1466	4	US-10-402-072A-4	Sequence 4, Appli	130	7.2	1818	5	US-10-705-165-28	Sequence 28, Appl
820	136	7.5	1466	4	US-10-402-072A-6	Sequence 6, Appli	130	7.2	1818	5	US-11-051-454-36	Sequence 36, Appl
821	136	7.5	1496	4	US-10-177-293-70	Sequence 70, Appl	130	7.2	1818	5	US-10-886-384-19	Sequence 19, Appl
822	136	7.5	1496	4	US-10-301-822-35	Sequence 35, Appl	130	7.2	1818	5	US-10-331-496A-26	Sequence 26, Appl
823	136	7.5	1496	4	US-10-236-031B-74	Sequence 74, Appl	130	7.2	1818	5	US-10-852-335A-155	Sequence 155, App
824	136	7.5	1496	4	US-10-468-091-22	Sequence 22, Appl	130	7.2	1818	5	US-10-468-091-26	Sequence 26, Appl
825	136	7.5	1496	4	US-10-788-792-248	Sequence 248, App	130	7.2	1818	5	US-09-918-715-252	Sequence 252, App
826	136	7.5	1496	5	US-10-287-436A-500	Sequence 500, App	130	7.2	1818	5	US-10-372-683-8	Sequence 8, Appli
827	136	7.5	1496	5	US-10-287-436A-589	Sequence 589, App	130	7.2	1818	5	US-10-474-794-252	Sequence 252, App
828	136	7.5	1496	5	US-10-287-436A-1194	Sequence 1194, Ap	130	7.2	1818	5	US-10-979-159-252	Sequence 252, App
829	136	7.5	1496	6	US-11-186-284-35	Sequence 35, Appl	130	7.2	1818	5	US-09-918-715-240	Sequence 240, App
830	135.5	7.4	551	4	US-10-055-569A-42	Sequence 42, Appl	130	7.2	1818	5	US-10-474-794-240	Sequence 240, App
831	135.5	7.4	576	4	US-10-055-569A-40	Sequence 40, Appl	130	7.2	1818	5	US-10-979-159-240	Sequence 240, App
832	135.5	7.4	576	5	US-10-998-142-13	Sequence 13, Appl	130	7.2	1818	5	US-10-745-393-3	Sequence 3, Appli
833	135.5	7.4	1786	4	US-10-476-924-23	Sequence 23, Appl	130	7.1	1818	5	US-10-425-114-56930	Sequence 56930, A
834	135	7.4	1366	4	US-10-402-089-10	Sequence 10, Appl	130	7.1	1818	5	US-10-367-094-85	Sequence 85, Appl
835	135	7.4	1366	4	US-10-402-072A-10	Sequence 10, Appl	130	7.1	1818	5	US-10-367-094-87	Sequence 87, Appl
836	134.5	7.4	1115	3	US-09-915-543-17	Sequence 17, Appl	130	7.1	1818	5	US-10-287-436A-443	Sequence 443, App
837	134.5	7.4	1115	4	US-10-322-579-17	Sequence 17, Appl	130	7.1	1818	5	US-10-287-436A-1144	Sequence 1144, Ap
838	134.5	7.4	1115	4	US-10-664-859-17	Sequence 17, Appl	130	7.1	1818	5	US-10-367-094-89	Sequence 89, Appl
839	134.5	7.4	1192	6	US-11-097-143-22671	Sequence 22671, A	130	7.1	1818	5	US-11-124-368A-329	Sequence 329, App
840	134.5	7.4	1497	4	US-10-468-091-23	Sequence 23, Appl	130	7.1	1818	5	US-09-795-061-4	Sequence 4, Appli
841	134.5	7.4	19662	4	US-10-044-846A-6	Sequence 6, Appli	130	7.1	1818	5	US-10-723-860-2660	Sequence 2660, Ap
842	134	7.3	262	4	US-10-133-234A-5	Sequence 5, Appli	129	5	1745	5	US-10-304-630-33	Sequence 33, Appl
843	134	7.3	262	6	US-11-211-401-5	Sequence 5, Appli	129	5	1745	5	US-11-140-416-33	Sequence 33, Appl
844	134	7.3	406	4	US-10-472-385-10	Sequence 10, Appl	129	5	1745	5	US-09-789-561-97	Sequence 97, Appl
845	134	7.3	493	4	US-10-425-115-243187	Sequence 243187, Ap	129	5	1745	5	US-09-833-245-2106	Sequence 2106, Ap
846	134	7.3	1767	5	US-10-741-600-1476	Sequence 1476, Ap	129	5	1745	5	US-10-411-120-72	Sequence 72, Appl
847	134	7.3	1767	5	US-10-741-600-1480	Sequence 1480, Ap	129	5	1745	5	US-10-883-936-97	Sequence 97, Appl
848	134	7.3	1767	5	US-10-995-561-911	Sequence 911, App	129	5	1745	5	US-11-264-096-2106	Sequence 2106, Ap

922	129.5	7.1	546	5	US-10-450-763-45976	Sequence 45976, A	995	126.5	6.9	1017	4	US-10-639-286-10	Sequence 10, Appl
923	129.5	7.1	1020	6	US-11-097-143-3705	Sequence 3705, A	996	126.5	6.9	1612	5	US-11-097-143-5022	Sequence 5022, Ap
924	129.5	7.1	1040	5	US-10-450-763-45093	Sequence 45093, A	997	126	6.9	3325	6	US-10-450-763-41286	Sequence 41286, A
925	129	7.1	284	4	US-10-437-963-152730	Sequence 152730, A	998	126	6.9	391	4	US-10-087-192-567	Sequence 567, App
926	129	7.1	577	4	US-10-055-569A-4	Sequence 4, Appli	999	126	6.9	416	4	US-10-232-175-25	Sequence 25, Appl
927	129	7.1	1008	4	US-10-276-774-1897	Sequence 1897, Ap	1000	126	6.9	416	6	US-11-139-377-25	Sequence 25, Appl
928	129	7.1	1013	5	US-10-450-763-38471	Sequence 38471, A	1001	126	6.9	498	5	US-10-901-816A-1	Sequence 1, Appli
929	129	7.1	2527	4	US-10-408-765A-2462	Sequence 2462, Ap	1002	126	6.9	498	5	US-10-901-816A-2	Sequence 2, Appli
930	129	7.1	2715	4	US-10-408-765A-866	Sequence 866, App	1003	126	6.9	500	4	US-10-232-175-22	Sequence 22, Appl
931	129	7.1	3530	5	US-10-723-860-1801	Sequence 1801, Ap	1004	126	6.9	500	6	US-11-139-377-22	Sequence 22, Appl
932	128.5	7.0	216	4	US-10-437-963-176612	Sequence 176612, A	1005	126	6.9	510	4	US-10-232-175-26	Sequence 26, Appl
933	128.5	7.0	370	5	US-10-450-763-39385	Sequence 39385, A	1006	126	6.9	510	6	US-11-139-377-26	Sequence 26, Appl
934	128.5	7.0	374	4	US-10-437-963-143400	Sequence 143400, A	1007	126	6.9	660	5	US-10-901-816A-3	Sequence 3, Appli
935	128.5	7.0	686	4	US-10-276-774-1767	Sequence 1767, Ap	1008	126	6.9	660	5	US-10-901-816A-4	Sequence 4, Appli
936	128.5	7.0	760	5	US-10-450-763-34227	Sequence 34227, A	1009	126	6.9	662	4	US-10-232-175-33	Sequence 33, Appl
937	128.5	7.0	906	4	US-10-375-592A-4	Sequence 4, Appli	1010	126	6.9	662	6	US-11-139-377-33	Sequence 33, Appl
938	128.5	7.0	1003	4	US-10-094-749-2528	Sequence 2528, Ap	1011	126	6.9	743	4	US-10-236-055A-32	Sequence 32, Appl
939	128.5	7.0	1003	4	US-10-476-397-3	Sequence 3, Appli	1012	126	6.9	1014	5	US-10-901-816A-5	Sequence 5, Appli
940	128	7.0	225	4	US-10-437-963-198086	Sequence 198086, A	1013	126	6.9	1014	5	US-10-901-816A-6	Sequence 6, Appli
941	128	7.0	481	4	US-10-437-963-176449	Sequence 176449, A	1014	126	6.9	1014	5	US-10-901-816A-7	Sequence 7, Appli
942	128	7.0	707	3	US-09-919-039-278	Sequence 278, App	1015	126	6.9	1014	5	US-10-901-816A-13	Sequence 13, Appl
943	128	7.0	838	5	US-10-287-436A-464	Sequence 464, App	1016	126	6.9	1057	4	US-10-104-889-16	Sequence 16, Appl
944	128	7.0	1838	5	US-10-287-436A-1161	Sequence 1161, Ap	1017	126	6.9	1057	4	US-10-104-889-20	Sequence 20, Appl
945	128	7.0	907	4	US-10-008-739A-2	Sequence 2, Appli	1018	126	6.9	1057	5	US-10-104-793-16	Sequence 16, Appl
946	128	7.0	1003	5	US-10-486-977-9	Sequence 9, Appli	1019	126	6.9	1057	5	US-10-104-793-20	Sequence 20, Appl
947	128	7.0	1531	5	US-10-330-773-142	Sequence 142, App	1020	126	6.9	1107	4	US-10-104-889-11	Sequence 11, Appl
948	128	7.0	1638	5	US-10-852-335A-162	Sequence 162, App	1021	126	6.9	1107	5	US-10-104-793-11	Sequence 11, Appl
949	128	7.0	707	5	US-10-784-004-1222	Sequence 1222, Ap	1022	126	6.9	1169	4	US-10-104-889-6	Sequence 6, Appli
950	128	7.0	1874	5	US-10-821-234-1182	Sequence 1182, Ap	1023	126	6.9	1169	5	US-10-104-793-6	Sequence 6, Appli
951	127.5	7.0	179	4	US-10-425-115-302253	Sequence 302253, A	1024	126	6.9	1171	4	US-10-104-889-8	Sequence 8, Appli
952	127.5	7.0	445	6	US-11-097-143-15996	Sequence 15996, A	1025	126	6.9	1171	5	US-10-104-793-8	Sequence 8, Appli
953	127.5	7.0	884	5	US-11-232-440-45	Sequence 45, Appl	1026	126	6.9	1341	4	US-10-058-124-18	Sequence 18, Appl
954	127.5	7.0	1149	5	US-10-450-763-33699	Sequence 33699, A	1027	126	6.9	1388	4	US-10-104-889-10	Sequence 10, Appl
955	127.5	7.0	1166	5	US-10-821-234-964	Sequence 964, App	1028	126	6.9	1388	5	US-10-104-793-10	Sequence 10, Appl
956	127.5	7.0	1453	5	US-10-784-004-344	Sequence 344, App	1029	126	6.9	1461	4	US-10-468-091-25	Sequence 25, Appl
957	127.5	7.0	1453	5	US-10-784-004-434	Sequence 434, App	1030	126	6.9	1464	3	US-09-918-715-261	Sequence 261, App
958	127.5	7.0	1453	5	US-10-784-004-918	Sequence 918, App	1031	126	6.9	1464	4	US-10-060-036-159	Sequence 159, App
959	127.5	7.0	1453	5	US-10-784-004-950	Sequence 950, App	1032	126	6.9	1464	4	US-10-171-311-36	Sequence 36, Appl
960	127.5	7.0	1466	3	US-09-918-715-226	Sequence 226, App	1033	126	6.9	1464	4	US-10-216-705-21	Sequence 21, Appl
961	127.5	7.0	1466	4	US-10-177-293-68	Sequence 68, Appl	1034	126	6.9	1464	4	US-10-149-352-2	Sequence 2, Appli
962	127.5	7.0	1466	4	US-10-301-822-33	Sequence 33, Appl	1035	126	6.9	1464	4	US-10-177-293-65	Sequence 65, Appl
963	127.5	7.0	1466	4	US-10-257-021-72	Sequence 72, Appl	1036	126	6.9	1464	4	US-10-301-822-28	Sequence 28, Appl
964	127.5	7.0	1466	4	US-10-357-851-3	Sequence 3, Appli	1037	126	6.9	1464	4	US-10-291-265-243	Sequence 243, App
965	127.5	7.0	1466	4	US-10-358-024-3	Sequence 3, Appli	1038	126	6.9	1464	4	US-10-764-425-114	Sequence 114, App
966	127.5	7.0	1466	4	US-10-734-564-103	Sequence 103, App	1039	126	6.9	1464	4	US-10-357-851-1	Sequence 1, Appli
967	127.5	7.0	1466	4	US-10-474-794-226	Sequence 226, App	1040	126	6.9	1464	4	US-10-358-024-1	Sequence 1, Appli
968	127.5	7.0	1466	5	US-10-852-335A-159	Sequence 159, App	1041	126	6.9	1464	4	US-10-734-564-79	Sequence 79, Appl
969	127.5	7.0	1466	5	US-10-979-159-226	Sequence 226, App	1042	126	6.9	1464	4	US-10-788-792-150	Sequence 150, App
970	127.5	7.0	1466	5	US-10-287-436A-451	Sequence 451, App	1043	126	6.9	1464	4	US-10-474-794-261	Sequence 261, App
971	127.5	7.0	1466	5	US-10-287-436A-494	Sequence 494, App	1044	126	6.9	1464	5	US-10-723-860-2289	Sequence 2289, Ap
972	127.5	7.0	1466	5	US-10-287-436A-1151	Sequence 1151, Ap	1045	126	6.9	1464	5	US-10-852-335A-157	Sequence 157, App
973	127.5	7.0	1466	5	US-10-287-436A-1189	Sequence 1189, Ap	1046	126	6.9	1464	5	US-10-979-159-261	Sequence 261, App
974	127.5	7.0	1466	6	US-11-186-284-33	Sequence 33, Appl	1047	126	6.9	1464	5	US-10-287-436A-491	Sequence 491, App
975	127.5	7.0	1469	5	US-10-450-763-45550	Sequence 45550, A	1048	126	6.9	1464	5	US-10-287-436A-1187	Sequence 1187, Ap
976	127.5	7.0	1485	5	US-10-489-740-129	Sequence 129, App	1049	126	6.9	1464	5	US-10-501-035-331	Sequence 331, App
977	127.5	7.0	1485	5	US-10-450-763-33817	Sequence 33817, A	1050	126	6.9	1464	6	US-11-000-463-243	Sequence 243, App
978	127.5	7.0	1642	4	US-10-786-720-39	Sequence 39, Appl	1051	126	6.9	1464	6	US-11-186-284-28	Sequence 28, Appl
979	127.5	7.0	1670	4	US-10-786-720-38	Sequence 38, Appl	1052	126	6.9	1464	6	US-11-021-603-2	Sequence 2, Appli
980	127	7.0	385	4	US-10-437-963-161558	Sequence 161558, A	1053	126	6.9	1467	5	US-10-821-234-1096	Sequence 1096, Ap
981	127	7.0	430	4	US-10-029-386-32401	Sequence 32401, A	1054	126	6.9	1518	5	US-10-450-763-53038	Sequence 53038, A
982	127	7.0	538	4	US-10-437-963-180554	Sequence 180554, A	1055	126	6.9	2309	6	US-11-097-143-25488	Sequence 25488, A
983	127	7.0	1014	5	US-10-901-816A-11	Sequence 11, Appl	1056	125.5	6.9	394	4	US-10-437-963-197292	Sequence 197292, A
984	127	7.0	1106	4	US-10-157-031-30	Sequence 30, Appl	1057	125.5	6.9	459	6	US-11-096-568A-21887	Sequence 21887, A
985	127	7.0	1106	4	US-10-930-723A-16	Sequence 16, Appl	1058	125.5	6.9	534	4	US-10-437-963-159995	Sequence 159995, A
986	127	7.0	1106	5	US-10-927-951A-16	Sequence 16, Appl	1059	125.5	6.9	605	4	US-10-411-120-65	Sequence 65, Appl
987	126.5	6.9	342	4	US-10-112-944-914	Sequence 914, App	1060	125.5	6.9	744	4	US-10-301-822-39	Sequence 39, Appl
988	126.5	6.9	531	3	US-09-925-300-1444	Sequence 1444, Ap	1061	125.5	6.9	744	5	US-10-758-846-71	Sequence 71, Appl
989	126.5	6.9	638	4	US-10-038-010-4	Sequence 4, Appli	1062	125.5	6.9	744	3	US-11-186-284-39	Sequence 39, Appl
990	126.5	6.9	668	4	US-10-240-154-20	Sequence 20, Appl	1063	125.5	6.9	752	3	US-09-159-469-61	Sequence 61, Appl
991	126.5	6.9	714	4	US-10-233-885-44	Sequence 44, Appl	1064	125.5	6.9	752	3	US-09-798-042-61	Sequence 61, Appl
992	126.5	6.9	714	4	US-10-231-581-44	Sequence 44, Appl	1065	125.5	6.9	752	3	US-09-798-042-89	Sequence 89, Appl
993	126.5	6.9	714	4	US-10-326-508A-15	Sequence 15, Appl	1066	125.5	6.9	752	3	US-09-953-108-61	Sequence 61, Appl
994	126.5	6.9	754	4	US-10-437-963-134895	Sequence 134895, A	1067	125.5	6.9	752	3	US-09-953-108-89	Sequence 89, Appl

1068	125.5	6.9	993	6	US-11-097-143-20001	Sequence 20001, A	1141	123	6.7	744	6	US-11-186-284-37	Sequence 37, Appl
1069	125.5	6.9	1121	4	US-10-437-963-196036	Sequence 196036,	1142	123	6.7	759	6	US-11-097-143-36930	Sequence 36930, A
1070	125.5	6.9	1450	4	US-10-381-2478-17	Sequence 17, Appl	1143	123	6.7	763	6	US-11-096-568A-32714	Sequence 32714, A
1071	125.5	6.9	1463	4	US-10-402-089-2	Sequence 2, Appli	1144	123	6.7	793	6	US-11-096-568A-32713	Sequence 32713, A
1072	125.5	6.9	1463	4	US-10-402-072A-2	Sequence 2, Appli	1145	123	6.7	1014	5	US-10-901-816A-8	Sequence 8, Appli
1073	125.5	6.9	1487	6	US-11-202-057-7	Sequence 7, Appli	1146	123	6.7	1014	5	US-10-901-816A-9	Sequence 9, Appli
1074	125.5	6.9	1494	4	US-10-381-247B-2	Sequence 2, Appli	1147	123	6.7	1039	6	US-11-097-143-14139	Sequence 14139, A
1075	125	6.9	301	4	US-10-424-599-236175	Sequence 236175,	1148	123	6.7	1251	4	US-10-399-645-7	Sequence 7, Appli
1076	125	6.9	636	5	US-10-784-004-428	Sequence 428, App	1149	123	6.7	1316	4	US-10-379-981-9	Sequence 9, Appli
1077	125	6.9	639	4	US-10-369-493-2275	Sequence 2275, Ap	1150	123	6.7	3067	5	US-10-631-467-1618	Sequence 1618, Ap
1078	125	6.9	700	4	US-10-437-963-145767	Sequence 145767,	1151	122.5	6.7	254	4	US-10-301-488A-24	Sequence 24, Appl
1079	125	6.9	895	5	US-10-476-724A-2	Sequence 2, Appli	1152	122.5	6.7	254	4	US-10-301-448-24	Sequence 24, Appl
1080	125	6.9	895	5	US-10-476-724A-2	Sequence 4, Appli	1153	122.5	6.7	272	3	US-09-774-639-167	Sequence 167, App
1081	125	6.9	910	5	US-10-723-860-2221	Sequence 2221, Ap	1154	122.5	6.7	272	3	US-09-969-730-120	Sequence 120, App
1082	125	6.9	1685	5	US-10-450-763-35198	Sequence 35198, A	1155	122.5	6.7	272	3	US-10-621-363-120	Sequence 120, App
1083	125	6.9	1693	5	US-10-450-763-45978	Sequence 45978, A	1156	122.5	6.7	272	5	US-10-986-501-120	Sequence 120, App
1084	125	6.9	1759	4	US-10-369-493-7032	Sequence 7032, Ap	1157	122.5	6.7	514	4	US-10-437-963-111701	Sequence 111701,
1085	124.5	6.8	282	4	US-10-424-599-259896	Sequence 259896,	1158	122.5	6.7	527	3	US-09-738-973-216	Sequence 216, App
1086	124.5	6.8	372	4	US-10-437-963-160362	Sequence 160362,	1159	122.5	6.7	527	3	US-09-854-133-216	Sequence 216, App
1087	124.5	6.8	450	4	US-10-437-963-175308	Sequence 175308,	1160	122.5	6.7	527	4	US-10-144-649A-216	Sequence 216, App
1088	124.5	6.8	1014	4	US-10-194-441A-1	Sequence 1, Appli	1161	122.5	6.7	937	5	US-10-450-763-50706	Sequence 50706, A
1089	124.5	6.8	1418	4	US-10-058-124-20	Sequence 20, Appl	1162	122.5	6.7	1078	4	US-10-058-124-21	Sequence 21, Appl
1090	124.5	6.8	1418	4	US-10-468-091-5	Sequence 5, Appli	1163	122.5	6.7	1373	5	US-10-840-512-180	Sequence 180, App
1091	124.5	6.8	1448	4	US-10-408-765A-998	Sequence 998, App	1164	122.5	6.7	1413	4	US-10-288-798-24	Sequence 24, Appl
1092	124.5	6.8	1487	5	US-10-756-149-4739	Sequence 4739, Ap	1165	122.5	6.7	1413	4	US-10-362-892-24	Sequence 24, Appl
1093	124.5	6.8	1487	6	US-11-202-057-3	Sequence 3, Appli	1166	122.5	6.7	1644	4	US-10-408-765A-919	Sequence 919, App
1094	124.5	6.8	1487	6	US-11-202-057-5	Sequence 5, Appli	1167	122.5	6.7	1644	4	US-10-210-130-38	Sequence 38, Appl
1095	124.5	6.8	19723	4	US-10-084-846A-5	Sequence 5, Appli	1168	122	6.7	264	4	US-10-304-630-24	Sequence 24, Appl
1096	124	6.8	178	4	US-10-437-963-111612	Sequence 111612,	1169	122	6.7	264	6	US-11-140-416-24	Sequence 24, Appl
1097	124	6.8	295	6	US-11-051-720-1444	Sequence 1444, Ap	1170	122	6.7	488	4	US-10-080-170-4	Sequence 4, Appli
1098	124	6.8	346	4	US-10-437-963-184670	Sequence 184670,	1171	122	6.7	488	4	US-10-080-170-4	Sequence 4, Appli
1099	124	6.8	439	4	US-10-115-984-2	Sequence 2, Appli	1172	122	6.7	488	4	US-10-468-356-4	Sequence 4, Appli
1100	124	6.8	630	4	US-10-322-281-428	Sequence 428, App	1173	122	6.7	574	4	US-10-168-097A-76	Sequence 76, Appl
1101	124	6.8	720	4	US-10-322-281-432	Sequence 432, App	1174	122	6.7	574	4	US-10-239-431A-38	Sequence 38, Appl
1102	124	6.8	881	3	US-09-816-860A-2	Sequence 2, Appli	1175	122	6.7	574	5	US-10-469-469-44	Sequence 44, Appl
1103	124	6.8	881	5	US-10-860-777-2	Sequence 3, Appli	1176	122	6.7	575	4	US-10-055-569A-41	Sequence 41, Appl
1104	124	6.8	895	5	US-10-461-862-36	Sequence 36, Appl	1177	122	6.7	668	5	US-10-805-684-40	Sequence 40, Appl
1105	124	6.8	903	4	US-10-408-765A-827	Sequence 827, App	1178	122	6.7	819	5	US-10-450-763-33928	Sequence 33928, A
1106	124	6.8	940	4	US-10-291-172-363	Sequence 363, App	1179	122	6.7	1014	5	US-10-901-816A-10	Sequence 10, Appl
1107	124	6.8	940	4	US-10-221-278-363	Sequence 363, App	1180	122	6.7	1038	5	US-10-739-930-5899	Sequence 5899, Ap
1108	124	6.8	968	4	US-10-231-172-739	Sequence 739, App	1181	122	6.7	1152	4	US-10-322-636-75	Sequence 75, Appl
1109	124	6.8	968	4	US-10-221-278-739	Sequence 739, App	1182	122	6.7	1259	4	US-10-260-715-8	Sequence 8, Appli
1110	124	6.8	1120	6	US-11-051-720-1733	Sequence 1733, Ap	1183	122	6.7	1259	5	US-10-491-188-8	Sequence 8, Appli
1111	124	6.8	1126	4	US-10-108-260A-3665	Sequence 3665, Ap	1184	122	6.7	1537	6	US-11-097-143-27759	Sequence 27759, A
1112	124	6.8	1305	6	US-11-051-720-1370	Sequence 1370, Ap	1185	122	6.7	1963	6	US-11-097-143-15249	Sequence 15249, A
1113	124	6.8	1326	5	US-10-461-862-30	Sequence 30, Appl	1186	122	6.7	3640	5	US-10-450-763-53388	Sequence 53388, A
1114	124	6.8	1326	5	US-10-461-862-40	Sequence 40, Appl	1187	121.5	6.7	254	4	US-10-304-630-20	Sequence 20, Appl
1115	124	6.8	1502	5	US-10-461-862-34	Sequence 34, Appl	1188	121.5	6.7	254	4	US-10-304-630-21	Sequence 21, Appl
1116	124	6.8	1502	5	US-10-461-862-42	Sequence 42, Appl	1189	121.5	6.7	254	4	US-10-304-630-22	Sequence 22, Appl
1117	124	6.8	1739	3	US-09-795-061-2	Sequence 2, Appli	1190	121.5	6.7	254	6	US-11-140-416-20	Sequence 20, Appl
1118	123.5	6.8	276	4	US-10-437-963-154928	Sequence 154928,	1191	121.5	6.7	254	6	US-11-140-416-21	Sequence 21, Appl
1119	123.5	6.8	318	4	US-10-437-963-127875	Sequence 127875,	1192	121.5	6.7	254	6	US-11-140-416-22	Sequence 22, Appl
1120	123.5	6.8	394	5	US-10-450-763-39772	Sequence 39772, A	1193	121.5	6.7	717	5	US-10-758-846-25	Sequence 25, Appl
1121	123.5	6.8	401	4	US-10-342-331-34	Sequence 34, Appl	1194	121.5	6.7	717	5	US-10-496-905-31	Sequence 31, Appl
1122	123.5	6.8	453	6	US-11-097-143-22710	Sequence 22710, A	1195	121.5	6.7	744	5	US-10-758-846-24	Sequence 24, Appl
1123	123.5	6.8	599	5	US-10-672-040-22	Sequence 22, Appl	1196	121.5	6.7	744	5	US-10-496-905-28	Sequence 28, Appl
1124	123.5	6.8	599	5	US-10-672-040-23	Sequence 23, Appl	1197	121.5	6.7	749	6	US-11-097-143-15537	Sequence 15537, A
1125	123.5	6.8	663	5	US-10-072-012-700	Sequence 700, App	1198	121.5	6.7	754	5	US-10-496-905-156	Sequence 156, App
1126	123.5	6.8	663	5	US-10-029-345A-40	Sequence 40, Appl	1199	121	6.6	256	4	US-10-346-190-84	Sequence 84, Appl
1127	123.5	6.8	663	6	US-11-143-984A-40	Sequence 40, Appl	1200	121	6.6	519	5	US-10-450-763-53075	Sequence 53075, A
1128	123.5	6.8	1458	5	US-10-461-862-38	Sequence 38, Appl	1201	121	6.6	606	4	US-10-276-774-1383	Sequence 1383, Ap
1129	123.5	6.8	1461	5	US-10-461-862-32	Sequence 32, Appl	1202	121	6.6	654	4	US-10-764-425-156	Sequence 156, App
1130	123.5	6.8	1516	4	US-10-060-036-166	Sequence 166, App	1203	121	6.6	726	4	US-10-437-963-197489	Sequence 197489,
1131	123.5	6.8	1516	4	US-10-431-642-3	Sequence 3, Appli	1204	121	6.6	759	4	US-10-156-761-10673	Sequence 10673, A
1132	123.5	6.8	1516	5	US-10-849-989-30	Sequence 30, Appl	1213	121	6.6	839	4	US-10-237-535-54	Sequence 54, Appl
1133	123.5	6.8	1516	5	US-10-220-824-8	Sequence 8, Appli	1222	121	6.6	839	4	US-10-239-196-54	Sequence 54, Appl
1134	123.5	6.8	1712	5	US-10-648-813-4	Sequence 4, Appli	1309	121	6.6	839	4	US-10-210-951-36	Sequence 36, Appl
1135	123	6.7	437	4	US-10-437-963-139039	Sequence 139039,	1312	121	6.6	839	4	US-10-211-884-36	Sequence 36, Appl
1136	123	6.7	469	4	US-10-437-963-136216	Sequence 136216,	1315	121	6.6	839	4	US-10-211-858-36	Sequence 36, Appl
1137	123	6.7	659	4	US-10-425-115-206708	Sequence 206708,	1330	121	6.6	862	6	US-11-051-720-1443	Sequence 1443, Ap
1138	123	6.7	744	4	US-10-171-311-40	Sequence 40, Appl	1331	121	6.6	1071	4	US-10-188-248-24	Sequence 24, Appl
1139	123	6.7	744	4	US-10-236-055A-30	Sequence 30, Appl	1332	121	6.6	1260	6	US-11-097-143-3972	Sequence 3972, Ap
1140	123	6.7	744	4	US-10-301-822-37	Sequence 37, Appl	1333	121	6.6	2280	6	US-11-097-143-11742	Sequence 11742, A

1334	121	6.6	19695	4	US-10-084-846A-3	Sequence 3, Appli	1407	119	6.5	1099	5	US-10-899-715-4	Sequence 4, Appli
1335	120.5	6.6	284	4	US-10-437-963-148869	Sequence 148869, A	1408	119	6.5	1099	6	US-11-213-326-10	Sequence 10, Appl
1336	120.5	6.6	329	4	US-10-425-114-59937	Sequence 59937, A	1409	119	6.5	1186	6	US-11-097-143-9768	Sequence 9768, Ap
1337	120.5	6.6	349	4	US-10-403-571-102	Sequence 102, App	1410	118.5	6.5	143	4	US-10-425-115-212479	Sequence 212479, S
1338	120.5	6.6	447	4	US-10-437-963-152072	Sequence 152072, A	1411	118.5	6.5	393	5	US-10-220-335-540	Sequence 540, App
1339	120.5	6.6	592	5	US-10-450-763-34450	Sequence 34450, A	1412	118.5	6.5	444	5	US-10-450-763-33800	Sequence 33800, A
1340	120.5	6.6	702	6	US-11-097-143-15984	Sequence 15984, A	1413	118.5	6.5	699	4	US-10-121-988-143	Sequence 143, App
1341	120.5	6.6	703	4	US-10-219-449-4	Sequence 4, Appli	1414	118.5	6.5	699	4	US-10-400-562-143	Sequence 143, App
1342	120.5	6.6	703	5	US-10-958-858-4	Sequence 4, Appli	1415	118.5	6.5	699	4	US-10-237-551-143	Sequence 143, App
1343	120.5	6.6	717	4	US-10-219-449-2	Sequence 2, Appli	1416	118.5	6.5	699	4	US-10-237-551-254	Sequence 254, App
1344	120.5	6.6	717	5	US-10-958-858-2	Sequence 2, Appli	1417	118.5	6.5	699	5	US-10-945-050-143	Sequence 143, App
1345	120.5	6.6	733	4	US-10-138-588-40	Sequence 40, Appl	1418	118.5	6.5	699	5	US-10-945-050-254	Sequence 254, App
1346	120.5	6.6	1016	5	US-10-481-596-4	Sequence 4, Appli	1419	118.5	6.5	818	6	US-11-097-143-37449	Sequence 37449, A
1347	120.5	6.6	1170	4	US-10-437-963-189133	Sequence 189133, A	1420	118.5	6.5	921	5	US-10-723-860-2056	Sequence 2056, Ap
1348	120.5	6.6	1277	5	US-10-893-315-106	Sequence 106, App	1421	118.5	6.5	991	5	US-10-784-004-1210	Sequence 1210, Ap
1349	120.5	6.6	1278	4	US-10-087-192-708	Sequence 708, App	1422	118.5	6.5	1643	5	US-10-732-923-8217	Sequence 8217, Ap
1350	120.5	6.6	1449	4	US-10-402-089-8	Sequence 8, Appli	1423	118.5	6.5	1870	4	US-10-408-765A-120	Sequence 120, App
1351	120.5	6.6	1449	4	US-10-402-072A-8	Sequence 8, Appli	1424	118	6.5	219	5	US-10-967-589-2	Sequence 2, Appli
1352	120.5	6.6	1712	3	US-09-961-403-9	Sequence 9, Appli	1425	118	6.5	255	3	US-09-943-306-4	Sequence 4, Appli
1353	120.5	6.6	3164	4	US-10-669-161-72	Sequence 72, Appl	1426	118	6.5	255	4	US-10-435-602-4	Sequence 4, Appli
1354	120.5	6.6	4952	4	US-10-051-874-56	Sequence 56, Appl	1427	118	6.5	255	5	US-10-475-558-4	Sequence 4, Appli
1355	120.5	6.6	5029	5	US-10-732-923-14989	Sequence 8219, Ap	1428	118	6.5	255	6	US-11-027-139-4	Sequence 4, Appli
1356	120.5	6.6	5159	4	US-10-085-198-112	Sequence 112, App	1429	118	6.5	256	3	US-09-823-494-22	Sequence 22, Appl
1357	120.5	6.6	5262	4	US-10-051-874-165	Sequence 165, App	1430	118	6.5	256	4	US-10-109-551-2	Sequence 2, Appli
1358	120	6.6	265	5	US-10-471-931-2	Sequence 2, Appli	1431	118	6.5	256	4	US-10-109-551-4	Sequence 4, Appli
1359	120	6.6	313	4	US-10-437-963-114711	Sequence 114711, A	1432	118	6.5	256	4	US-10-301-488A-28	Sequence 28, Appl
1360	120	6.6	334	6	US-11-097-143-24261	Sequence 24261, A	1433	118	6.5	256	4	US-10-105-616-5	Sequence 5, Appli
1361	120	6.6	421	4	US-10-411-120-76	Sequence 76, Appl	1434	118	6.5	256	4	US-10-410-907A-11	Sequence 11, Appl
1362	120	6.6	492	4	US-10-639-286-11	Sequence 11, Appl	1435	118	6.5	256	4	US-10-410-907A-12	Sequence 12, Appl
1363	120	6.6	617	5	US-10-658-989A-2	Sequence 2, Appli	1436	118	6.5	256	4	US-10-346-190-81	Sequence 81, Appl
1364	120	6.6	821	5	US-10-658-989A-3	Sequence 3, Appli	1437	118	6.5	256	4	US-10-346-190-88	Sequence 88, Appl
1365	120	6.6	932	5	US-10-732-923-14989	Sequence 14989, A	1438	118	6.5	256	4	US-10-301-448-28	Sequence 28, Appl
1366	120	6.6	1014	4	US-10-194-441A-18	Sequence 48, Appl	1439	118	6.5	256	4	US-10-479-218-1	Sequence 1, Appli
1367	120	6.6	1286	4	US-10-425-115-206578	Sequence 206578, A	1440	118	6.5	256	4	US-10-479-218-3	Sequence 3, Appli
1368	120	6.6	187	4	US-10-468-091-6	Sequence 6, Appli	1441	118	6.5	256	4	US-10-479-218-5	Sequence 5, Appli
1369	119.5	6.6	186	4	US-10-425-115-269376	Sequence 269376, A	1442	118	6.5	256	4	US-10-479-218-6	Sequence 6, Appli
1370	119.5	6.6	264	4	US-10-304-630-27	Sequence 27, Appl	1443	118	6.5	256	4	US-10-479-218-7	Sequence 7, Appli
1371	119.5	6.6	264	6	US-11-140-416-27	Sequence 27, Appl	1444	118	6.5	256	4	US-10-479-218-8	Sequence 8, Appli
1372	119.5	6.6	268	4	US-10-437-963-127271	Sequence 127271, A	1445	118	6.5	256	4	US-10-479-218-9	Sequence 9, Appli
1373	119.5	6.6	333	4	US-10-232-175-27	Sequence 27, Appl	1446	118	6.5	256	4	US-10-479-218-10	Sequence 10, Appl
1374	119.5	6.6	333	6	US-11-139-377-27	Sequence 27, Appl	1447	118	6.5	256	4	US-10-479-218-11	Sequence 11, Appl
1375	119.5	6.6	413	4	US-10-424-599-240403	Sequence 240403, A	1448	118	6.5	256	4	US-10-479-218-12	Sequence 12, Appl
1376	119.5	6.6	442	4	US-10-437-963-197867	Sequence 197867, A	1449	118	6.5	256	4	US-10-479-218-13	Sequence 13, Appl
1377	119.5	6.6	638	4	US-10-001-887-108	Sequence 108, App	1450	118	6.5	256	4	US-10-479-218-14	Sequence 14, Appl
1378	119.5	6.6	638	4	US-10-138-588-42	Sequence 42, Appl	1451	118	6.5	256	4	US-10-479-218-15	Sequence 15, Appl
1379	119.5	6.6	638	5	US-10-958-863-108	Sequence 108, App	1452	118	6.5	256	4	US-10-479-218-16	Sequence 16, Appl
1380	119.5	6.6	914	5	US-10-450-763-57757	Sequence 57757, A	1453	118	6.5	256	4	US-10-479-218-17	Sequence 17, Appl
1381	119.5	6.6	1094	4	US-10-437-963-181712	Sequence 181712, A	1454	118	6.5	256	4	US-10-479-218-18	Sequence 18, Appl
1382	119.5	6.6	1241	5	US-10-930-723A-18	Sequence 18, Appl	1455	118	6.5	256	4	US-10-479-218-19	Sequence 19, Appl
1383	119.5	6.6	1241	5	US-10-927-951A-18	Sequence 18, Appl	1456	118	6.5	256	4	US-10-479-218-20	Sequence 20, Appl
1384	119.5	6.6	1523	4	US-10-473-576-5	Sequence 5, Appli	1457	118	6.5	256	5	US-10-949-880-1	Sequence 1, Appli
1385	119.5	6.6	1603	5	US-10-723-860-4225	Sequence 4225, Ap	1458	118	6.5	256	5	US-10-917-646-6	Sequence 6, Appli
1386	119	6.5	243	4	US-10-437-963-196787	Sequence 196787, A	1459	118	6.5	256	6	US-11-056-950-6	Sequence 6, Appli
1387	119	6.5	256	4	US-10-109-551-6	Sequence 6, Appli	1460	118	6.5	256	3	US-09-823-494-21	Sequence 21, Appl
1388	119	6.5	256	4	US-10-109-551-8	Sequence 8, Appli	1461	118	6.5	264	4	US-10-209-194-2	Sequence 2, Appli
1389	119	6.5	256	4	US-10-109-551-10	Sequence 10, Appl	1462	118	6.5	264	4	US-10-301-488A-30	Sequence 30, Appl
1390	119	6.5	256	4	US-10-301-488A-29	Sequence 29, Appl	1463	118	6.5	264	4	US-10-301-488A-33	Sequence 33, Appl
1391	119	6.5	256	4	US-10-346-190-82	Sequence 82, Appl	1464	118	6.5	264	4	US-10-410-907A-13	Sequence 13, Appl
1392	119	6.5	256	4	US-10-346-190-83	Sequence 83, Appl	1465	118	6.5	264	4	US-10-346-190-80	Sequence 80, Appl
1393	119	6.5	256	4	US-10-301-448-29	Sequence 29, Appl	1466	118	6.5	264	4	US-10-417-964A-32	Sequence 32, Appl
1394	119	6.5	256	5	US-10-917-646-8	Sequence 8, Appli	1467	118	6.5	264	4	US-10-417-964A-19	Sequence 19, Appl
1395	119	6.5	256	5	US-10-917-646-9	Sequence 9, Appli	1468	118	6.5	264	4	US-10-301-448-33	Sequence 30, Appl
1396	119	6.5	256	5	US-10-917-646-10	Sequence 10, Appl	1469	118	6.5	264	4	US-10-301-448-33	Sequence 33, Appl
1397	119	6.5	256	5	US-10-917-646-11	Sequence 11, Appl	1470	118	6.5	264	4	US-10-479-218-2	Sequence 2, Appli
1398	119	6.5	256	6	US-11-056-950-8	Sequence 8, Appli	1471	118	6.5	264	5	US-10-949-880-2	Sequence 2, Appli
1399	119	6.5	256	6	US-11-056-950-9	Sequence 9, Appli	1472	118	6.5	264	5	US-10-917-646-5	Sequence 5, Appli
1400	119	6.5	256	6	US-11-056-950-10	Sequence 10, Appl	1473	118	6.5	264	5	US-10-966-012-1	Sequence 1, Appli
1401	119	6.5	256	6	US-11-056-950-11	Sequence 11, Appl	1474	118	6.5	264	6	US-11-056-950-5	Sequence 5, Appli
1402	119	6.5	492	4	US-10-639-286-12	Sequence 12, Appl	1475	118	6.5	396	4	US-10-437-963-176490	Sequence 176490, A
1403	119	6.5	731	4	US-10-086-464-8	Sequence 8, Appli	1476	118	6.5	397	5	US-10-450-763-34229	Sequence 34229, A
1404	119	6.5	1099	3	US-09-881-654-4	Sequence 4, Appli	1477	118	6.5	421	4	US-10-411-120-51	Sequence 51, Appl
1405	119	6.5	1099	4	US-10-637-323-4	Sequence 4, Appli	1478	118	6.5	421	4	US-10-411-120-77	Sequence 77, Appl
1406	119	6.5	1099	4	US-10-658-782-6	Sequence 6, Appli	1479	118	6.5	437	4	US-10-437-963-168762	Sequence 168762, A

1480	118	6.5	900	5	US-10-450-763-57406	Sequence 57406, A
1481	118	6.5	2289	4	US-10-437-963-162531	Sequence 162531,
1482	117.5	6.4	246	4	US-10-276-774-2466	Sequence 2466, Ap
1483	117.5	6.4	261	6	US-11-096-568A-20320	Sequence 20320, A
1484	117.5	6.4	270	4	US-10-425-115-273687	Sequence 273687,
1485	117.5	6.4	355	4	US-10-437-963-191965	Sequence 191965,
1486	117.5	6.4	384	4	US-10-437-963-200395	Sequence 200395,
1487	117.5	6.4	443	4	US-10-425-115-366467	Sequence 366467,
1488	117.5	6.4	755	3	US-09-919-497-57	Sequence 57, Appl
1489	117.5	6.4	817	4	US-10-437-963-154523	Sequence 154523,
1490	117.5	6.4	1045	6	US-11-097-143-14307	Sequence 14307, A
1491	117.5	6.4	1318	4	US-10-200-562-197	Sequence 197, App
1492	117.5	6.4	1318	4	US-10-237-551-197	Sequence 197, App
1493	117.5	6.4	1318	5	US-10-945-050-197	Sequence 197, App
1494	117.5	6.4	1780	4	US-10-115-479-10	Sequence 10, Appl
1495	117	6.4	256	4	US-10-479-218-4	Sequence 4, Appli
1496	117	6.4	306	4	US-10-437-963-146544	Sequence 146544,
1497	117	6.4	367	4	US-10-437-963-151076	Sequence 151076,
1498	117	6.4	408	4	US-10-437-963-184023	Sequence 184023,
1499	117	6.4	445	4	US-10-437-963-161789	Sequence 161789,
1500	117	6.4	481	4	US-10-156-761-12906	Sequence 12906, A

Search completed: July 30, 2007, 17:01:01

Job time : 159 secs

GenCore version 6.2.1
 Copyright (c) 1993 - 2007 Bioceleration Ltd.
 OM protein - protein search, using sw model
 Run on: July 30, 2007, 16:58:44 ; Search time 99 Seconds
 (without alignments)
 1137.554 Million cell updates/sec

Perfect score: 1824
 Sequence: 1 MGRVAGSCAPIGLLLVCLH.....SSWNIPAGFPNPPSPRLONG 325

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1425058 seqs, 346516376 residues

Total number of hits satisfying chosen parameters: 1425058

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1500 summaries

Database : Published Applications AA_New:
 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB pep.*
 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB pep.*
 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB pep.*
 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US03_NEW_PUB pep.*
 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB pep.*
 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB pep.*
 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US16_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
4	1824	100.0	325	7 US-11-101-316-64	Sequence 64, Appl
5	1824	100.0	325	7 US-11-376-673-64	Sequence 64, Appl
6	1824	100.0	325	7 US-11-102-284-64	Sequence 64, Appl
7	1810	99.2	325	7 US-11-294-760-6	Sequence 6, Appl
8	1810	99.2	325	7 US-11-443-428A-876877	Sequence 876877, Appl
9	595	32.6	125	7 US-11-486-448-79955	Sequence 79955, A
10	571	31.3	144	7 US-11-486-448-79954	Sequence 79954, A
11	191.5	10.5	300	7 US-11-443-428A-815332	Sequence 815332, A
12	191.5	10.5	300	7 US-11-443-428A-815333	Sequence 815333, A
13	191.5	10.5	300	7 US-11-443-428A-815334	Sequence 815334, A
14	191.5	10.5	300	7 US-11-443-428A-815335	Sequence 815335, A
15	191.5	10.5	300	7 US-11-443-428A-815339	Sequence 815339, A
16	191.5	10.5	300	7 US-11-443-428A-815341	Sequence 815341, A
17	191.5	10.5	300	7 US-11-443-428A-815342	Sequence 815342, A
18	191.5	10.5	300	7 US-11-443-428A-815345	Sequence 815345, A
19	191.5	10.5	300	7 US-11-443-428A-815347	Sequence 815347, A
20	191.5	10.5	304	7 US-11-443-428A-815337	Sequence 815337, A
21	191.5	10.5	304	7 US-11-443-428A-815340	Sequence 815340, A
22	191.5	10.5	314	7 US-11-443-428A-815336	Sequence 815336, A
23	179	9.8	239	7 US-11-443-428A-815338	Sequence 815338, A
24	173	9.5	1348	7 US-11-090-997-554	Sequence 554, Appl
25	169	9.3	1497	7 US-11-443-428A-908957	Sequence 908957, A
26	163	8.9	708	7 US-11-443-428A-908972	Sequence 908972, A
27	163	8.9	1086	6 US-10-990-328-13128	Sequence 13128, A
28	163	8.9	1207	7 US-11-443-428A-908986	Sequence 908986, A
29	163	8.9	1234	7 US-11-443-428A-908978	Sequence 908978, A

30	163	8.9	1282	7 US-11-443-428A-908969	Sequence 908969, A
31	163	8.9	1303	7 US-11-443-428A-908968	Sequence 908968, A
32	163	8.9	1340	7 US-11-443-428A-908985	Sequence 908985, A
33	163	8.9	1356	7 US-11-443-428A-908963	Sequence 908963, A
34	163	8.9	1356	7 US-11-443-428A-908963	Sequence 908963, A
35	163	8.9	1356	7 US-11-443-428A-908975	Sequence 908975, A
36	163	8.9	1356	7 US-11-443-428A-908976	Sequence 908976, A
37	163	8.9	1356	7 US-11-443-428A-908977	Sequence 908977, A
38	163	8.9	1356	7 US-11-443-428A-908983	Sequence 908983, A
39	163	8.9	1389	7 US-11-443-428A-908953	Sequence 908953, A
40	163	8.9	1389	7 US-11-443-428A-908954	Sequence 908954, A
41	163	8.9	1389	7 US-11-443-428A-908955	Sequence 908955, A
42	163	8.9	1614	6 US-10-990-328-13133	Sequence 13133, A
43	163	8.9	1647	6 US-10-990-328-13127	Sequence 13127, A
44	163	8.9	1647	6 US-10-990-328-13130	Sequence 13130, A
45	163	8.9	1647	6 US-10-990-328-13131	Sequence 13131, A
46	163	8.9	1647	7 US-11-090-997-1466	Sequence 1466, Ap
47	163	8.9	1647	7 US-11-582-861-8070	Sequence 8070, Ap
48	163	8.9	1679	6 US-10-990-328-13129	Sequence 13129, A
49	163	8.9	1679	7 US-11-090-997-1468	Sequence 1468, Ap
50	162.5	8.9	665	7 US-11-443-428A-836074	Sequence 836074, A
51	159	8.7	559	6 US-10-557-444-18	Sequence 18, Appl
52	154.5	8.5	293	7 US-11-443-428A-815343	Sequence 815343, A
53	153.5	8.4	245	7 US-11-371-354-13877	Sequence 13877, A
54	153.5	8.4	245	7 US-11-371-354-58451	Sequence 58451, A
55	153.5	8.4	245	7 US-11-371-354-78626	Sequence 78626, A
56	153.5	8.4	300	7 US-11-431-855-27810	Sequence 27810, A
57	153.5	8.4	338	7 US-11-443-428A-807581	Sequence 807581, A
58	153.5	8.4	386	7 US-11-443-428A-807596	Sequence 807596, A
59	153.5	8.4	418	7 US-11-443-428A-807579	Sequence 807579, A
60	153.5	8.4	436	7 US-11-443-428A-807580	Sequence 807580, A
61	153.5	8.4	464	7 US-11-443-428A-807568	Sequence 807568, A
62	153.5	8.4	464	7 US-11-443-428A-807570	Sequence 807570, A
63	153.5	8.4	464	7 US-11-443-428A-807571	Sequence 807571, A
64	153.5	8.4	464	7 US-11-443-428A-807572	Sequence 807572, A
65	153.5	8.4	464	7 US-11-443-428A-807573	Sequence 807573, A
66	153.5	8.4	464	7 US-11-443-428A-807574	Sequence 807574, A
67	153.5	8.4	464	7 US-11-443-428A-807577	Sequence 807577, A
68	153.5	8.4	464	7 US-11-443-428A-807578	Sequence 807578, A
69	153.5	8.4	464	7 US-11-443-428A-807589	Sequence 807589, A
70	153.5	8.4	464	7 US-11-443-428A-807590	Sequence 807590, A
71	153.5	8.4	464	7 US-11-443-428A-807593	Sequence 807593, A
72	153.5	8.4	464	7 US-11-443-428A-807594	Sequence 807594, A
73	153.5	8.4	490	7 US-11-443-428A-807595	Sequence 807595, A
74	151.5	8.3	328	7 US-11-218-141-3894	Sequence 3894, Ap
75	151.5	8.3	388	6 US-10-534-893-5447	Sequence 5447, Ap
76	151	8.3	1366	6 US-10-985-570-3	Sequence 3, Appl
77	151	8.3	1366	7 US-11-443-428A-1025025	Sequence 1025025, A
78	151	8.3	1366	7 US-11-443-428A-1025026	Sequence 1025026, A
79	151	8.3	1366	7 US-11-443-428A-1025027	Sequence 1025027, A
80	150	8.2	680	6 US-10-219-051B-11803	Sequence 11803, A
81	150	8.2	680	7 US-11-226-554-83	Sequence 83, Appl
82	150	8.2	680	7 US-11-248-718-83	Sequence 83, Appl
83	150	8.2	680	7 US-11-538-552-83	Sequence 83, Appl
84	150	8.2	680	7 US-11-538-764-118	Sequence 118, Appl
85	150	8.2	680	7 US-11-443-428A-756250	Sequence 756250, A
86	150	8.2	680	7 US-11-443-428A-756252	Sequence 756252, A
87	150	8.2	680	7 US-11-443-428A-756253	Sequence 756253, A
88	148.5	8.1	737	7 US-11-214-063A-1110	Sequence 1110, Ap
89	147.5	8.1	278	6 US-10-917-503-11151	Sequence 11151, A
90	147.5	8.1	377	7 US-11-443-428A-872375	Sequence 872375, A
91	147.5	8.1	388	7 US-11-371-354-70407	Sequence 70407, A
92	147.5	8.1	388	7 US-11-443-428A-872362	Sequence 872362, A
93	147.5	8.1	388	7 US-11-443-428A-872366	Sequence 872366, A
94	147.5	8.1	388	7 US-11-443-428A-872367	Sequence 872367, A
95	147.5	8.1	388	7 US-11-443-428A-872368	Sequence 872368, A
96	147.5	8.1	388	7 US-11-443-428A-872369	Sequence 872369, A
97	147.5	8.1	388	7 US-11-443-428A-872370	Sequence 872370, A
98	147.5	8.1	388	7 US-11-443-428A-872377	Sequence 872377, A
99	147.5	8.1	388	7 US-11-443-428A-872378	Sequence 872378, A
100	147.5	8.1	388	7 US-11-443-428A-872379	Sequence 872379, A
101	147.5	8.1	388	7 US-11-443-428A-872381	Sequence 872381, A
102	147.5	8.1	388	7 US-11-582-861-11032	Sequence 11032, A

103 147.5 8.1 723 7 US-11-443-428A-815569 Sequence 815569, 176
104 147 8.1 544 6 US-10-934-893-1378 Sequence 1378, Ap 177
105 147 8.1 552 7 US-11-443-428A-917626 Sequence 917626, 178
106 147 8.1 812 7 US-11-293-697-3673 Sequence 3673, Ap 179
107 147 8.1 812 7 US-11-090-997-1776 Sequence 1776, Ap 180
108 147 8.1 812 7 US-11-371-354-70915 Sequence 70915, A 181
109 147 8.1 812 7 US-11-443-428A-917624 Sequence 917624, 182
110 147 8.1 812 7 US-11-443-428A-917627 Sequence 917627, 183
111 147 8.1 821 6 US-10-533-520-4750 Sequence 4750, Ap 184
112 147 8.1 821 7 US-11-090-997-1774 Sequence 1774, Ap 185
113 146.5 8.0 229 7 US-11-443-428A-815344 Sequence 815344, 186
114 146.5 8.0 1046 7 US-11-431-855-19583 Sequence 19583, A 187
115 146 8.0 636 7 US-11-443-428A-920762 Sequence 920762, 188
116 146 8.0 1040 7 US-11-048-197-30 Sequence 197, 30, Appl 189
117 146 8.0 1040 7 US-11-048-197-32 Sequence 32, Appl 190
118 146 8.0 1227 6 US-10-405-027-3917 Sequence 3917, Ap 191
119 146 8.0 1366 6 US-10-700-439-136 Sequence 136, App 192
120 146 8.0 1366 6 US-10-574-398-195 Sequence 195, App 193
121 146 8.0 1366 6 US-10-574-398-309 Sequence 309, App 194
122 146 8.0 1366 7 US-11-105-233-159 Sequence 159, App 195
123 146 8.0 1366 7 US-11-510-530-38 Sequence 38, Appl 196
124 146 8.0 1366 7 US-11-582-861-6589 Sequence 6589, Ap 197
125 146 8.0 1372 6 US-10-219-051B-5579 Sequence 5579, Ap 198
126 146 8.0 1372 6 US-10-219-051B-5583 Sequence 5583, Ap 199
127 146 8.0 1372 6 US-10-219-051B-10581 Sequence 10581, A 200
128 146 8.0 1372 6 US-10-219-051B-11270 Sequence 11270, A 201
129 146 8.0 1372 6 US-10-219-051B-13225 Sequence 13225, A 202
130 145.5 8.0 477 6 US-10-669-920-737 Sequence 737, App 203
131 145.5 8.0 566 7 US-11-241-607-26850 Sequence 26850, A 204
132 145.5 8.0 601 7 US-11-241-607-26849 Sequence 26849, A 205
133 145.5 8.0 914 6 US-10-557-444-7 Sequence 7, Appl 206
134 145.5 8.0 988 6 US-10-669-920-731 Sequence 731, App 207
135 145.5 8.0 988 6 US-10-669-920-735 Sequence 735, App 208
136 145.5 8.0 1312 7 US-11-443-428A-912390 Sequence 912390, 209
137 145.5 8.0 1354 6 US-10-669-920-725 Sequence 725, App 210
138 145.5 8.0 1368 6 US-10-669-920-727 Sequence 727, App 211
139 145.5 8.0 1368 6 US-10-669-920-729 Sequence 729, App 212
140 145.5 8.0 1388 7 US-11-443-428A-912387 Sequence 912387, 213
141 145.5 8.0 1388 7 US-11-443-428A-912388 Sequence 912388, 214
142 145.5 8.0 1388 7 US-11-443-428A-912389 Sequence 912389, 215
143 145.5 8.0 1388 7 US-11-443-428A-912392 Sequence 912392, 216
144 145.5 8.0 1684 7 US-11-218-141-3225 Sequence 3225, Ap 217
145 145 7.9 276 6 US-10-703-032-136520 Sequence 136520, 218
146 145 7.9 1277 7 US-11-443-428A-890862 Sequence 890862, 219
147 144.5 7.9 404 6 US-10-917-503-15782 Sequence 15782, A 220
148 144.5 7.9 540 7 US-11-371-354-64613 Sequence 64613, A 221
149 144.5 7.9 540 7 US-11-443-428A-898561 Sequence 898561, 222
150 144.5 7.9 540 7 US-11-443-428A-898562 Sequence 898562, 223
151 144.5 7.9 540 7 US-11-443-428A-898563 Sequence 898563, 224
152 144.5 7.9 540 7 US-11-443-428A-898565 Sequence 898565, 225
153 144.5 7.9 540 7 US-11-443-428A-898567 Sequence 898567, 226
154 144.5 7.9 540 7 US-11-443-428A-898568 Sequence 898568, 227
155 144.5 7.9 540 7 US-11-443-428A-898569 Sequence 898569, 228
156 144.5 7.9 540 7 US-11-650-501-170 Sequence 170, App 229
157 144 7.9 336 7 US-11-443-428A-837831 Sequence 837831, 230
158 144 7.9 599 7 US-11-443-428A-837817 Sequence 837817, 231
159 144 7.9 599 7 US-11-443-428A-837818 Sequence 837818, 232
160 144 7.9 599 7 US-11-443-428A-837819 Sequence 837819, 233
161 144 7.9 599 7 US-11-443-428A-837821 Sequence 837821, 234
162 144 7.9 599 7 US-11-443-428A-837822 Sequence 837822, 235
163 144 7.9 599 7 US-11-443-428A-837823 Sequence 837823, 236
164 144 7.9 599 7 US-11-443-428A-837824 Sequence 837824, 237
165 144 7.9 599 7 US-11-443-428A-837825 Sequence 837825, 238
166 144 7.9 599 7 US-11-443-428A-837826 Sequence 837826, 239
167 144 7.9 599 7 US-11-443-428A-837827 Sequence 837827, 240
168 144 7.9 599 7 US-11-443-428A-837828 Sequence 837828, 241
169 144 7.9 599 7 US-11-443-428A-837832 Sequence 837832, 242
170 144 7.9 599 7 US-11-443-428A-837834 Sequence 837834, 243
171 144 7.9 599 7 US-11-443-428A-837835 Sequence 837835, 244
172 144 7.9 599 7 US-11-443-428A-837836 Sequence 837836, 245
173 144 7.9 599 7 US-11-443-428A-837839 Sequence 837839, 246
174 144 7.9 599 7 US-11-443-428A-837840 Sequence 837840, 247
175 144 7.9 732 7 US-11-443-428A-872613 Sequence 872613, 248

7 732 7 US-11-443-428A-872617 Sequence 872617, 249
6 631 6 US-10-760-320A-3161 Sequence 3161, Ap 250
7 757 7 US-11-443-428A-872614 Sequence 872614, 251
6 1735 6 US-10-533-519-2409 Sequence 2409, Ap 252
7 1735 6 US-10-219-051B-8300 Sequence 8300, Ap 253
6 1735 6 US-10-219-051B-11860 Sequence 11860, A 254
7 1735 6 US-10-529-348-2342 Sequence 2342, Ap 255
6 1735 6 US-11-395-172-1 Sequence 1, Appl 256
7 637 7 US-11-443-428A-890877 Sequence 890877, 257
7 682 7 US-11-443-428A-890876 Sequence 890876, 258
7 926 7 US-11-443-428A-890875 Sequence 890875, 259
7 1086 7 US-11-443-428A-890863 Sequence 890863, 260
7 1142 7 US-11-443-428A-890869 Sequence 890869, 261
7 1142 7 US-11-443-428A-890866 Sequence 890866, 262
7 1151 7 US-11-443-428A-890874 Sequence 890874, 263
7 1189 7 US-11-443-428A-890859 Sequence 890859, 264
7 1189 7 US-11-443-428A-890860 Sequence 890860, 265
7 1283 7 US-11-443-428A-890861 Sequence 890861, 266
7 1283 7 US-11-443-428A-890868 Sequence 890868, 267
7 1283 7 US-11-443-428A-890868 Sequence 271, App 268
7 1006 7 US-11-250-779-271 Sequence 271, App 269
7 1231 7 US-11-250-779-273 Sequence 273, App 270
7 1334 7 US-11-443-428A-890864 Sequence 890864, 271
6 437 6 US-10-703-032-125651 Sequence 125651, 272
7 793 7 US-11-582-861-10326 Sequence 10326, A 273
7 1355 7 US-11-582-861-10326 Sequence 6587, Ap 274
6 1740 6 US-10-556-747-19 Sequence 19, Appl 275
7 1740 7 US-11-582-861-6207 Sequence 6207, Ap 276
7 1740 7 US-11-598-148-70 Sequence 70, Appl 277
6 2145 6 US-10-567-867-746 Sequence 746, App 278
7 2145 7 US-11-582-861-8349 Sequence 8349, Ap 279
6 2157 6 US-10-567-867-738 Sequence 738, App 280
7 2157 7 US-11-582-861-8347 Sequence 8347, Ap 281
6 560 6 US-10-449-502-53037 Sequence 53037, A 282
7 985 7 US-11-443-428A-767169 Sequence 767169, 283
7 1033 7 US-11-431-855-17215 Sequence 17215, A 284
7 1639 7 US-11-443-428A-767166 Sequence 767166, 285
7 1700 7 US-11-443-428A-767163 Sequence 767163, 286
6 1723 6 US-10-743-643-176 Sequence 176, App 287
7 1723 7 US-11-218-141-1257 Sequence 1257, Ap 288
7 1723 7 US-11-443-428A-767160 Sequence 767160, 289
6 1727 6 US-10-521-748-11 Sequence 6148, Ap 290
7 1727 7 US-11-582-861-6148 Sequence 6148, Ap 291
6 2892 6 US-10-533-520-2892 Sequence 2892, Ap 292
7 1759 7 US-11-443-428A-767161 Sequence 767161, 293
7 1759 7 US-11-443-428A-767162 Sequence 767162, 294
6 654 6 US-10-276-817B-13276 Sequence 13276, A 295
6 924 6 US-10-760-320A-3282 Sequence 3282, Ap 296
7 145 7 US-11-486-448-71476 Sequence 71476, A 297
6 664 6 US-10-276-817B-14707 Sequence 14707, A 298
7 744 7 US-11-443-428A-895296 Sequence 895296, 299
7 1695 7 US-11-443-428A-825827 Sequence 825827, 300
7 1711 7 US-11-443-428A-825851 Sequence 825851, 301
6 1777 7 US-11-443-428A-825835 Sequence 825835, 302
6 1823 6 US-10-767-471-1268 Sequence 1268, Ap 303
7 1823 6 US-10-796-280-1344 Sequence 1344, Ap 304
6 1823 6 US-10-796-307-872 Sequence 872, App 305
7 1823 7 US-11-066-316A-1128 Sequence 1128, Ap 306
7 1696 7 US-11-443-428A-825832 Sequence 825832, 307
7 2028 7 US-11-443-428A-825831 Sequence 825831, 308
6 2028 6 US-10-767-471-1269 Sequence 1269, Ap 309
6 2108 6 US-10-796-280-1345 Sequence 1345, Ap 310
7 2108 7 US-10-796-307-873 Sequence 873, App 311
6 2108 6 US-11-066-316A-1127 Sequence 1127, Ap 312
7 2128 7 US-11-443-428A-825844 Sequence 825844, 313
7 2128 7 US-11-443-428A-825847 Sequence 825847, 314

249	139	7.6	2155	7	US-11-443-428A-825830	Sequence 825830,	322	135.5	7.4	1799	7	US-11-443-428A-813018	Sequence 813018,
250	139	7.6	2157	6	US-10-767-471-1271	Sequence 1271, Ap	323	135.5	7.4	1812	7	US-11-443-428A-813019	Sequence 813019,
251	139	7.6	2157	6	US-10-796-280-1347	Sequence 1347, Ap	324	135.5	7.4	1842	7	US-11-443-428A-813021	Sequence 813021,
252	139	7.6	2157	6	US-10-796-307-875	Sequence 875, App	325	135.5	7.4	1842	7	US-11-443-428A-813022	Sequence 813022,
253	139	7.6	2157	7	US-11-066-316A-1125	Sequence 1125, Ap	326	135.5	7.4	1842	7	US-11-443-428A-813023	Sequence 813023,
254	139	7.6	2195	7	US-11-443-428A-825829	Sequence 825829,	327	135.5	7.4	1842	7	US-11-443-428A-813024	Sequence 813024,
255	139	7.6	2212	7	US-11-443-428A-825823	Sequence 825823,	328	135.5	7.4	1842	7	US-11-443-428A-813027	Sequence 813027,
256	139	7.6	2216	7	US-11-443-428A-825825	Sequence 825825,	329	135.5	7.4	2178	7	US-11-582-861-6116	Sequence 6176, Ap
257	139	7.6	2231	7	US-11-443-428A-825841	Sequence 825841,	330	135.5	7.4	2191	7	US-11-582-861-6118	Sequence 6175, Ap
258	139	7.6	2237	7	US-11-443-428A-825846	Sequence 825846,	331	135.5	7.4	2231	7	US-11-582-861-6180	Sequence 6180, Ap
259	139	7.6	2272	7	US-11-443-428A-825826	Sequence 825826,	332	135	7.4	449	7	US-11-443-428A-837201	Sequence 837201,
260	139	7.6	2296	7	US-11-443-428A-825824	Sequence 825824,	333	135	7.4	625	7	US-11-443-428A-900890	Sequence 900890,
261	139	7.6	2303	7	US-11-443-428A-825828	Sequence 825828,	334	135	7.4	1003	7	US-11-330-403-10079	Sequence 10079, A
262	138.5	7.6	361	7	US-11-443-428A-872363	Sequence 872363,	335	135	7.4	1003	7	US-11-431-855-22693	Sequence 22693, A
263	138.5	7.6	361	7	US-11-582-861-11034	Sequence 11034, A	336	135	7.4	1030	6	US-10-245-882-263	Sequence 263, App
264	138.5	7.6	383	7	US-11-443-428A-817537	Sequence 817537,	337	135	7.4	1070	7	US-11-431-855-10193	Sequence 10193, A
265	138.5	7.6	649	7	US-11-443-428A-815572	Sequence 815572,	338	135	7.4	1369	7	US-11-443-428A-900887	Sequence 900887,
266	138.5	7.6	903	7	US-11-443-428A-817759	Sequence 817759,	339	135	7.4	1369	7	US-11-443-428A-900888	Sequence 900888,
267	138.5	7.6	991	7	US-11-443-428A-817757	Sequence 817757,	340	135	7.4	1315	7	US-11-443-428A-900889	Sequence 900889,
268	138.5	7.6	1374	7	US-11-582-861-9914	Sequence 9914, Ap	341	134.5	7.4	650	7	US-11-443-428A-890878	Sequence 890878,
269	138.5	7.6	1500	7	US-11-443-428A-817753	Sequence 817753,	342	134.5	7.4	1029	7	US-11-582-861-6649	Sequence 6649, Ap
270	138.5	7.6	1530	7	US-11-443-428A-817755	Sequence 817755,	343	134.5	7.4	1489	7	US-11-582-861-6606	Sequence 6606, Ap
271	138.5	7.6	1717	7	US-11-443-428A-817745	Sequence 817745,	344	134	7.3	314	6	US-10-557-444-6	Sequence 6, Appli
272	138.5	7.6	1726	7	US-11-443-428A-817752	Sequence 817752,	345	134	7.3	1391	7	US-11-598-148-43	Sequence 43, Appli
273	138.5	7.6	1902	7	US-11-443-428A-817749	Sequence 817749,	346	134	7.3	1811	7	US-11-443-428A-816245	Sequence 816245,
274	138.5	7.6	2068	7	US-11-582-861-9913	Sequence 9913, Ap	347	134	7.3	1806	6	US-10-245-882-202	Sequence 202, App
275	138.5	7.6	2285	6	US-10-556-747-20	Sequence 20, Appl	348	134	7.3	1806	7	US-11-043-842-348	Sequence 348, App
276	138.5	7.6	2411	7	US-11-443-428A-817744	Sequence 817744,	349	134	7.3	1806	7	US-11-043-842-349	Sequence 349, App
277	138.5	7.6	2411	7	US-11-443-428A-817748	Sequence 817748,	350	134	7.3	1806	7	US-11-050-875-633	Sequence 633, App
278	138.5	7.6	2411	7	US-11-443-428A-817750	Sequence 817750,	351	134	7.3	1806	7	US-11-050-875-634	Sequence 634, App
279	138.5	7.6	2411	7	US-11-443-428A-817751	Sequence 817751,	352	134	7.3	1807	7	US-11-443-428A-816242	Sequence 816242,
280	138.5	7.6	2411	7	US-11-443-428A-817754	Sequence 817754,	353	133.5	7.3	616	6	US-10-245-882-264	Sequence 837376,
281	138.5	7.6	2411	7	US-11-443-428A-817756	Sequence 817756,	354	133.5	7.3	788	6	US-10-449-902-41167	Sequence 264, App
282	137.5	7.5	360	6	US-10-449-902-31341	Sequence 31341, A	355	133.5	7.3	788	6	US-10-449-902-41167	Sequence 41167, A
283	137.5	7.5	814	6	US-10-669-920-733	Sequence 733, App	356	133.5	7.3	1004	6	US-10-805-394-5676	Sequence 5676, Ap
284	137	7.5	368	6	US-10-525-573-446	Sequence 446, App	357	133.5	7.3	1004	7	US-11-431-855-15282	Sequence 15282, A
285	137	7.5	368	7	US-11-371-354-13577	Sequence 13577, A	358	133.5	7.3	1038	7	US-11-443-428A-882182	Sequence 882182,
286	137	7.5	368	7	US-11-371-354-72595	Sequence 72595, A	359	133	7.3	285	7	US-11-582-861-6468	Sequence 6468, Ap
287	137	7.5	368	7	US-11-371-354-78203	Sequence 78203, A	360	133	7.3	332	6	US-10-419-128-17541	Sequence 17541, A
288	137	7.5	368	7	US-11-443-428A-872360	Sequence 872360,	361	133	7.3	404	7	US-11-166-372-3089	Sequence 3089, Ap
289	137	7.5	368	7	US-11-582-861-11033	Sequence 11033, A	362	133	7.3	565	7	US-11-443-428A-837837	Sequence 837837,
290	137	7.5	387	7	US-11-443-428A-943720	Sequence 943720,	363	133	7.3	767	7	US-11-443-428A-837815	Sequence 837815,
291	137	7.5	546	7	US-11-443-428A-890879	Sequence 890879,	364	133	7.3	1639	7	US-11-582-861-6588	Sequence 6588, Ap
292	136.5	7.5	425	7	US-11-041-504-466	Sequence 466, App	365	133	7.3	1639	7	US-11-443-428A-758404	Sequence 758404,
293	136.5	7.5	1004	7	US-11-041-504-464	Sequence 464, App	366	133	7.3	2285	7	US-11-582-861-7345	Sequence 7345, Ap
294	136	7.5	510	7	US-11-520-715-72837	Sequence 72837, A	367	132.5	7.3	497	7	US-11-443-428A-795003	Sequence 795003,
295	136	7.5	1340	7	US-11-443-428A-1030171	Sequence 1030171,	368	132.5	7.3	497	7	US-11-582-861-11342	Sequence 11342, A
296	136	7.5	1340	7	US-11-443-428A-1030172	Sequence 1030172,	369	132.5	7.3	531	7	US-11-241-607-59305	Sequence 59305, A
297	136	7.5	1340	7	US-11-443-428A-1030174	Sequence 1030174,	370	132.5	7.3	704	6	US-10-219-051B-3575	Sequence 3575, Ap
298	136	7.5	1340	7	US-11-443-428A-1030175	Sequence 1030175,	371	132.5	7.3	704	7	US-11-518-868-18	Sequence 18, Appl
299	136	7.5	1340	7	US-11-443-428A-1030176	Sequence 1030176,	372	132	7.2	400	7	US-11-443-428A-1031607	Sequence 1031607,
300	136	7.5	1340	7	US-11-443-428A-1030177	Sequence 1030177,	373	132	7.2	417	7	US-11-443-428A-1031606	Sequence 1031606,
301	136	7.5	1340	7	US-11-443-428A-1030178	Sequence 1030178,	374	132	7.2	1548	7	US-11-443-428A-795843	Sequence 795843,
302	136	7.5	1340	7	US-11-443-428A-1030179	Sequence 1030179,	375	132	7.2	2167	7	US-11-443-428A-795842	Sequence 795842,
303	136	7.5	1495	7	US-11-443-428A-756165	Sequence 756165,	376	132	7.2	2162	7	US-11-443-428A-795844	Sequence 795844,
304	136	7.5	1496	6	US-10-700-439-104	Sequence 104, App	377	131.5	7.2	673	7	US-11-443-428A-793242	Sequence 793242,
305	136	7.5	1496	6	US-10-219-051B-7098	Sequence 7098, Ap	378	131.5	7.2	690	6	US-10-934-893-5270	Sequence 5270, Ap
306	136	7.5	1496	7	US-11-582-861-10325	Sequence 10325, A	379	131.5	7.2	690	7	US-11-330-403-4347	Sequence 4347, Ap
307	135.5	7.4	297	6	US-10-612-783-4246	Sequence 4246, Ap	380	131.5	7.2	739	7	US-11-443-428A-793248	Sequence 793248,
308	135.5	7.4	349	7	US-11-582-861-6177	Sequence 6177, Ap	381	131.5	7.2	960	7	US-11-090-997-1962	Sequence 1962, Ap
309	135.5	7.4	576	6	US-10-917-503-17064	Sequence 17064, A	382	131.5	7.2	1219	7	US-11-443-428A-793250	Sequence 793250,
310	135.5	7.4	576	7	US-11-443-428A-836068	Sequence 836068,	383	131.5	7.2	1447	7	US-11-443-428A-793249	Sequence 793249,
311	135.5	7.4	576	7	US-11-443-428A-836069	Sequence 836069,	384	131.5	7.2	1551	7	US-11-443-428A-793244	Sequence 793244,
312	135.5	7.4	634	7	US-11-443-428A-836070	Sequence 836070,	385	131.5	7.2	1551	7	US-11-443-428A-793245	Sequence 793245,
313	135.5	7.4	634	7	US-11-443-428A-813031	Sequence 813031,	386	131.5	7.2	1590	7	US-11-443-428A-793246	Sequence 793246,
314	135.5	7.4	662	7	US-11-443-428A-836073	Sequence 836073,	387	131.5	7.2	1740	7	US-11-582-861-6690	Sequence 6690, Ap
315	135.5	7.4	689	7	US-11-443-428A-836075	Sequence 836075,	388	131	7.2	438	7	US-11-443-428A-881345	Sequence 881345,
316	135.5	7.4	716	7	US-11-443-428A-813035	Sequence 813035,	389	131	7.2	595	6	US-10-573-166-3	Sequence 3, Appli
317	135.5	7.4	742	7	US-11-443-428A-813029	Sequence 813029,	390	131	7.2	696	7	US-11-443-428A-872616	Sequence 872616,
318	135.5	7.4	787	7	US-11-443-428A-813032	Sequence 813032,	391	131	7.2	696	7	US-11-443-428A-872619	Sequence 872619,
319	135.5	7.4	1078	6	US-10-449-902-54534	Sequence 54534, A	392	131	7.2	711	6	US-10-573-166-2	Sequence 2, Appli
320	135.5	7.4	1542	7	US-11-443-428A-813030	Sequence 813030,	393	131	7.2	920	6	US-10-529-348-2169	Sequence 2169, Ap
321	135.5	7.4	1659	7	US-11-443-428A-813020	Sequence 813020,	394	131	7.2	920	7	US-11-283-329-108	Sequence 108, App

395	131	7.2	920	7	US-11-516-717-6	Sequence 6, Appli	468	129.5	7.1	2087	6	US-10-743-643-2443	Sequence 2443, Ap
396	131	7.2	921	7	US-11-443-428A-899297	Sequence 899297,	469	129	7.1	594	7	US-11-443-428A-821674	Sequence 821674,
397	131	7.2	951	7	US-11-443-428A-899298	Sequence 899298,	470	129	7.1	594	7	US-11-443-428A-821675	Sequence 821675,
398	131	7.2	957	6	US-10-419-128-20408	Sequence 20408, A	471	129	7.1	594	7	US-11-443-428A-821677	Sequence 821677,
399	131	7.2	980	7	US-11-443-428A-876595	Sequence 876595,	472	129	7.1	594	7	US-11-443-428A-821683	Sequence 821683,
400	131	7.2	997	7	US-11-443-428A-876594	Sequence 876594,	473	129	7.1	596	7	US-11-443-428A-821686	Sequence 821686,
401	131	7.2	997	7	US-11-582-861-8941	Sequence 8941, Ap	474	129	7.1	608	7	US-11-443-428A-821830	Sequence 821830,
402	131	7.2	1067	7	US-11-443-428A-876593	Sequence 876593,	475	129	7.1	625	7	US-11-443-428A-821830	Sequence 821830,
403	131	7.2	1067	7	US-11-443-428A-876596	Sequence 876596,	476	129	7.1	668	7	US-11-443-428A-821672	Sequence 821672,
404	131	7.2	1067	7	US-11-443-428A-876601	Sequence 876601,	477	129	7.1	880	7	US-11-443-428A-828762	Sequence 828762,
405	131	7.2	1067	7	US-11-443-428A-876602	Sequence 876602,	478	129	7.1	1263	7	US-11-090-997-1956	Sequence 1956, Ap
406	131	7.2	1067	7	US-11-443-428A-876604	Sequence 876604,	479	129	7.1	1752	7	US-11-443-428A-828746	Sequence 828746,
407	131	7.2	1067	7	US-11-443-428A-876605	Sequence 876605,	480	129	7.1	1840	6	US-10-743-643-1001	Sequence 1001, Ap
408	131	7.2	1067	7	US-11-443-428A-876606	Sequence 876606,	481	129	7.1	2571	7	US-11-443-428A-850026	Sequence 850026,
409	131	7.2	1067	7	US-11-582-861-8940	Sequence 8940, Ap	482	129	7.1	2661	7	US-11-443-428A-850031	Sequence 850031,
410	131	7.2	1195	7	US-11-443-428A-899293	Sequence 899293,	483	129	7.1	2715	7	US-11-443-428A-850024	Sequence 850024,
411	131	7.2	1815	7	US-11-443-428A-899295	Sequence 899295,	484	129	7.1	2715	7	US-11-443-428A-850027	Sequence 850027,
412	131	7.2	1815	7	US-11-443-428A-899299	Sequence 899299,	485	129	7.1	2715	7	US-11-443-428A-850028	Sequence 850028,
413	131	7.2	1815	7	US-11-443-428A-899301	Sequence 899301,	486	129	7.1	2715	7	US-11-443-428A-850033	Sequence 850033,
414	131	7.2	1815	7	US-11-443-428A-899303	Sequence 899303,	487	128.5	7.0	316	6	US-10-449-902-40133	Sequence 40133, A
415	131	7.2	1815	7	US-11-443-428A-899301	Sequence 899301,	488	128.5	7.0	587	7	US-11-443-428A-803116	Sequence 803116,
416	130.5	7.2	731	7	US-11-443-428A-755813	Sequence 755813,	489	128.5	7.0	723	7	US-11-443-428A-755811	Sequence 755811,
417	130.5	7.2	898	6	US-10-523-899-8	Sequence 8, Appli	490	128.5	7.0	819	7	US-11-443-428A-791710	Sequence 791710,
418	130.5	7.2	919	6	US-10-521-748-1	Sequence 1, Appli	491	128.5	7.0	819	7	US-11-443-428A-791711	Sequence 791711,
419	130.5	7.2	919	6	US-10-521-748-1	Sequence 1, Appli	492	128.5	7.0	819	7	US-11-443-428A-791712	Sequence 791712,
420	130.5	7.2	919	6	US-10-705-165-28	Sequence 28, Appl	493	128.5	7.0	906	6	US-10-529-348-927	Sequence 927, App
421	130.5	7.2	919	6	US-11-565-589-25	Sequence 25, Appl	494	128.5	7.0	917	7	US-11-443-428A-803118	Sequence 803118,
422	130.5	7.2	921	7	US-11-443-428A-755810	Sequence 755810,	495	128.5	7.0	920	7	US-11-443-428A-755812	Sequence 755812,
423	130.5	7.2	1119	7	US-11-443-428A-828747	Sequence 828747,	496	128.5	7.0	965	7	US-11-443-428A-1017276	Sequence 1017276,
424	130.5	7.2	1164	6	US-10-523-899-7	Sequence 7, Appli	497	128.5	7.0	967	7	US-11-443-428A-1017277	Sequence 1017277,
425	130.5	7.2	1297	7	US-11-443-428A-854191	Sequence 854191,	498	128.5	7.0	1003	7	US-11-443-428A-803112	Sequence 803112,
426	130.5	7.2	1605	7	US-11-443-428A-854176	Sequence 854176,	499	128.5	7.0	1003	7	US-11-443-428A-803113	Sequence 803113,
427	130.5	7.2	1649	7	US-11-443-428A-854177	Sequence 854177,	500	128.5	7.0	1003	7	US-11-443-428A-803113	Sequence 803113,
428	130.5	7.2	1651	7	US-11-443-428A-854181	Sequence 854181,	501	128.5	7.0	1003	7	US-11-443-428A-803114	Sequence 803114,
429	130.5	7.2	1663	7	US-11-443-428A-828754	Sequence 828754,	502	128.5	7.0	1003	7	US-11-443-428A-803119	Sequence 803119,
430	130.5	7.2	1669	7	US-11-443-428A-854175	Sequence 854175,	503	128.5	7.0	1003	7	US-11-443-428A-803120	Sequence 803120,
431	130.5	7.2	1669	7	US-11-443-428A-854179	Sequence 854179,	504	128.5	7.0	1003	7	US-11-582-861-6664	Sequence 6664, Ap
432	130.5	7.2	1669	7	US-11-443-428A-854185	Sequence 854185,	505	128.5	7.0	2056	7	US-10-419-128-24320	Sequence 24320, A
433	130.5	7.2	1669	7	US-11-443-428A-854186	Sequence 854186,	506	128	7.0	247	6	US-10-419-128-24320	Sequence 24320, A
434	130.5	7.2	1669	7	US-11-443-428A-854187	Sequence 854187,	507	128	7.0	432	7	US-11-443-428A-916172	Sequence 916172, A
435	130.5	7.2	1669	7	US-11-443-428A-854188	Sequence 854188,	508	128	7.0	669	7	US-11-582-861-10443	Sequence 10443, A
436	130.5	7.2	1669	7	US-11-443-428A-854190	Sequence 854190,	509	128	7.0	707	6	US-10-219-051B-740	Sequence 740, App
437	130.5	7.2	1669	7	US-11-443-428A-854194	Sequence 854194,	510	128	7.0	707	6	US-10-219-051B-743	Sequence 743, App
438	130.5	7.2	1669	7	US-11-443-428A-854195	Sequence 854195,	511	128	7.0	707	6	US-10-219-051B-746	Sequence 746, App
439	130.5	7.2	1681	7	US-11-443-428A-854183	Sequence 854183,	512	128	7.0	707	6	US-10-219-051B-749	Sequence 749, App
440	130.5	7.2	1735	7	US-11-582-861-8240	Sequence 8240, Ap	513	128	7.0	707	6	US-10-219-051B-752	Sequence 752, App
441	130.5	7.2	1744	7	US-11-443-428A-828760	Sequence 828760,	514	128	7.0	707	6	US-10-219-051B-755	Sequence 755, App
442	130.5	7.2	1777	7	US-11-443-428A-828761	Sequence 828761,	515	128	7.0	707	7	US-11-582-861-10442	Sequence 10442, A
443	130.5	7.2	1855	7	US-11-443-428A-828744	Sequence 828744,	516	128	7.0	707	7	US-11-417-264-168	Sequence 168, App
444	130.5	7.2	1855	7	US-11-443-428A-828745	Sequence 828745,	517	128	7.0	977	6	US-10-419-128-16655	Sequence 1655, A
445	130.5	7.2	1855	7	US-11-443-428A-828750	Sequence 828750,	518	128	7.0	1073	6	US-10-449-902-41088	Sequence 41088, A
446	130.5	7.2	1855	7	US-11-443-428A-828751	Sequence 828751,	519	128	7.0	1531	6	US-10-540-898-142	Sequence 142, App
447	130.5	7.2	1855	7	US-11-443-428A-828752	Sequence 828752,	520	128	7.0	1588	6	US-11-090-997-1786	Sequence 1786, App
448	130.5	7.2	1855	7	US-11-443-428A-828753	Sequence 828753,	521	128	7.0	1838	6	US-10-574-398-177	Sequence 177, App
449	130.5	7.2	1855	7	US-11-443-428A-828764	Sequence 828764,	522	128	7.0	1838	6	US-10-219-051B-1383	Sequence 1383, Ap
450	130.5	7.2	1855	7	US-11-443-428A-828765	Sequence 828765,	523	128	7.0	1838	6	US-10-219-051B-1387	Sequence 1387, Ap
451	130.5	7.2	1855	7	US-11-443-428A-828766	Sequence 828766,	524	128	7.0	1838	7	US-11-443-428A-767060	Sequence 767060,
452	130	7.1	417	6	US-10-526-572-31	Sequence 31, Appl	525	128	7.0	1838	7	US-11-443-428A-767061	Sequence 767061,
453	130	7.1	622	7	US-11-443-428A-821818	Sequence 821818,	526	128	7.0	1838	7	US-11-443-428A-767062	Sequence 767062,
454	130	7.1	845	7	US-11-520-715-56930	Sequence 56930, A	527	128	7.0	1838	7	US-11-443-428A-767063	Sequence 767063,
455	130	7.1	966	6	US-10-449-902-41240	Sequence 41240, A	528	128	7.0	1838	7	US-11-443-428A-767064	Sequence 767064,
456	130	7.1	1492	7	US-11-443-428A-739155	Sequence 739155,	529	128	7.0	1838	7	US-11-443-428A-767065	Sequence 767065,
457	130	7.1	1620	7	US-11-443-428A-832697	Sequence 832697,	530	128	7.0	1838	7	US-11-443-428A-767066	Sequence 767066,
458	130	7.1	1745	7	US-11-443-428A-739152	Sequence 739152,	531	128	7.0	1838	7	US-11-443-428A-767067	Sequence 767067,
459	130	7.1	1745	7	US-11-443-428A-739153	Sequence 739153,	532	128	7.0	1838	7	US-11-443-428A-767073	Sequence 767073,
460	130	7.1	1745	7	US-11-582-861-10618	Sequence 10618, A	533	128	7.0	1838	7	US-11-582-861-6605	Sequence 6605, Ap
461	130	7.1	1776	7	US-11-443-428A-739154	Sequence 739154,	534	127.5	7.0	333	7	US-11-056-355B-9738	Sequence 9738, Ap
462	129.5	7.1	164	7	US-11-486-448-82922	Sequence 82922, A	535	127.5	7.0	383	7	US-11-241-607-51479	Sequence 51479, A
463	129.5	7.1	289	6	US-10-990-328-10116	Sequence 10116, A	536	127.5	7.0	445	6	US-10-527-571A-321	Sequence 321, App
464	129.5	7.1	309	7	US-11-443-428A-754561	Sequence 754561,	537	127.5	7.0	616	7	US-11-443-428A-849160	Sequence 849160,
465	129.5	7.1	309	7	US-11-443-428A-754562	Sequence 754562,	538	127.5	7.0	681	7	US-11-443-428A-849167	Sequence 849167,
466	129.5	7.1	459	7	US-11-001-793-11084	Sequence 11084, A	539	127.5	7.0	695	6	US-10-276-817B-14869	Sequence 14869, A
467	129.5	7.1	459	7	US-11-545-766-2106	Sequence 2106, Ap	540	127.5	7.0	699	7	US-11-296-571-13	Sequence 13, Appl

541	127.5	7.0	761	7	US-11-443-428A-758598	Sequence 758598,	614	127.5	7.0	1604	6	US-10-554-068-14	Sequence 14, Appl
542	127.5	7.0	774	7	US-11-443-428A-849158	Sequence 849158,	615	127.5	7.0	1642	7	US-11-443-428A-758147	Sequence 758147,
543	127.5	7.0	854	7	US-11-443-428A-849154	Sequence 849154,	616	127.5	7.0	1670	6	US-10-219-051B-12751	Sequence 12751, A
544	127.5	7.0	861	7	US-11-443-428A-758552	Sequence 758552,	617	127.5	7.0	1670	6	US-11-443-428A-758143	Sequence 758143,
545	127.5	7.0	866	7	US-11-443-428A-758597	Sequence 758597,	618	127.5	7.0	1950	6	US-10-554-068-10	Sequence 10, Appl
546	127.5	7.0	878	7	US-11-443-428A-758596	Sequence 758596,	619	127	7.0	1106	6	US-10-567-867-632	Sequence 632, App
547	127.5	7.0	884	7	US-11-371-354-60727	Sequence 60727, A	620	127	7.0	1106	7	US-11-407-702-76	Sequence 76, Appl
548	127.5	7.0	891	7	US-11-443-428A-758573	Sequence 758573,	621	127	7.0	1106	7	US-11-443-428A-804243	Sequence 804243,
549	127.5	7.0	905	7	US-11-443-428A-758574	Sequence 758574,	622	127	7.0	1106	7	US-11-443-428A-804245	Sequence 804245,
550	127.5	7.0	916	7	US-11-443-428A-849155	Sequence 849155,	623	127	7.0	1185	7	US-11-443-428A-858376	Sequence 858376,
551	127.5	7.0	916	7	US-11-443-428A-849163	Sequence 849163,	624	127	7.0	1231	7	US-11-443-428A-858383	Sequence 858383,
552	127.5	7.0	916	7	US-11-443-428A-849164	Sequence 849164,	625	126.5	6.9	341	7	US-11-443-428A-872365	Sequence 872365,
553	127.5	7.0	916	7	US-11-443-428A-849165	Sequence 849165,	626	126.5	6.9	442	6	US-10-419-128-30607	Sequence 30607, A
554	127.5	7.0	927	7	US-11-443-428A-849156	Sequence 849156,	627	126.5	6.9	496	7	US-11-443-428A-821833	Sequence 821833,
555	127.5	7.0	938	7	US-11-443-428A-758578	Sequence 758578,	628	126.5	6.9	534	7	US-11-443-428A-821826	Sequence 821826,
556	127.5	7.0	941	7	US-11-443-428A-849157	Sequence 849157,	629	126.5	6.9	524	7	US-11-443-428A-821827	Sequence 821827,
557	127.5	7.0	1096	7	US-11-443-428A-758572	Sequence 758572,	630	126.5	6.9	524	7	US-11-443-428A-821829	Sequence 821829,
558	127.5	7.0	1163	7	US-11-371-354-56961	Sequence 56961, A	631	126.5	6.9	526	7	US-11-443-428A-837838	Sequence 837838,
559	127.5	7.0	1163	7	US-11-582-861-10182	Sequence 10182, A	632	126.5	6.9	548	7	US-11-443-428A-821817	Sequence 821817,
560	127.5	7.0	1170	7	US-11-443-428A-758595	Sequence 758595,	633	126.5	6.9	586	7	US-11-443-428A-821828	Sequence 821828,
561	127.5	7.0	1192	7	US-11-443-428A-758570	Sequence 758570,	634	126.5	6.9	613	7	US-11-443-428A-821825	Sequence 821825,
562	127.5	7.0	1204	7	US-11-443-428A-758571	Sequence 758571,	635	126.5	6.9	639	7	US-11-443-428A-821819	Sequence 821819,
563	127.5	7.0	1328	7	US-11-443-428A-758594	Sequence 758594,	636	126.5	6.9	639	7	US-11-443-428A-821823	Sequence 821823,
564	127.5	7.0	1342	7	US-11-443-428A-758569	Sequence 758569,	637	126.5	6.9	639	7	US-11-443-428A-821824	Sequence 821824,
565	127.5	7.0	1346	7	US-11-443-428A-758554	Sequence 758554,	638	126.5	6.9	639	7	US-11-443-428A-821837	Sequence 821837,
566	127.5	7.0	1365	7	US-11-443-428A-758568	Sequence 758568,	639	126.5	6.9	639	7	US-11-443-428A-821838	Sequence 821838,
567	127.5	7.0	1373	7	US-11-443-428A-758593	Sequence 758593,	640	126.5	6.9	668	7	US-11-518-868-20	Sequence 20, Appl
568	127.5	7.0	1381	7	US-11-443-428A-758551	Sequence 758551,	641	126.5	6.9	881	7	US-11-443-428A-910861	Sequence 910861,
569	127.5	7.0	1399	7	US-11-443-428A-758585	Sequence 758585,	642	126.5	6.9	891	7	US-11-582-861-9931	Sequence 9931, Ap
570	127.5	7.0	1424	7	US-11-188-417A-23	Sequence 23, Appl	643	126	6.9	2499	7	US-11-443-428A-973677	Sequence 973677,
571	127.5	7.0	1424	7	US-11-495-015-78	Sequence 78, Appl	644	126	6.9	296	7	US-11-443-428A-973677	Sequence 973677,
572	127.5	7.0	1427	7	US-11-443-428A-758567	Sequence 758567,	645	126	6.9	483	7	US-11-289-102-332	Sequence 332, App
573	127.5	7.0	1428	7	US-11-443-428A-758559	Sequence 758559,	645	126	6.9	760	6	US-10-505-928-50	Sequence 50, Appl
574	127.5	7.0	1428	7	US-11-443-428A-758562	Sequence 758562,	646	126	6.9	779	7	US-11-490-760-8	Sequence 8, Appl
575	127.5	7.0	1428	7	US-11-443-428A-758591	Sequence 758591,	647	126	6.9	779	7	US-11-519-399-8	Sequence 8, Appl
576	127.5	7.0	1429	7	US-11-443-428A-758550	Sequence 758550,	648	126	6.9	1040	6	US-10-574-398-48	Sequence 48, Appl
577	127.5	7.0	1429	7	US-11-443-428A-758555	Sequence 758555,	649	126	6.9	1057	7	US-11-048-197-16	Sequence 16, Appl
578	127.5	7.0	1429	7	US-11-443-428A-758556	Sequence 758556,	650	126	6.9	1057	7	US-11-048-197-16	Sequence 20, Appl
579	127.5	7.0	1429	7	US-11-443-428A-758560	Sequence 758560,	651	126	6.9	1107	7	US-11-048-197-11	Sequence 11, Appl
580	127.5	7.0	1429	7	US-11-443-428A-758561	Sequence 758561,	652	126	6.9	1169	7	US-11-048-197-6	Sequence 6, Appl
581	127.5	7.0	1429	7	US-11-443-428A-758563	Sequence 758563,	653	126	6.9	1171	7	US-11-048-197-8	Sequence 8, Appl
582	127.5	7.0	1429	7	US-11-443-428A-758564	Sequence 758564,	654	126	6.9	1388	7	US-11-048-197-10	Sequence 10, Appl
583	127.5	7.0	1429	7	US-11-443-428A-758586	Sequence 758586,	655	126	6.9	1464	6	US-10-985-570-2	Sequence 2, Appl
584	127.5	7.0	1429	7	US-11-443-428A-758565	Sequence 758565,	656	126	6.9	1464	6	US-10-700-439-125	Sequence 125, App
585	127.5	7.0	1429	7	US-11-443-428A-758579	Sequence 758579,	657	126	6.9	1464	6	US-10-219-051B-10483	Sequence 10483, A
586	127.5	7.0	1429	7	US-11-443-428A-758580	Sequence 758580,	658	126	6.9	1464	6	US-10-219-051B-10487	Sequence 10487, A
587	127.5	7.0	1429	7	US-11-443-428A-758581	Sequence 758581,	659	126	6.9	1464	6	US-10-219-051B-10491	Sequence 10491, A
588	127.5	7.0	1429	7	US-11-443-428A-758584	Sequence 758584,	660	126	6.9	1464	6	US-10-566-878-1	Sequence 1, Appl
589	127.5	7.0	1429	7	US-11-443-428A-758586	Sequence 758586,	661	126	6.9	1464	6	US-10-348-119-331	Sequence 331, App
590	127.5	7.0	1429	7	US-11-443-428A-758587	Sequence 758587,	662	126	6.9	1464	7	US-11-105-233-143	Sequence 143, App
591	127.5	7.0	1429	7	US-11-443-428A-758588	Sequence 758588,	663	126	6.9	1464	7	US-11-399-543-199	Sequence 199, App
592	127.5	7.0	1429	7	US-11-443-428A-758589	Sequence 758589,	664	126	6.9	1464	7	US-11-510-530-36	Sequence 36, Appl
593	127.5	7.0	1436	7	US-11-443-428A-758592	Sequence 758592,	665	126	6.9	1464	7	US-11-582-861-5834	Sequence 5834, Ap
594	127.5	7.0	1437	7	US-11-443-428A-813025	Sequence 813025,	666	126	6.9	1477	7	US-11-417-264-60	Sequence 60, Appl
595	127.5	7.0	1445	6	US-11-443-428A-758146	Sequence 758146,	667	126	6.9	415	7	US-11-582-861-10426	Sequence 10426, A
596	127.5	7.0	1453	6	US-10-219-051B-10481	Sequence 10481, A	668	125.5	6.9	415	7	US-11-056-355B-5415	Sequence 5415, Ap
597	127.5	7.0	1453	6	US-10-219-051B-10485	Sequence 10485, A	669	125.5	6.9	459	7	US-10-505-928-493	Sequence 493, App
598	127.5	7.0	1453	6	US-10-219-051B-10489	Sequence 10489, A	670	125.5	6.9	744	6	US-10-505-928-493	Sequence 758186,
599	127.5	7.0	1453	6	US-10-219-051B-10437	Sequence 14037, A	671	125.5	6.9	744	7	US-11-443-428A-758187	Sequence 758187,
600	127.5	7.0	1453	6	US-10-219-051B-14041	Sequence 14041, A	672	125.5	6.9	744	7	US-11-443-428A-758189	Sequence 758189,
601	127.5	7.0	1453	6	US-10-219-051B-14045	Sequence 14045, A	673	125.5	6.9	744	7	US-11-443-428A-758190	Sequence 758190,
602	127.5	7.0	1466	6	US-10-985-570-1	Sequence 1, Appl	674	125.5	6.9	753	7	US-11-443-428A-815575	Sequence 815575,
603	127.5	7.0	1466	6	US-10-700-439-140	Sequence 140, App	675	125.5	6.9	798	7	US-11-443-428A-815558	Sequence 815558,
604	127.5	7.0	1466	7	US-11-105-233-44	Sequence 44, Appl	676	125.5	6.9	798	7	US-11-443-428A-881583	Sequence 881583,
605	127.5	7.0	1466	7	US-11-105-233-167	Sequence 167, App	677	125.5	6.9	1263	7	US-11-582-861-7012	Sequence 7012, App
606	127.5	7.0	1466	7	US-11-582-861-10183	Sequence 10183, A	678	125.5	6.9	2948	7	US-11-598-148-628	Sequence 628, App
607	127.5	7.0	1466	7	US-11-417-264-52	Sequence 52, Appl	679	125.5	6.9	358	7	US-11-443-428A-808256	Sequence 807591,
608	127.5	7.0	1470	7	US-11-443-428A-758566	Sequence 758566,	680	125	6.9	316	7	US-11-443-428A-880256	Sequence 880256,
609	127.5	7.0	1485	7	US-11-582-861-6179	Sequence 6179, Ap	681	125	6.9	585	6	US-10-557-444-4	Sequence 4, Appl
610	127.5	7.0	1494	7	US-11-443-428A-758148	Sequence 758148,	682	125	6.9	647	7	US-11-443-428A-872025	Sequence 872025,
611	127.5	7.0	1498	7	US-11-443-428A-758144	Sequence 758144,	683	125	6.9	655	7	US-11-443-428A-872019	Sequence 872019,
612	127.5	7.0	1498	7	US-11-443-428A-758145	Sequence 758145,	684	125	6.9	663	7	US-11-443-428A-872026	Sequence 872026,
613	127.5	7.0	1572	6	US-10-554-068-27	Sequence 27, Appl	686	125	6.9	679	7	US-11-443-428A-872016	Sequence 872016,

687	125	6.9	736	7	US-11-443-428A-872018	Sequence 872018,	760	123.5	6.8	1336	7	US-11-582-861-10424	Sequence 10424, A
688	125	6.9	834	7	US-11-443-428A-872017	Sequence 872017,	761	123.5	6.8	1355	6	US-11-443-428A-848836	Sequence 848836,
689	125	6.9	845	7	US-11-443-428A-872021	Sequence 872021,	762	123.5	6.8	1516	6	US-10-533-520-2157	Sequence 2157, Ap
690	125	6.9	845	7	US-11-443-428A-872024	Sequence 872024,	763	123.5	6.8	1516	7	US-11-431-526-8	Sequence 8, Appli
691	125	6.9	845	7	US-11-582-861-8972	Sequence 8972, Ap	764	123.5	6.8	1516	7	US-11-431-663-8	Sequence 8, Appli
692	125	6.9	896	7	US-11-443-428A-872014	Sequence 872014,	765	123.5	6.8	1516	7	US-11-521-715-3	Sequence 3, Appli
693	125	6.9	940	7	US-11-582-861-7913	Sequence 7913, Ap	766	123.5	6.8	1516	7	US-11-582-861-10425	Sequence 10425, A
694	125	6.9	1087	7	US-11-443-428A-911691	Sequence 911691,	767	123.5	6.8	1530	7	US-11-443-428A-848824	Sequence 848824,
695	125	6.9	1604	7	US-11-443-428A-911688	Sequence 911688,	768	123.5	6.8	1530	7	US-11-443-428A-848825	Sequence 848825,
696	125	6.9	1616	7	US-11-443-428A-911686	Sequence 911686,	769	123.5	6.8	1530	7	US-11-443-428A-848826	Sequence 848826,
697	125	6.9	1670	7	US-11-443-428A-911684	Sequence 911684,	770	123.5	6.8	1530	7	US-11-443-428A-848827	Sequence 848827,
698	125	6.9	1688	7	US-11-443-428A-911681	Sequence 911681,	771	123.5	6.8	1530	7	US-11-443-428A-848831	Sequence 848831,
699	125	6.9	1688	7	US-11-443-428A-911682	Sequence 911682,	772	123.5	6.8	1530	7	US-11-443-428A-848835	Sequence 848835,
700	125	6.9	1691	7	US-11-371-354-69607	Sequence 69607, A	773	123.5	6.8	1535	7	US-11-443-428A-848832	Sequence 848832,
701	124.5	6.8	223	7	US-11-443-428A-872364	Sequence 872364,	774	123.5	6.8	1535	7	US-11-443-428A-848833	Sequence 848833,
702	124.5	6.8	287	7	US-11-443-428A-777233	Sequence 777233,	775	123	6.7	577	7	US-11-443-428A-979450	Sequence 979450,
703	124.5	6.8	468	7	US-11-443-428A-829773	Sequence 829773,	776	123	6.7	670	7	US-11-371-354-57013	Sequence 57013, A
704	124.5	6.8	662	6	US-10-276-817B-14812	Sequence 14812, A	777	123	6.7	673	7	US-11-443-428A-928279	Sequence 928279,
705	124.5	6.8	1004	7	US-11-431-855-23803	Sequence 23803, A	778	123	6.7	687	7	US-11-443-428A-872618	Sequence 872618,
706	124.5	6.8	1014	7	US-11-482-553-1	Sequence 1, Appli	779	123	6.7	716	7	US-11-443-428A-872624	Sequence 872624,
707	124.5	6.8	1041	7	US-11-443-428A-760889	Sequence 760889,	780	123	6.7	718	7	US-11-443-428A-1020179	Sequence 1020179,
708	124.5	6.8	1286	7	US-11-443-428A-910863	Sequence 910863,	781	123	6.7	744	7	US-11-510-530-40	Sequence 40, Appli
709	124.5	6.8	1303	7	US-11-443-428A-910862	Sequence 910862,	782	123	6.7	1020	7	US-11-443-428A-896754	Sequence 896754,
710	124.5	6.8	1418	7	US-11-443-428A-910864	Sequence 910864,	783	123	6.7	1197	6	US-10-917-503-17169	Sequence 17169, A
711	124.5	6.8	1487	5	US-09-976-858-124	Sequence 124, App	784	123	6.7	1209	7	US-11-443-428A-896757	Sequence 896757,
712	124.5	6.8	1487	7	US-11-212-799-124	Sequence 124, App	785	123	6.7	1242	7	US-11-443-428A-896753	Sequence 896753,
713	124.5	6.8	1487	7	US-11-443-428A-872963	Sequence 872963,	786	123	6.7	1313	6	US-10-529-708-3	Sequence 3, Appli
714	124.5	6.8	3530	7	US-11-443-428A-872963	Sequence 872963,	787	123	6.7	1316	7	US-11-443-428A-896756	Sequence 896756,
715	124.5	6.8	3530	7	US-11-598-148-618	Sequence 618, App	788	123	6.7	2142	7	US-11-582-861-8348	Sequence 8348, Ap
716	124	6.8	239	6	US-10-419-128-17615	Sequence 17615, A	789	122.5	6.7	234	6	US-10-558-276-6	Sequence 6, Appli
717	124	6.8	304	7	US-11-056-355B-46079	Sequence 46079, A	790	122.5	6.7	272	7	US-11-375-414-120	Sequence 120, Ap
718	124	6.8	304	7	US-11-056-355B-50799	Sequence 50799, A	791	122.5	6.7	272	7	US-11-001-793-8025	Sequence 8025, Ap
719	124	6.8	608	7	US-11-443-428A-754261	Sequence 754261,	792	122.5	6.7	293	7	US-11-486-448-65080	Sequence 65080, A
720	124	6.8	608	6	US-10-539-228-428	Sequence 428, App	793	122.5	6.7	293	7	US-11-443-428A-787508	Sequence 787508,
721	124	6.8	655	7	US-11-443-428A-836707	Sequence 836707,	794	122.5	6.7	502	7	US-11-443-428A-847446	Sequence 847446,
722	124	6.8	655	7	US-11-443-428A-836708	Sequence 836708,	795	122.5	6.7	554	7	US-11-443-428A-847440	Sequence 847440,
723	124	6.8	655	7	US-11-443-428A-836709	Sequence 836709,	796	122.5	6.7	554	7	US-11-443-428A-847454	Sequence 847454,
724	124	6.8	655	7	US-11-443-428A-836715	Sequence 836715,	797	122.5	6.7	589	6	US-10-419-128-28836	Sequence 28836, A
725	124	6.8	683	7	US-11-443-428A-872622	Sequence 872622,	798	122.5	6.7	620	6	US-10-505-928-284	Sequence 284, App
726	124	6.8	693	7	US-11-443-428A-754260	Sequence 754260,	799	122.5	6.7	620	6	US-10-533-520-1939	Sequence 1939, Ap
727	124	6.8	694	7	US-11-443-428A-872620	Sequence 872620,	800	122.5	6.7	620	6	US-11-371-354-73307	Sequence 73307, A
728	124	6.8	720	6	US-10-539-228-432	Sequence 432, App	801	122.5	6.7	620	7	US-11-371-354-78070	Sequence 78070, A
729	124	6.8	730	7	US-11-443-428A-836716	Sequence 836716,	802	122.5	6.7	620	7	US-11-443-428A-847447	Sequence 847447,
730	124	6.8	800	7	US-11-443-428A-836716	Sequence 836716,	803	122.5	6.7	627	7	US-11-443-428A-847450	Sequence 847450,
731	124	6.8	840	7	US-11-443-428A-754263	Sequence 754263,	804	122.5	6.7	700	7	US-11-443-428A-847444	Sequence 847444,
732	124	6.8	840	7	US-11-443-428A-754273	Sequence 754273,	805	122.5	6.7	757	7	US-11-443-428A-817758	Sequence 817758,
733	124	6.8	853	7	US-11-443-428A-754268	Sequence 754268,	806	122.5	6.7	757	7	US-11-443-428A-847436	Sequence 847436,
734	124	6.8	853	7	US-11-443-428A-754272	Sequence 754272,	807	122.5	6.7	757	7	US-11-443-428A-847438	Sequence 847438,
735	124	6.8	854	7	US-11-443-428A-754259	Sequence 754259,	808	122.5	6.7	757	7	US-11-443-428A-847439	Sequence 847439,
736	124	6.8	881	7	US-11-443-428A-754258	Sequence 754258,	809	122.5	6.7	757	7	US-11-443-428A-847441	Sequence 847441,
737	124	6.8	898	7	US-11-090-997-1960	Sequence 1960, Ap	810	122.5	6.7	757	7	US-11-443-428A-847445	Sequence 847445,
738	124	6.8	916	7	US-11-066-316A-1136	Sequence 1136, Ap	811	122.5	6.7	1038	6	US-10-529-708-2	Sequence 2, Appli
739	124	6.8	940	7	US-11-443-428A-836704	Sequence 836704,	812	122.5	6.7	1277	6	US-11-443-428A-768160	Sequence 768160,
740	124	6.8	940	7	US-11-443-428A-836705	Sequence 836705,	813	122.5	6.7	1313	6	US-10-529-708-1	Sequence 1, Appli
741	124	6.8	940	7	US-11-443-428A-836714	Sequence 836714,	814	122.5	6.7	1420	6	US-10-534-538A-3	Sequence 3, Appli
742	124	6.8	940	7	US-11-582-861-7912	Sequence 7912, Ap	815	122.5	6.7	1460	7	US-11-247-437-14	Sequence 14, Appli
743	124	6.8	974	7	US-11-443-428A-836706	Sequence 836706,	816	122.5	6.7	1480	7	US-11-443-428A-844316	Sequence 844316,
744	124	6.8	990	7	US-11-443-428A-749930	Sequence 749930,	817	122	6.7	312	7	US-11-443-428A-824726	Sequence 824726,
745	124	6.8	1034	7	US-11-443-428A-749938	Sequence 749938,	818	122	6.7	369	7	US-11-443-428A-777222	Sequence 777222,
746	124	6.8	1041	7	US-11-443-428A-819197	Sequence 819197,	819	122	6.7	369	7	US-11-443-428A-777231	Sequence 777231,
747	124	6.8	1126	7	US-11-293-697-3665	Sequence 3665, Ap	820	122	6.7	575	6	US-10-219-051B-529	Sequence 529, App
748	124	6.8	1142	7	US-11-443-428A-793105	Sequence 793105,	821	122	6.7	575	7	US-11-287-157A-254	Sequence 254, App
749	124	6.8	1282	7	US-11-443-428A-749929	Sequence 749929,	822	122	6.7	585	7	US-11-443-428A-890880	Sequence 890880,
750	124	6.8	1282	7	US-11-443-428A-819204	Sequence 819204,	823	122	6.7	586	7	US-11-443-428A-824688	Sequence 824688,
751	124	6.8	1300	7	US-11-443-428A-819203	Sequence 819203,	824	122	6.7	783	7	US-11-330-403-15564	Sequence 15564, A
752	124	6.8	1310	7	US-11-443-428A-819196	Sequence 819196,	825	122	6.7	902	7	US-11-413-976-8	Sequence 8, Appli
753	124	6.8	1310	7	US-11-443-428A-819199	Sequence 819199,	826	122	6.7	1016	6	US-11-443-428A-835076	Sequence 835076,
754	124	6.8	1396	7	US-11-443-428A-758577	Sequence 758577,	827	122	6.7	1150	6	US-10-669-920-1266	Sequence 1266, Ap
755	124	6.8	1709	7	US-11-582-861-7159	Sequence 7159, Ap	828	121.5	6.7	331	6	US-10-219-051B-11408	Sequence 11408, A
756	124	6.8	1963	7	US-11-582-861-7160	Sequence 7160, Ap	829	121.5	6.7	625	6	US-10-550-786-3	Sequence 3, Appli
757	123.5	6.8	503	6	US-10-560-790A-17	Sequence 17, Appli	830	121	6.6	279	6	US-10-703-032-108000	Sequence 108000,
758	123.5	6.8	698	7	US-11-443-428A-848839	Sequence 848839,	831	121	6.6	568	7	US-11-443-428A-815584	Sequence 815584,
759	123.5	6.8	935	7	US-11-443-428A-848838	Sequence 848838,	832	121	6.6	622	7	US-11-443-428A-815561	Sequence 815561,

833	121	6.6	642	7	US-11-443-428A-815565	Sequence 815565,	906	120.5	6.6	1808	7	US-11-443-428A-846823	Sequence 846823,
834	121	6.6	645	7	US-11-443-428A-815566	Sequence 815566,	907	120.5	6.6	1808	7	US-11-443-428A-846824	Sequence 846824,
835	121	6.6	645	7	US-11-443-428A-815567	Sequence 815567,	908	120.5	6.6	1808	7	US-11-443-428A-846825	Sequence 846825,
836	121	6.6	645	7	US-11-443-428A-815571	Sequence 815571,	909	120.5	6.6	1808	7	US-11-443-428A-846826	Sequence 846826,
837	121	6.6	654	6	US-10-219-051B-7772	Sequence 7772, Ap	910	120.5	6.6	3164	7	US-11-506-450-36	Sequence 36, Appl
838	121	6.6	654	6	US-10-219-051B-9799	Sequence 9799, Ap	911	120.5	6.6	4332	7	US-11-443-428A-794675	Sequence 794675,
839	121	6.6	654	6	US-10-567-867-61	Sequence 61, Appl	912	120.5	6.6	4364	7	US-11-443-428A-794674	Sequence 794674,
840	121	6.6	657	7	US-11-443-428A-815559	Sequence 815559,	913	120.5	6.6	4391	6	US-10-529-348-1733	Sequence 1733, Ap
841	121	6.6	657	7	US-11-443-428A-815576	Sequence 815576,	914	120.5	6.6	5262	7	US-11-582-861-10450	Sequence 10450, A
842	121	6.6	657	7	US-11-443-428A-815577	Sequence 815577,	915	120.5	6.6	5265	7	US-11-582-861-10499	Sequence 10499, A
843	121	6.6	657	7	US-11-443-428A-815579	Sequence 815579,	916	120	6.6	197	7	US-11-486-448-71477	Sequence 71477, A
844	121	6.6	684	7	US-11-443-428A-815563	Sequence 815563,	917	120	6.6	405	6	US-10-105-299-6164	Sequence 6164, Ap
845	121	6.6	688	7	US-11-296-571-12	Sequence 12, Appl	918	120	6.6	405	6	US-10-868-184-5160	Sequence 5160, Ap
846	121	6.6	696	7	US-11-443-428A-815554	Sequence 815554,	919	120	6.6	405	6	US-10-994-608-6164	Sequence 6164, Ap
847	121	6.6	696	7	US-11-443-428A-815557	Sequence 815557,	920	120	6.6	424	7	US-11-241-607-7210	Sequence 7210, Ap
848	121	6.6	696	7	US-11-443-428A-815560	Sequence 815560,	921	120	6.6	427	7	US-11-241-607-7209	Sequence 7209, Ap
849	121	6.6	696	7	US-11-443-428A-815568	Sequence 815568,	922	120	6.6	427	6	US-10-917-503-12413	Sequence 12413, A
850	121	6.6	696	7	US-11-443-428A-815570	Sequence 815570,	923	120	6.6	441	7	US-11-174-307B-5246	Sequence 5246, Ap
851	121	6.6	696	7	US-11-443-428A-815573	Sequence 815573,	924	120	6.6	441	7	US-11-241-607-7208	Sequence 7208, Ap
852	121	6.6	696	7	US-11-443-428A-815574	Sequence 815574,	925	120	6.6	565	7	US-11-443-428A-821839	Sequence 821839,
853	121	6.6	709	6	US-10-449-902-41387	Sequence 41387, A	926	120	6.6	617	6	US-10-540-167A-1	Sequence 1, Appl
854	121	6.6	709	7	US-11-443-428A-815578	Sequence 815578,	927	120	6.6	635	7	US-11-218-141-1460	Sequence 1460, Ap
855	121	6.6	714	7	US-11-443-428A-815564	Sequence 815564,	928	120	6.6	644	7	US-11-218-141-3428	Sequence 3428, Ap
856	121	6.6	726	7	US-11-443-428A-815562	Sequence 815562,	929	120	6.6	932	7	US-11-371-354-59621	Sequence 59621, A
857	121	6.6	726	7	US-11-443-428A-815580	Sequence 815580,	930	120	6.6	932	7	US-11-443-428A-905165	Sequence 905165,
858	121	6.6	726	7	US-11-443-428A-815581	Sequence 815581,	931	120	6.6	932	7	US-11-443-428A-905167	Sequence 905167,
859	121	6.6	726	7	US-11-443-428A-815582	Sequence 815582,	932	120	6.6	932	7	US-11-443-428A-905169	Sequence 905169,
860	121	6.6	733	7	US-11-443-428A-815583	Sequence 815583,	933	120	6.6	932	7	US-11-443-428A-905184	Sequence 905184,
861	121	6.6	783	7	US-11-443-428A-918649	Sequence 918649,	934	120	6.6	932	7	US-11-443-428A-905185	Sequence 905185,
862	121	6.6	1101	7	US-11-443-428A-848840	Sequence 848840,	935	120	6.6	932	7	US-11-443-428A-905186	Sequence 905186,
863	121	6.6	1189	6	US-10-449-902-41223	Sequence 41223, A	936	120	6.6	1014	7	US-11-482-553-48	Sequence 48, Appl
864	121	6.6	1419	6	US-10-219-051B-1513	Sequence 1513, Ap	937	120	6.6	1678	7	US-11-443-428A-756589	Sequence 756589,
865	120.5	6.6	339	7	US-11-520-715-59937	Sequence 59937, A	938	120	6.6	1877	7	US-11-443-428A-757677	Sequence 757677,
866	120.5	6.6	336	7	US-11-443-428A-899169	Sequence 899169,	939	120	6.6	2142	7	US-11-443-428A-757675	Sequence 757675,
867	120.5	6.6	421	7	US-11-443-428A-897399	Sequence 897399,	940	119.5	6.6	196	7	US-11-241-607-54693	Sequence 54693, A
868	120.5	6.6	442	7	US-11-443-428A-835077	Sequence 835077,	941	119.5	6.6	331	6	US-11-443-428A-872645	Sequence 872645,
869	120.5	6.6	477	7	US-11-443-428A-899174	Sequence 899174,	942	119.5	6.6	337	6	US-10-419-128-31851	Sequence 31851, A
870	120.5	6.6	497	7	US-11-241-607-61259	Sequence 61259, A	943	119.5	6.6	634	7	US-11-443-428A-861913	Sequence 861913,
871	120.5	6.6	573	7	US-11-443-428A-760153	Sequence 760153,	944	119.5	6.6	634	7	US-11-443-428A-861919	Sequence 861919,
872	120.5	6.6	699	7	US-11-296-571-11	Sequence 11, Appl	945	119.5	6.6	669	7	US-11-443-428A-861918	Sequence 861918,
873	120.5	6.6	795	7	US-11-478-193-411	Sequence 411, Appl	946	119.5	6.6	831	7	US-11-443-428A-756377	Sequence 756377,
874	120.5	6.6	814	7	US-11-443-428A-846817	Sequence 846817,	947	119.5	6.6	855	7	US-11-443-428A-910865	Sequence 910865,
875	120.5	6.6	819	7	US-11-443-428A-768906	Sequence 768906,	948	119.5	6.6	918	6	US-10-449-902-47854	Sequence 47854, A
876	120.5	6.6	829	7	US-11-443-428A-846818	Sequence 846818,	949	119.5	6.6	1036	6	US-10-760-320A-2902	Sequence 2902, Ap
877	120.5	6.6	857	7	US-11-443-428A-846828	Sequence 846828,	950	119.5	6.6	1241	7	US-11-407-702-77	Sequence 77, Appl
878	120.5	6.6	1016	6	US-10-567-867-1462	Sequence 1462, Ap	951	119.5	6.6	1241	7	US-11-443-428A-748580	Sequence 748580,
879	120.5	6.6	1016	7	US-11-443-428A-899168	Sequence 899168,	952	119.5	6.6	1258	7	US-11-443-428A-748579	Sequence 748579,
880	120.5	6.6	1016	7	US-11-443-428A-899170	Sequence 899170,	953	119.5	6.6	1291	6	US-10-419-128-19504	Sequence 19504, A
881	120.5	6.6	1016	7	US-11-443-428A-899171	Sequence 899171,	954	119.5	6.6	1523	7	US-11-582-861-7373	Sequence 7373, Ap
882	120.5	6.6	1016	7	US-11-443-428A-899175	Sequence 899175,	955	119.5	6.6	1603	7	US-11-582-861-6405	Sequence 6405, Ap
883	120.5	6.6	1086	7	US-11-443-428A-867856	Sequence 867856,	956	119.5	6.6	1604	7	US-11-443-428A-867854	Sequence 867854,
884	120.5	6.6	1095	7	US-11-443-428A-867856	Sequence 867856,	957	119	6.5	256	6	US-10-558-276-3	Sequence 3, Appl
885	120.5	6.6	1122	7	US-11-443-428A-846815	Sequence 846815,	958	119	6.5	256	6	US-10-558-276-4	Sequence 4, Appl
886	120.5	6.6	1140	7	US-11-443-428A-846815	Sequence 846815,	959	119	6.5	256	6	US-10-558-276-5	Sequence 5, Appl
887	120.5	6.6	1181	6	US-10-533-519-62	Sequence 62, Appl	960	119	6.5	256	6	US-10-558-276-9	Sequence 9, Appl
888	120.5	6.6	1195	7	US-11-443-428A-867862	Sequence 867862,	961	119	6.5	256	7	US-11-518-091-8	Sequence 8, Appl
889	120.5	6.6	1246	7	US-11-443-428A-844313	Sequence 844313,	962	119	6.5	256	7	US-11-518-091-9	Sequence 9, Appl
890	120.5	6.6	1338	7	US-11-582-861-7029	Sequence 7029, Ap	963	119	6.5	256	7	US-11-518-091-10	Sequence 10, Appl
891	120.5	6.6	1363	7	US-11-443-428A-846816	Sequence 846816,	964	119	6.5	256	7	US-11-518-091-11	Sequence 11, Appl
892	120.5	6.6	1460	7	US-11-443-428A-867852	Sequence 867852,	965	119	6.5	329	7	US-11-443-428A-868491	Sequence 868491,
893	120.5	6.6	1509	7	US-11-443-428A-895360	Sequence 895360,	966	119	6.5	346	7	US-11-443-428A-868492	Sequence 868492,
894	120.5	6.6	1509	7	US-11-443-428A-895361	Sequence 895361,	967	119	6.5	436	6	US-10-276-817B-14810	Sequence 14810, A
895	120.5	6.6	1509	7	US-11-443-428A-895362	Sequence 895362,	968	119	6.5	450	7	US-11-443-428A-764280	Sequence 764280,
896	120.5	6.6	1509	7	US-11-443-428A-895363	Sequence 895363,	969	119	6.5	462	7	US-11-443-428A-868494	Sequence 868494,
897	120.5	6.6	1509	7	US-11-443-428A-895364	Sequence 895364,	970	119	6.5	462	7	US-11-443-428A-868495	Sequence 868495,
898	120.5	6.6	1565	7	US-11-443-428A-867861	Sequence 867861,	971	119	6.5	462	7	US-11-443-428A-868496	Sequence 868496,
899	120.5	6.6	1599	7	US-11-443-428A-867845	Sequence 867845,	972	119	6.5	462	7	US-11-443-428A-868499	Sequence 868499,
900	120.5	6.6	1599	7	US-11-443-428A-924506	Sequence 924506,	973	119	6.5	462	7	US-11-443-428A-868503	Sequence 868503,
901	120.5	6.6	1690	7	US-11-443-428A-867846	Sequence 867846,	974	119	6.5	543	7	US-11-443-428A-821831	Sequence 821831,
902	120.5	6.6	1712	6	US-10-796-307-777	Sequence 777, App	975	119	6.5	546	7	US-11-443-428A-902531	Sequence 902531,
903	120.5	6.6	1808	7	US-11-443-428A-846810	Sequence 846810,	976	119	6.5	608	6	US-10-760-320A-3237	Sequence 3237, Ap
904	120.5	6.6	1808	7	US-11-443-428A-846811	Sequence 846811,	977	119	6.5	656	7	US-11-443-428A-902527	Sequence 902527,
905	120.5	6.6	1808	7	US-11-443-428A-846814	Sequence 846814,	978	119	6.5	681	7	US-11-443-428A-902528	Sequence 902528,

979	119	6.5	715	7	US-11-443-428A-902526	Sequence 902526,	1052	117.5	6.4	751	7	US-11-443-428A-851729	Sequence 851729,
980	119	6.5	722	7	US-11-443-428A-902529	Sequence 902529,	1053	117.5	6.4	759	7	US-11-371-354-57951	Sequence 57951, A
981	119	6.5	772	7	US-11-056-355B-75114	Sequence 75114, A	1054	117.5	6.4	759	7	US-11-582-861-57951	Sequence 57951, Ap
982	119	6.5	772	7	US-11-241-607-28243	Sequence 28243, A	1055	117.5	6.4	881	7	US-11-443-428A-906530	Sequence 906530, Ap
983	119	6.5	1069	7	US-11-443-428A-911683	Sequence 911683,	1056	117.5	6.4	938	7	US-11-443-428A-864586	Sequence 864586,
984	119	6.5	1361	7	US-11-443-428A-911689	Sequence 911689,	1057	117.5	6.4	958	7	US-11-443-428A-864577	Sequence 864577,
985	119	6.5	1691	7	US-11-443-428A-756590	Sequence 756590,	1058	117.5	6.4	989	7	US-11-443-428A-864588	Sequence 864588,
986	119	6.5	1691	7	US-11-598-148-51	Sequence 51, Appl	1059	117.5	6.4	1082	7	US-11-443-428A-868407	Sequence 868407,
987	118.5	6.5	371	7	US-11-443-428A-801867	Sequence 801867,	1060	117.5	6.4	1082	7	US-11-443-428A-868408	Sequence 868408,
988	118.5	6.5	477	7	US-11-443-428A-801866	Sequence 801866,	1061	117.5	6.4	1082	7	US-11-443-428A-868413	Sequence 868413,
989	118.5	6.5	511	6	US-10-419-128-26078	Sequence 26078, A	1062	117.5	6.4	1082	7	US-11-443-428A-868415	Sequence 868415,
990	118.5	6.5	550	7	US-10-419-128-21295	Sequence 21295, A	1063	117.5	6.4	1141	7	US-11-443-428A-864575	Sequence 864575,
991	118.5	6.5	552	7	US-11-443-428A-801864	Sequence 801864,	1064	117.5	6.4	1141	7	US-11-443-428A-864576	Sequence 864576,
992	118.5	6.5	603	7	US-11-443-428A-788231	Sequence 788231,	1065	117.5	6.4	1141	7	US-11-443-428A-864580	Sequence 864580,
993	118.5	6.5	633	7	US-11-443-428A-855018	Sequence 855018,	1066	117.5	6.4	1141	7	US-11-443-428A-864587	Sequence 864587,
994	118.5	6.5	653	7	US-11-443-428A-855011	Sequence 855011,	1067	117.5	6.4	1336	7	US-11-443-428A-864583	Sequence 864583,
995	118.5	6.5	678	7	US-11-443-428A-801863	Sequence 801863,	1068	117.5	6.4	1685	7	US-11-443-428A-906521	Sequence 906521,
996	118.5	6.5	699	7	US-11-296-571-1	Sequence 1, Appli	1069	117.5	6.4	1701	7	US-11-443-428A-906520	Sequence 906520,
997	118.5	6.5	921	6	US-10-560-790A-15	Sequence 15, Appl	1070	117.5	6.4	1701	7	US-11-443-428A-906529	Sequence 906529,
998	118.5	6.5	921	7	US-11-443-428A-801862	Sequence 801862,	1071	117.5	6.4	1706	7	US-11-443-428A-906531	Sequence 906531,
999	118.5	6.5	921	7	US-11-443-428A-801865	Sequence 801865,	1072	117	6.4	288	6	US-10-449-902-40102	Sequence 40102, A
1000	118.5	6.5	1301	7	US-11-443-428A-811261	Sequence 811261,	1073	117	6.4	394	6	US-10-419-128-19344	Sequence 19344, A
1001	118.5	6.5	1301	7	US-11-443-428A-811261	Sequence 811261,	1074	117	6.4	448	7	US-11-443-428A-825549	Sequence 825549,
1002	118.5	6.5	1323	6	US-11-443-428A-811262	Sequence 811262, A	1075	117	6.4	524	7	US-11-443-428A-888610	Sequence 888610,
1003	118.5	6.5	1326	7	US-11-090-997-1950	Sequence 1950, A	1076	117	6.4	524	7	US-11-443-428A-888611	Sequence 888611,
1004	118.5	6.5	1339	7	US-11-090-997-1952	Sequence 1952, Ap	1077	117	6.4	524	7	US-11-443-428A-888612	Sequence 888612,
1005	118.5	6.5	1608	6	US-10-567-867-1723	Sequence 1723, Ap	1078	117	6.4	524	7	US-11-443-428A-888613	Sequence 888613,
1006	118	6.5	256	6	US-10-558-276-8	Sequence 8, Appli	1079	117	6.4	524	7	US-11-443-428A-888614	Sequence 888614,
1007	118	6.5	256	7	US-11-518-091-6	Sequence 6, Appli	1080	117	6.4	524	7	US-11-443-428A-888615	Sequence 888615,
1008	118	6.5	284	6	US-10-558-276-2	Sequence 2, Appli	1081	117	6.4	524	7	US-11-443-428A-888622	Sequence 888622,
1009	118	6.5	284	6	US-10-558-276-18	Sequence 18, Appl	1082	117	6.4	524	7	US-11-443-428A-888623	Sequence 888623,
1010	118	6.5	288	7	US-11-443-428A-922487	Sequence 922487,	1083	117	6.4	524	7	US-11-443-428A-888624	Sequence 888624,
1011	118	6.5	302	7	US-11-486-448-67346	Sequence 67346, A	1084	117	6.4	524	7	US-11-443-428A-888625	Sequence 888625,
1012	118	6.5	416	6	US-10-419-128-24575	Sequence 24575, A	1085	117	6.4	524	7	US-11-443-428A-888626	Sequence 888626,
1013	118	6.5	421	6	US-10-513-957-2	Sequence 2, Appli	1086	117	6.4	524	7	US-11-443-428A-888627	Sequence 888627,
1014	118	6.5	421	7	US-11-001-793-9001	Sequence 9001, Ap	1087	117	6.4	535	7	US-11-443-428A-837841	Sequence 837841,
1015	118	6.5	468	6	US-10-777-288A-3173	Sequence 3173, Ap	1088	117	6.4	690	7	US-11-296-571-10	Sequence 10, Appl
1016	118	6.5	508	7	US-11-443-428A-817746	Sequence 817746,	1089	117	6.4	788	6	US-10-530-187-275	Sequence 275, App
1017	118	6.5	508	7	US-11-443-428A-742149	Sequence 742149,	1090	117	6.4	788	6	US-11-582-861-5651	Sequence 5651, Ap
1018	118	6.5	681	7	US-11-443-428A-817765	Sequence 817765,	1091	117	6.4	925	6	US-10-934-893-4327	Sequence 4327, Ap
1019	118	6.5	690	7	US-11-443-428A-742148	Sequence 742148,	1092	117	6.4	1367	7	US-11-443-428A-828335	Sequence 828335,
1020	118	6.5	690	7	US-11-443-428A-742150	Sequence 742150,	1093	117	6.4	1783	7	US-11-443-428A-828328	Sequence 828328,
1021	118	6.5	690	7	US-11-443-428A-742151	Sequence 742151,	1094	116.5	6.4	265	7	US-11-518-091-5	Sequence 5, Appli
1022	118	6.5	690	7	US-11-443-428A-742156	Sequence 742156,	1095	116.5	6.4	280	6	US-10-953-349-18921	Sequence 18921, A
1023	118	6.5	690	7	US-11-443-428A-742157	Sequence 742157,	1096	116.5	6.4	280	7	US-11-056-355B-54673	Sequence 54673, A
1024	118	6.5	691	7	US-11-443-428A-742158	Sequence 742158,	1097	116.5	6.4	305	7	US-11-443-428A-901651	Sequence 901651,
1025	118	6.5	710	7	US-11-443-428A-742152	Sequence 742152,	1098	116.5	6.4	327	6	US-10-523-834-287	Sequence 287, App
1026	118	6.5	738	7	US-11-443-428A-742154	Sequence 742154,	1099	116.5	6.4	357	7	US-11-443-428A-777232	Sequence 777232,
1027	118	6.5	756	7	US-11-443-428A-742147	Sequence 742147,	1100	116.5	6.4	361	7	US-11-371-354-12501	Sequence 12501, A
1028	118	6.5	775	7	US-11-443-428A-817762	Sequence 817762,	1101	116.5	6.4	361	7	US-11-371-354-55737	Sequence 55737, A
1029	118	6.5	780	7	US-11-443-428A-742145	Sequence 742145,	1102	116.5	6.4	361	7	US-11-371-354-76399	Sequence 76399, A
1030	118	6.5	780	7	US-11-443-428A-742146	Sequence 742146,	1103	116.5	6.4	361	7	US-11-443-428A-777230	Sequence 777230,
1031	118	6.5	780	7	US-11-443-428A-742153	Sequence 742153,	1104	116.5	6.4	361	7	US-11-443-428A-777234	Sequence 777234,
1032	118	6.5	785	7	US-11-443-428A-817764	Sequence 817764,	1105	116.5	6.4	361	7	US-11-443-428A-777235	Sequence 777235,
1033	118	6.5	864	7	US-11-443-428A-817763	Sequence 817763,	1106	116.5	6.4	389	7	US-11-443-428A-781098	Sequence 781098,
1034	118	6.5	971	6	US-10-777-288A-2468	Sequence 2468, Ap	1107	116.5	6.4	424	7	US-11-371-354-73171	Sequence 73171, A
1035	118	6.5	1003	6	US-10-276-817B-14803	Sequence 14803, A	1108	116.5	6.4	424	7	US-11-443-428A-901643	Sequence 901643,
1036	118	6.5	1045	7	US-11-443-428A-867847	Sequence 867847, Ap	1109	116.5	6.4	441	7	US-11-443-428A-901644	Sequence 901644,
1037	118	6.5	1079	6	US-10-276-817B-14951	Sequence 14951, A	1110	116.5	6.4	441	7	US-11-443-428A-901648	Sequence 901648,
1038	118	6.5	1248	7	US-11-428-415-33	Sequence 33, Appl	1111	116.5	6.4	446	7	US-11-443-428A-901649	Sequence 901649,
1039	118	6.5	1248	7	US-11-066-316A-1137	Sequence 1137, Ap	1112	116.5	6.4	470	7	US-11-443-428A-901650	Sequence 901650,
1040	118	6.5	1270	7	US-11-443-428A-749928	Sequence 749928,	1113	116.5	6.4	660	6	US-10-419-128-32842	Sequence 32842, A
1041	118	6.5	1270	7	US-11-443-428A-749928	Sequence 749928,	1114	116.5	6.4	1035	6	US-10-533-519-790	Sequence 790, App
1042	118	6.5	1270	7	US-11-443-428A-749932	Sequence 749932,	1115	116.5	6.4	1036	6	US-10-743-643-301	Sequence 301, App
1043	117.5	6.4	261	7	US-11-056-355B-9529	Sequence 9529, Ap	1116	116.5	6.4	1036	6	US-10-743-643-1750	Sequence 1750, Ap
1044	117.5	6.4	261	7	US-11-241-607-22987	Sequence 22987, A	1117	116.5	6.4	1036	6	US-11-248-956-2	Sequence 2, Appli
1045	117.5	6.4	368	7	US-11-443-428A-829774	Sequence 829774,	1118	116.5	6.4	1036	7	US-11-121-133-355	Sequence 255, App
1046	117.5	6.4	473	7	US-11-218-141-1916	Sequence 1916, Ap	1119	116.5	6.4	1036	7	US-11-121-133-256	Sequence 256, App
1047	117.5	6.4	478	7	US-11-443-428A-808771	Sequence 808771,	1120	116.5	6.4	1324	6	US-10-219-051B-13625	Sequence 13625, A
1048	117.5	6.4	484	7	US-11-218-141-3743	Sequence 3743, Ap	1121	116.5	6.4	1324	6	US-10-219-051B-14626	Sequence 14626, A
1049	117.5	6.4	675	7	US-11-443-428A-785612	Sequence 785612,	1122	116.5	6.4	3288	7	US-11-506-450-38	Sequence 38, Appl
1050	117.5	6.4	698	7	US-11-443-428A-906532	Sequence 906532,	1123	116	6.4	253	6	US-10-276-817B-9981	Sequence 9981, Ap
1051	117.5	6.4	746	7	US-11-218-141-1775	Sequence 1775, Ap	1124	116	6.4	315	6	US-10-419-128-18926	Sequence 18926, A

1125	116	6.4	385	6	US-10-990-328-10369	Sequence 10369, A	1198	115	6.3	548	7	US-11-371-354-55725	Sequence 55725, A
1126	116	6.4	385	7	US-11-371-354-71939	Sequence 71939, A	1199	115	6.3	548	7	US-11-371-354-76590	Sequence 76590, A
1127	116	6.4	385	7	US-11-443-428A-798025	Sequence 798025, A	1200	115	6.3	548	7	US-11-443-428A-808769	Sequence 808769, A
1128	116	6.4	391	7	US-11-472-437-1	Sequence 1, Appl	1201	115	6.3	548	7	US-11-443-428A-808773	Sequence 808773, A
1129	116	6.4	443	7	US-11-241-607-60571	Sequence 60571, A	1202	115	6.3	548	7	US-11-443-428A-808774	Sequence 808774, A
1130	116	6.4	533	6	US-10-533-519-1023	Sequence 1023, Ap	1203	115	6.3	548	7	US-11-443-428A-808775	Sequence 808775, A
1131	116	6.4	533	6	US-10-533-519-1025	Sequence 1025, Ap	1204	115	6.3	548	7	US-11-443-428A-808776	Sequence 808776, A
1132	116	6.4	533	7	US-11-365-989-98	Sequence 98, Appl	1205	115	6.3	560	7	US-11-443-428A-808770	Sequence 808770, A
1133	116	6.4	533	7	US-11-371-354-13296	Sequence 13296, A	1206	115	6.3	588	7	US-11-443-428A-849162	Sequence 849162, A
1134	116	6.4	533	7	US-11-371-354-56315	Sequence 56315, A	1207	115	6.3	639	6	US-10-419-128-28453	Sequence 28453, A
1135	116	6.4	533	7	US-11-371-354-77805	Sequence 77805, A	1208	115	6.3	675	7	US-11-443-428A-900047	Sequence 900047, A
1136	116	6.4	533	7	US-11-371-354-77805	Sequence 77805, A	1209	115	6.3	775	7	US-11-443-428A-837820	Sequence 837820, A
1137	116	6.4	602	7	US-11-443-428A-1024909	Sequence 1024909, A	1210	115	6.3	806	7	US-11-056-355B-43358	Sequence 43358, A
1138	116	6.4	632	7	US-11-443-428A-821832	Sequence 821832, A	1211	115	6.3	833	7	US-11-056-355B-43357	Sequence 43357, A
1139	116	6.4	684	7	US-11-090-997-1954	Sequence 1954, Ap	1212	115	6.3	845	7	US-11-582-861-8973	Sequence 8973, Ap
1140	116	6.4	858	7	US-11-443-428A-804244	Sequence 804244, A	1213	115	6.3	895	7	US-11-056-355B-43356	Sequence 43356, A
1141	116	6.4	1124	7	US-11-431-855-23456	Sequence 23456, A	1214	115	6.3	919	6	US-10-449-902-53543	Sequence 53543, A
1142	116	6.4	1324	7	US-11-090-997-17028	Sequence 17028, Ap	1215	115	6.3	937	7	US-11-443-428A-900046	Sequence 900046, A
1143	116	6.4	1470	7	US-11-443-428A-825842	Sequence 825842, A	1216	115	6.3	1094	7	US-11-371-354-12556	Sequence 12556, A
1144	116	6.4	1812	7	US-11-443-428A-825848	Sequence 825848, A	1217	115	6.3	1094	7	US-11-371-354-76486	Sequence 76486, A
1145	115.5	6.3	134	7	US-11-443-428A-1019452	Sequence 1019452, A	1218	115	6.3	1152	6	US-10-219-051B-5341	Sequence 5341, Ap
1146	115.5	6.3	195	6	US-10-703-032-177731	Sequence 177731, A	1219	115	6.3	1153	7	US-11-443-428A-900028	Sequence 900028, A
1147	115.5	6.3	211	7	US-11-134-228A-19	Sequence 19, Appl	1220	115	6.3	1269	7	US-11-443-428A-900029	Sequence 900029, A
1148	115.5	6.3	254	6	US-10-516-211-23	Sequence 23, Appl	1221	115	6.3	1290	7	US-11-443-428A-823194	Sequence 823194, A
1149	115.5	6.3	254	7	US-11-419-688-10	Sequence 10, Appl	1222	115	6.3	1369	7	US-11-443-428A-823193	Sequence 823193, A
1150	115.5	6.3	254	7	US-11-518-091-2	Sequence 2, Appl	1223	115	6.3	1374	7	US-11-443-428A-823191	Sequence 823191, A
1151	115.5	6.3	254	7	US-11-518-091-7	Sequence 7, Appl	1224	115	6.3	1374	7	US-11-443-428A-823195	Sequence 823195, A
1152	115.5	6.3	326	7	US-11-443-428A-754266	Sequence 754266, A	1225	115	6.3	1374	7	US-11-443-428A-823196	Sequence 823196, A
1153	115.5	6.3	329	7	US-11-293-697-2847	Sequence 2847, Ap	1226	115	6.3	1374	7	US-11-443-428A-823197	Sequence 823197, A
1154	115.5	6.3	364	7	US-11-443-428A-917483	Sequence 917483, A	1227	115	6.3	1374	7	US-11-443-428A-823199	Sequence 823199, A
1155	115.5	6.3	369	7	US-11-293-697-3622	Sequence 3622, Ap	1228	115	6.3	1374	7	US-11-443-428A-823200	Sequence 823200, A
1156	115.5	6.3	371	7	US-11-443-428A-754265	Sequence 754265, A	1229	115	6.3	1374	7	US-11-443-428A-823201	Sequence 823201, A
1157	115.5	6.3	374	7	US-11-443-428A-754264	Sequence 754264, A	1230	115	6.3	1422	7	US-11-443-428A-900045	Sequence 900045, A
1158	115.5	6.3	395	7	US-11-443-428A-808776	Sequence 808776, A	1231	115	6.3	1490	7	US-11-443-428A-900027	Sequence 900027, A
1159	115.5	6.3	409	6	US-10-990-328-10370	Sequence 10370, A	1232	115	6.3	1497	7	US-11-443-428A-1029350	Sequence 1029350, A
1160	115.5	6.3	410	7	US-11-443-428A-754262	Sequence 754262, A	1233	115	6.3	1532	7	US-11-582-861-10836	Sequence 10836, A
1161	115.5	6.3	454	6	US-10-934-893-2557	Sequence 2557, Ap	1234	115	6.3	1537	7	US-11-443-428A-823192	Sequence 823192, A
1162	115.5	6.3	462	7	US-11-443-428A-829768	Sequence 829768, A	1235	115	6.3	1541	6	US-10-574-398-223	Sequence 223, App
1163	115.5	6.3	625	6	US-10-419-128-19871	Sequence 19871, A	1236	115	6.3	1541	6	US-10-567-867-844	Sequence 844, App
1164	115.5	6.3	726	6	US-10-917-503-17690	Sequence 17690, A	1237	115	6.3	1573	6	US-10-990-328-14412	Sequence 14412, A
1165	115.5	6.3	803	6	US-10-917-503-14810	Sequence 14810, A	1238	115	6.3	1573	6	US-10-990-328-14413	Sequence 14413, A
1166	115.5	6.3	803	7	US-11-443-428A-754253	Sequence 754253, A	1239	115	6.3	1573	6	US-10-219-051B-1403	Sequence 1403, Ap
1167	115.5	6.3	803	7	US-11-443-428A-754257	Sequence 754257, A	1240	115	6.3	1576	6	US-10-990-328-14414	Sequence 14414, A
1168	115.5	6.3	803	7	US-11-443-428A-754271	Sequence 754271, A	1241	115	6.3	1589	7	US-11-443-428A-896382	Sequence 896382, A
1169	115.5	6.3	808	7	US-11-520-715-69225	Sequence 69225, A	1242	115	6.3	1589	7	US-11-443-428A-896383	Sequence 896383, A
1170	115.5	6.3	1677	7	US-11-582-861-9995	Sequence 9995, Ap	1243	115	6.3	1589	7	US-11-443-428A-896384	Sequence 896384, A
1171	115	6.3	244	7	US-11-486-448-80811	Sequence 80811, A	1244	115	6.3	1597	7	US-11-443-428A-896386	Sequence 896386, A
1172	115	6.3	252	7	US-11-443-428A-1034164	Sequence 1034164, A	1245	115	6.3	1597	7	US-11-443-428A-900043	Sequence 900043, A
1173	115	6.3	295	7	US-11-443-428A-942513	Sequence 942513, A	1246	115	6.3	1722	7	US-11-443-428A-900025	Sequence 900025, A
1174	115	6.3	315	7	US-11-443-428A-948892	Sequence 948892, A	1247	115	6.3	1894	7	US-11-443-428A-900024	Sequence 900024, A
1175	115	6.3	318	6	US-10-703-032-114664	Sequence 114664, A	1248	115	6.3	2012	7	US-11-443-428A-900023	Sequence 900023, A
1176	115	6.3	351	6	US-10-934-893-2413	Sequence 2413, Ap	1249	115	6.3	2226	6	US-10-990-328-8257	Sequence 8257, Ap
1177	115	6.3	393	7	US-11-443-428A-919088	Sequence 919088, A	1250	115	6.3	2307	6	US-11-443-428A-900022	Sequence 900022, A
1178	115	6.3	394	7	US-11-443-428A-876210	Sequence 876210, A	1251	115	6.3	2397	7	US-11-443-428A-900041	Sequence 900041, A
1179	115	6.3	454	7	US-11-443-428A-799377	Sequence 799377, A	1252	115	6.3	2438	7	US-10-533-520-6352	Sequence 6352, Ap
1180	115	6.3	457	7	US-11-301-457-19	Sequence 19, Appl	1253	115	6.3	2442	6	US-10-990-328-8256	Sequence 8256, Ap
1181	115	6.3	457	7	US-11-371-354-67161	Sequence 67161, A	1254	115	6.3	2442	6	US-10-990-328-8258	Sequence 8258, Ap
1182	115	6.3	457	7	US-11-443-428A-807400	Sequence 807400, A	1255	115	6.3	2442	6	US-10-990-328-8258	Sequence 8258, Ap
1183	115	6.3	462	7	US-11-443-428A-876212	Sequence 876212, A	1256	115	6.3	2442	7	US-11-443-428A-900019	Sequence 900019, A
1184	115	6.3	463	6	US-10-419-128-29731	Sequence 29731, A	1257	115	6.3	2442	7	US-11-443-428A-900020	Sequence 900020, A
1185	115	6.3	466	6	US-10-219-051B-13285	Sequence 13285, A	1258	115	6.3	2442	7	US-11-443-428A-900039	Sequence 900039, A
1186	115	6.3	466	7	US-11-371-354-72965	Sequence 72965, A	1259	115	6.3	2442	7	US-11-443-428A-900042	Sequence 900042, A
1187	115	6.3	466	7	US-11-443-428A-876214	Sequence 876214, A	1260	115	6.3	2442	7	US-11-443-428A-900044	Sequence 900044, A
1188	115	6.3	466	7	US-11-582-861-11349	Sequence 11349, A	1261	115	6.3	2442	7	US-11-582-861-7317	Sequence 7317, Ap
1189	115	6.3	467	7	US-11-443-428A-876208	Sequence 876208, A	1262	115	6.3	2476	7	US-11-443-428A-900040	Sequence 900040, A
1190	115	6.3	489	7	US-11-443-428A-876202	Sequence 876202, A	1263	115	6.3	2780	7	US-11-443-428A-900021	Sequence 900021, A
1191	115	6.3	489	7	US-11-443-428A-876205	Sequence 876205, A	1264	114.5	6.3	224	7	US-11-443-428A-814243	Sequence 814243, A
1192	115	6.3	489	7	US-11-443-428A-876204	Sequence 876204, A	1265	114.5	6.3	261	7	US-11-520-715-63205	Sequence 63205, A
1193	115	6.3	489	7	US-11-443-428A-876213	Sequence 876213, A	1266	114.5	6.3	283	7	US-11-443-428A-940346	Sequence 940346, A
1194	115	6.3	489	7	US-11-443-428A-876218	Sequence 876218, A	1267	114.5	6.3	292	7	US-11-443-428A-971137	Sequence 971137, A
1195	115	6.3	490	7	US-11-443-428A-876206	Sequence 876206, A	1268	114.5	6.3	354	6	US-10-553-098-830	Sequence 830, App
1196	115	6.3	490	7	US-11-443-428A-876211	Sequence 876211, A	1269	114.5	6.3	361	6	US-10-533-520-1185	Sequence 1185, Ap
1197	115	6.3	548	7	US-11-371-354-12625	Sequence 12625, A	1270	114.5	6.3	361	6	US-10-533-520-2498	Sequence 2498, Ap

1271	114.5	6.3	377	6	US-10-572-004-36	Sequence 36, Appl	1344	113.5	6.2	231	7	US-11-443-428A-824712	Sequence 824712,
1272	114.5	6.3	443	7	US-11-443-428A-829767	Sequence 829767,	1345	113.5	6.2	260	7	US-11-443-428A-999490	Sequence 999490,
1273	114.5	6.3	485	7	US-11-443-428A-881359	Sequence 881359,	1346	113.5	6.2	263	6	US-10-558-276-14	Sequence 14, Appl
1274	114.5	6.3	488	7	US-11-582-861-11350	Sequence 11350, A	1347	113.5	6.2	369	7	US-11-486-448-79618	Sequence 79618, A
1275	114.5	6.3	511	7	US-11-443-428A-876203	Sequence 876203,	1348	113.5	6.2	373	7	US-11-486-448-68185	Sequence 68185, A
1276	114.5	6.3	675	6	US-10-449-902-48447	Sequence 48447, A	1349	113.5	6.2	430	6	US-10-419-128-16681	Sequence 16681, A
1277	114.5	6.3	675	6	US-10-449-902-50618	Sequence 50618, A	1350	113.5	6.2	443	6	US-10-511-937-2464	Sequence 2464, Ap
1278	114.5	6.3	717	7	US-11-443-428A-786272	Sequence 786272,	1351	113.5	6.2	443	6	US-10-529-348-826	Sequence 826, App
1279	114.5	6.3	720	6	US-10-419-128-23212	Sequence 23212, A	1352	113.5	6.2	443	6	US-10-533-520-2289	Sequence 2289, Ap
1280	114.5	6.3	941	7	US-11-443-428A-1029453	Sequence 1029453,	1353	113.5	6.2	443	7	US-11-289-102-300	Sequence 300, App
1281	114.5	6.3	1208	6	US-10-990-328-12368	Sequence 12368, A	1354	113.5	6.2	443	7	US-11-289-102-354	Sequence 354, App
1282	114.5	6.3	1208	7	US-11-415-100-4	Sequence 4, Appli	1355	113.5	6.2	443	7	US-11-289-102-379	Sequence 379, App
1283	114.5	6.3	1208	7	US-11-477-604-4	Sequence 4, Appli	1356	113.5	6.2	443	7	US-11-335-927-17	Sequence 17, Appl
1284	114.5	6.3	1320	7	US-11-443-428A-1029450	Sequence 1029450,	1357	113.5	6.2	443	7	US-11-371-354-72117	Sequence 72117, A
1285	114.5	6.3	1320	7	US-11-443-428A-1029452	Sequence 1029452,	1358	113.5	6.2	443	7	US-11-371-354-75845	Sequence 75845, A
1286	114.5	6.3	1320	7	US-11-443-428A-1029454	Sequence 1029454,	1359	113.5	6.2	444	7	US-11-371-354-68805	Sequence 68805, A
1287	114.5	6.3	1682	7	US-11-582-861-6354	Sequence 6354, Ap	1360	113.5	6.2	444	7	US-11-443-428A-907748	Sequence 907748,
1288	114	6.2	204	7	US-11-371-354-73237	Sequence 73237, A	1361	113.5	6.2	444	7	US-11-443-428A-907749	Sequence 907749,
1289	114	6.2	264	7	US-11-419-688-11	Sequence 11, Appl	1362	113.5	6.2	444	7	US-11-443-428A-907750	Sequence 907750,
1290	114	6.2	307	7	US-11-443-428A-1010396	Sequence 1010396,	1363	113.5	6.2	451	6	US-10-219-051B-8271	Sequence 8271, Ap
1291	114	6.2	397	7	US-11-443-428A-748893	Sequence 748893,	1364	113.5	6.2	453	6	US-11-443-428A-760152	Sequence 760152,
1292	114	6.2	426	7	US-11-443-428A-823784	Sequence 823784,	1365	113.5	6.2	453	6	US-10-703-032-106094	Sequence 106094,
1293	114	6.2	441	7	US-11-443-428A-851751	Sequence 851751,	1366	113.5	6.2	453	6	US-11-443-428A-837829	Sequence 837829,
1294	114	6.2	472	7	US-11-443-428A-837833	Sequence 837833,	1367	113.5	6.2	479	7	US-11-443-428A-837829	Sequence 837829,
1295	114	6.2	496	7	US-11-090-997-1958	Sequence 1958, Ap	1368	113.5	6.2	507	7	US-11-134-068-24	Sequence 24, Appl
1296	114	6.2	503	7	US-11-134-068-2	Sequence 2, Appli	1369	113.5	6.2	507	7	US-11-443-428A-854178	Sequence 854178,
1297	114	6.2	509	7	US-11-443-428A-852855	Sequence 852855,	1370	113.5	6.2	509	7	US-11-443-428A-834636	Sequence 834636,
1298	114	6.2	548	6	US-10-567-867-41	Sequence 41, Appl	1371	113.5	6.2	615	7	US-11-443-428A-760154	Sequence 760154,
1299	114	6.2	548	6	US-10-348-119-217	Sequence 217, App	1372	113.5	6.2	670	7	US-11-443-428A-854192	Sequence 854192,
1300	114	6.2	553	7	US-11-443-428A-916745	Sequence 916745,	1373	113.5	6.2	674	7	US-11-443-428A-872623	Sequence 872623,
1301	114	6.2	554	7	US-11-443-428A-852859	Sequence 852859,	1374	113.5	6.2	675	7	US-11-443-428A-814560	Sequence 814560,
1302	114	6.2	572	7	US-11-443-428A-851730	Sequence 851730,	1375	113.5	6.2	788	7	US-11-443-428A-814557	Sequence 814557,
1303	114	6.2	572	7	US-11-443-428A-851732	Sequence 851732,	1376	113.5	6.2	788	7	US-11-443-428A-814558	Sequence 814558,
1304	114	6.2	586	7	US-11-443-428A-851731	Sequence 851731,	1377	113.5	6.2	843	7	US-11-443-428A-834635	Sequence 834635,
1305	114	6.2	648	7	US-11-443-428A-817766	Sequence 817766,	1378	113.5	6.2	966	7	US-11-582-861-6706	Sequence 6706, Ap
1306	114	6.2	669	6	US-10-567-867-552	Sequence 552, App	1379	113.5	6.2	1007	7	US-11-582-861-7753	Sequence 7753, Ap
1307	114	6.2	669	7	US-11-443-428A-852858	Sequence 852858,	1380	113.5	6.2	1045	7	US-11-443-428A-834633	Sequence 834633,
1308	114	6.2	677	7	US-11-443-428A-851738	Sequence 851738,	1381	113.5	6.2	1065	7	US-11-582-861-7488	Sequence 7488, Ap
1309	114	6.2	684	7	US-11-371-354-57949	Sequence 57949, A	1382	113.5	6.2	1214	7	US-11-582-861-7488	Sequence 7488, Ap
1310	114	6.2	684	7	US-11-443-428A-851740	Sequence 851740,	1383	113.5	6.2	1294	7	US-11-443-428A-904455	Sequence 904455,
1311	114	6.2	684	7	US-11-443-428A-851741	Sequence 851741,	1384	113.5	6.2	1294	7	US-11-443-428A-904462	Sequence 904462,
1312	114	6.2	684	7	US-11-443-428A-851743	Sequence 851743,	1385	113.5	6.2	1611	7	US-11-520-715-54372	Sequence 54372, A
1313	114	6.2	705	6	US-10-567-867-550	Sequence 550, App	1386	113.5	6.2	1690	6	US-10-516-780-28	Sequence 28, Appl
1314	114	6.2	705	7	US-11-443-428A-852853	Sequence 852853,	1387	113.5	6.2	1798	6	US-10-796-280-1055	Sequence 1055, Ap
1315	114	6.2	705	7	US-11-443-428A-852854	Sequence 852854,	1388	113.5	6.2	1798	7	US-11-443-428A-834630	Sequence 834630,
1316	114	6.2	705	7	US-11-443-428A-852857	Sequence 852857,	1389	113.5	6.2	1798	7	US-11-443-428A-834639	Sequence 834639,
1317	114	6.2	707	7	US-11-443-428A-748891	Sequence 748891,	1390	113.5	6.2	1798	7	US-11-443-428A-834643	Sequence 834643,
1318	114	6.2	710	7	US-11-443-428A-823792	Sequence 823792,	1391	113.5	6.2	1888	7	US-11-443-428A-834640	Sequence 834640,
1319	114	6.2	727	7	US-11-443-428A-748892	Sequence 748892,	1392	113.5	6.2	1899	7	US-11-582-861-9710	Sequence 9710, Ap
1320	114	6.2	732	7	US-11-443-428A-851745	Sequence 851745,	1393	113.5	6.2	1993	7	US-11-443-428A-834632	Sequence 834632,
1321	114	6.2	791	7	US-11-443-428A-748889	Sequence 748889,	1394	113.5	6.2	1996	7	US-11-443-428A-834641	Sequence 834641,
1322	114	6.2	901	7	US-11-443-428A-748885	Sequence 748885,	1395	113.5	6.2	2414	6	US-10-990-328-14694	Sequence 14694, A
1323	114	6.2	901	7	US-11-443-428A-748890	Sequence 748890,	1396	113.5	6.2	2414	7	US-11-283-329-176	Sequence 176, App
1324	114	6.2	961	7	US-11-443-428A-748883	Sequence 748883,	1397	113.5	6.2	2414	7	US-11-443-428A-1024857	Sequence 1024857,
1325	114	6.2	961	7	US-11-443-428A-823776	Sequence 823776,	1398	113.5	6.2	2414	7	US-11-582-861-5756	Sequence 5756, Ap
1326	114	6.2	961	7	US-11-443-428A-823794	Sequence 823794,	1399	113.5	6.2	2414	7	US-11-605-202-2	Sequence 2, Appli
1327	114	6.2	1022	7	US-11-443-428A-823777	Sequence 823777,	1400	113.5	6.2	3063	7	US-11-443-428A-814552	Sequence 814552,
1328	114	6.2	1042	7	US-11-443-428A-823791	Sequence 823791,	1401	113.5	6.2	3063	7	US-11-443-428A-814554	Sequence 814554,
1329	114	6.2	1094	7	US-11-443-428A-823771	Sequence 823771,	1402	113.5	6.2	3063	7	US-11-443-428A-814555	Sequence 814555,
1330	114	6.2	1094	7	US-11-443-428A-823772	Sequence 823772,	1403	113.5	6.2	3064	7	US-11-582-861-9711	Sequence 9711, Ap
1331	114	6.2	1094	7	US-11-443-428A-823773	Sequence 823773,	1404	113	6.2	150	7	US-11-443-428A-940699	Sequence 940699,
1332	114	6.2	1094	7	US-11-443-428A-823774	Sequence 823774,	1405	113	6.2	212	7	US-11-134-228A-21	Sequence 21, Appl
1333	114	6.2	1094	7	US-11-443-428A-823778	Sequence 823778,	1406	113	6.2	247	7	US-11-443-428A-837386	Sequence 837386,
1334	114	6.2	1094	7	US-11-443-428A-823779	Sequence 823779,	1407	113	6.2	254	6	US-10-558-276-10	Sequence 10, Appl
1335	114	6.2	1094	7	US-11-443-428A-823781	Sequence 823781,	1408	113	6.2	254	7	US-11-518-091-4	Sequence 4, Appli
1336	114	6.2	1094	7	US-11-443-428A-823782	Sequence 823782,	1409	113	6.2	257	6	US-10-558-276-16	Sequence 16, Appl
1337	114	6.2	1094	7	US-11-443-428A-823783	Sequence 823783,	1410	113	6.2	258	6	US-10-558-276-11	Sequence 11, Appl
1338	114	6.2	1094	7	US-11-443-428A-823785	Sequence 823785,	1411	113	6.2	348	7	US-11-241-607-36045	Sequence 36045, A
1339	114	6.2	1094	7	US-11-443-428A-823789	Sequence 823789,	1412	113	6.2	366	7	US-11-443-428A-867850	Sequence 867850,
1340	114	6.2	1094	7	US-11-443-428A-823793	Sequence 823793,	1413	113	6.2	366	7	US-11-443-428A-867857	Sequence 867857,
1341	114	6.2	1114	7	US-11-443-428A-776406	Sequence 776406,	1414	113	6.2	366	7	US-11-443-428A-867858	Sequence 867858,
1342	114	6.2	1336	6	US-10-533-520-4080	Sequence 4080, Ap	1415	113	6.2	366	7	US-11-443-428A-867859	Sequence 867859,
1343	114	6.2	1484	7	US-11-443-428A-776407	Sequence 776407,	1416	113	6.2	448	7	US-11-443-428A-997806	Sequence 997806,

1417	113	6.2	477	6	US-10-419-128-19831	Sequence 19831, A	1490	112	6.1	1338	6	US-10-533-519-1397	Sequence 1397, Ap
1418	113	6.2	529	6	US-10-511-937-2534	Sequence 2534, Ap	1491	112	6.1	1338	6	US-10-533-520-2183	Sequence 2183, Ap
1419	113	6.2	529	6	US-10-529-348-620	Sequence 620, App	1492	112	6.1	1376	7	US-11-582-861-7387	Sequence 7387, Ap
1420	113	6.2	536	7	US-11-443-428A-828073	Sequence 828073, A	1493	112	6.1	1469	7	US-11-443-428A-794979	Sequence 794979, A
1421	113	6.2	536	7	US-11-443-428A-867849	Sequence 867849, A	1494	111.5	6.1	155	7	US-11-486-448-108475	Sequence 108475, A
1422	113	6.2	595	6	US-10-557-444-20	Sequence 20, Appl	1495	111.5	6.1	190	7	US-11-443-428A-940213	Sequence 940213, A
1423	113	6.2	812	7	US-11-443-428A-917030	Sequence 917030, A	1496	111.5	6.1	219	7	US-11-048-197-44	Sequence 44, Appl
1424	113	6.2	824	7	US-11-443-428A-917031	Sequence 917031, A	1497	111.5	6.1	219	7	US-11-048-197-44	Sequence 44, Appl
1425	113	6.2	896	6	US-10-743-643-413	Sequence 413, App	1498	111.5	6.1	231	7	US-11-443-428A-940326	Sequence 940326, A
1426	113	6.2	1352	7	US-11-443-428A-767071	Sequence 767071, A	1499	111.5	6.1	247	7	US-11-486-448-67345	Sequence 67345, A
1427	112.5	6.2	285	6	US-10-703-032-110699	Sequence 110699, A	1500	111.5	6.1	255	6	US-10-558-276-15	Sequence 15, Appl
1428	112.5	6.2	366	7	US-11-486-448-72494	Sequence 72494, A							
1429	112.5	6.2	391	6	US-10-529-348-298	Sequence 298, App							
1430	112.5	6.2	406	6	US-10-553-661-2	Sequence 2, Appl							
1431	112.5	6.2	413	7	US-11-443-428A-825544	Sequence 825544, A							
1432	112.5	6.2	416	6	US-10-419-128-16734	Sequence 16734, A							
1433	112.5	6.2	445	7	US-11-443-428A-829772	Sequence 829772, A							
1434	112.5	6.2	463	6	US-10-219-051B-13283	Sequence 13283, A							
1435	112.5	6.2	477	6	US-10-276-817B-8472	Sequence 8472, Ap							
1436	112.5	6.2	479	6	US-10-419-128-21297	Sequence 21297, A							
1437	112.5	6.2	493	7	US-11-443-428A-1025028	Sequence 1025028, A							
1438	112.5	6.2	530	7	US-11-443-428A-905468	Sequence 905468, A							
1439	112.5	6.2	676	7	US-11-443-428A-837433	Sequence 837433, A							
1440	112.5	6.2	753	6	US-10-276-817B-8999	Sequence 8999, Ap							
1441	112.5	6.2	771	6	US-10-276-817B-14097	Sequence 14097, A							
1442	112.5	6.2	1464	7	US-11-443-428A-905471	Sequence 905471, A							
1443	112.5	6.2	1620	7	US-11-443-428A-905469	Sequence 905469, A							
1444	112.5	6.2	1621	7	US-11-443-428A-905472	Sequence 905472, A							
1445	112.5	6.2	1626	7	US-11-598-148-42	Sequence 42, Appl							
1446	112.5	6.2	1626	7	US-11-584-250-2	Sequence 2, Appl							
1447	112.5	6.2	2388	7	US-11-443-428A-862687	Sequence 862687, A							
1448	112.5	6.2	2668	7	US-11-443-428A-862686	Sequence 862686, A							
1449	112.5	6.2	2703	7	US-11-443-428A-862691	Sequence 862691, A							
1450	112.5	6.2	2844	6	US-10-567-867-372	Sequence 372, App							
1451	112.5	6.2	2844	7	US-11-443-428A-862690	Sequence 862690, A							
1452	112.5	6.2	3023	7	US-11-443-428A-862685	Sequence 862685, A							
1453	112	6.1	211	6	US-10-703-032-110284	Sequence 110284, A							
1454	112	6.1	224	7	US-11-443-428A-939845	Sequence 939845, A							
1455	112	6.1	225	6	US-10-558-276-7	Sequence 7, Appl							
1456	112	6.1	254	6	US-10-219-051B-2116	Sequence 2116, Ap							
1457	112	6.1	314	7	US-11-443-428A-748922	Sequence 748922, A							
1458	112	6.1	324	7	US-11-520-715-47182	Sequence 47182, A							
1459	112	6.1	383	7	US-11-443-428A-917914	Sequence 917914, A							
1460	112	6.1	481	7	US-11-520-715-59250	Sequence 59250, A							
1461	112	6.1	527	7	US-11-443-428A-858486	Sequence 858486, A							
1462	112	6.1	557	7	US-11-520-715-53934	Sequence 53934, A							
1463	112	6.1	590	6	US-10-917-503-18859	Sequence 18859, A							
1464	112	6.1	602	7	US-11-443-428A-858489	Sequence 858489, A							
1465	112	6.1	606	7	US-11-443-428A-811922	Sequence 811922, A							
1466	112	6.1	606	7	US-11-443-428A-811923	Sequence 811923, A							
1467	112	6.1	616	7	US-11-371-354-54993	Sequence 54993, A							
1468	112	6.1	616	7	US-11-371-354-77337	Sequence 77337, A							
1469	112	6.1	616	7	US-11-443-428A-858476	Sequence 858476, A							
1470	112	6.1	616	7	US-11-443-428A-858477	Sequence 858477, A							
1471	112	6.1	616	7	US-11-443-428A-858479	Sequence 858479, A							
1472	112	6.1	616	7	US-11-443-428A-858485	Sequence 858485, A							
1473	112	6.1	616	7	US-11-443-428A-858487	Sequence 858487, A							
1474	112	6.1	616	7	US-11-443-428A-858488	Sequence 858488, A							
1475	112	6.1	679	7	US-11-443-428A-858478	Sequence 858478, A							
1476	112	6.1	691	7	US-11-443-428A-794984	Sequence 794984, A							
1477	112	6.1	699	7	US-11-056-355B-79574	Sequence 79574, A							
1478	112	6.1	702	7	US-11-443-428A-794983	Sequence 794983, A							
1479	112	6.1	830	6	US-10-419-128-22004	Sequence 22004, A							
1480	112	6.1	945	6	US-10-449-902-45439	Sequence 45439, A							
1481	112	6.1	945	7	US-11-443-428A-877981	Sequence 877981, A							
1482	112	6.1	950	6	US-10-419-128-25927	Sequence 25927, A							
1483	112	6.1	957	7	US-11-371-354-65363	Sequence 65363, A							
1484	112	6.1	1021	7	US-11-443-428A-794982	Sequence 794982, A							
1485	112	6.1	1034	6	US-10-669-920-1271	Sequence 1271, Ap							
1486	112	6.1	1138	6	US-10-669-920-1273	Sequence 1273, Ap							
1487	112	6.1	1142	7	US-11-443-428A-882193	Sequence 882193, A							
1488	112	6.1	1270	7	US-11-582-861-7386	Sequence 7386, Ap							
1489	112	6.1	1328	7	US-11-598-148-625	Sequence 625, App							

Search completed: July 30, 2007, 17:02:40

Job time : 115 secs

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 30, 2007, 16:40:58 ; Search time 241 Seconds
(without alignments)
1445.811 Million cell updates/sec

Title: US-10-063-569-64

Perfect score: 1824

Sequence: 1 MQRVAGSCAPGLLLVCLH.....SSWNIPAGFPNPPSPRLQWG 325

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : UniProt_8.4.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1818	99.7	325	1 CF015 HUMAN	O6uxa7 homo sapien
2	1802	98.8	325	2 Q2L6G7 HUMAN	Q2L6g7 homo sapien
3	1789	98.1	347	2 Q1X113_PANTR	Q1x113 pan troglod
4	1591.5	87.3	314	1 CF015_MACMU	Q9bgl9 macaca mula
5	841	46.1	240	2 Q767M7_PIG	Q767m7 sus scrofa
6	681.5	37.4	349	2 Q3KN13_MOUSE	Q3kni3 mus musculus
7	675.5	37.0	349	2 Q8BM15_MOUSE	Q8bm15 mus musculus
8	428	23.5	250	2 Q3KN14_MOUSE	Q3kni4 mus musculus
9	192	10.5	1118	2 Q9VR13_DROME	Q9vrl3 drosophila
10	191	10.5	1159	2 Q61SL3_CABER	Q61sl3 caenorhabdi
11	176	9.6	606	2 Q3BDW0_BRARE	Q3bdw0 brachydanio
12	176	9.6	606	2 Q5K0E1_BRARE	Q5k0e1 brachydanio
13	176	9.6	606	2 Q5OJ87_BRARE	Q5oj87 brachydanio
14	175	9.6	606	2 Q32PN3_BRARE	Q32pn3 brachydanio
15	174	9.5	1613	2 Q8K1P7_RAT	Q8k1p7 rattus norv
16	173	9.5	580	2 Q8BQ54_MOUSE	Q8bq54 m 12 days e
17	173	9.5	587	2 Q7TQL1_MOUSE	Q7tql1 mus musculus
18	173	9.5	590	2 Q6P8K2_MOUSE	Q6p8k2 mus musculus
19	173	9.5	1348	2 Q6PAL9_MOUSE	Q6pal9 mus musculus
20	173	9.5	1613	2 Q3TKt4_MOUSE	Q3tkr4 mus musculus
21	173	9.5	1614	2 Q6AXG8_MOUSE	Q6axg8 m swi/snf r
22	173	9.5	1617	2 Q3TUD7_MOUSE	Q3tud7 mus musculus
23	167.5	9.2	2206	2 Q7PUR9_ANOGA	Q7pur9 anopheles g
24	165.5	9.1	2556	2 Q7KSE8_DROME	Q7kse8 drosophila
25	165.5	9.1	2716	1 QSA_DROME	Q8in94 drosophila
26	165	9.0	930	2 Q25TV8_MYCVN	Q25tv8 mycobacteri
27	164.5	9.0	240	2 Q17QF3_BOVIN	Q17qf3 bos taurus
28	164.5	9.0	431	2 Q2QJ8D4_FRASC	Q2jq8d4 frankia sp.
29	163.5	9.0	239	1 QNO32_BOVIN	Q5e913 bos taurus
30	163.5	9.0	545	2 Q8CGJ5_MOUSE	Q8cgj5 mus musculus
31	163.5	9.0	843	2 Q4W7T7_9CRUS	Q4w7t7 moina macro

32	163	8.9	1647	1	SMCA4_HUMAN	P51532 h probable
33	163	8.9	1679	2	Q9HBD4_HUMAN	Q9hbd4 homo sapien
34	161.5	8.9	420	2	Q1D3Z1_MYXXA	Q1d3z1 myxococcus
35	159.5	8.7	297	2	Q4P2F5_USTWA	Q4p2f5 ustilago ma
36	159.5	8.7	1268	2	Q5Z229_NOCFA	Q5z229 nocardia fa
37	159	8.7	7192	2	Q5Z1N5_NOCFA	Q5z1n5 nocardia fa
38	157	8.6	1241	2	Q3TUE2_MOUSE	Q3tue2 mus musculus
39	157	8.6	1372	1	CO1A2_MOUSE	Q01a19 mus musculus
40	157	8.6	1372	2	Q3TX57_MOUSE	Q3tx57 m osteoclas
41	157	8.6	1372	2	Q3TU64_MOUSE	Q3tu64 mus musculus
42	156.5	8.6	1164	2	Q59FZ6_HUMAN	Q59fz6 homo sapien
43	155.5	8.5	241	1	QNO32_MOUSE	Q8bh93 mus musculus
44	155.5	8.5	1175	2	P70200_MOUSE	P70200 mus musculus
45	155	8.5	585	2	Q41935_MHV68	Q41935 murid herpe
46	155	8.5	1062	2	Q2J728_FRASC	Q2j728 frankia sp.
47	154	8.4	244	1	QNO32_MACFA	Q4r3b7 macaca fasc
48	154	8.4	514	2	Q3WBL7_9ACTO	Q3wbl7 frankia sp.
49	154	8.4	2304	2	Q4IR34_GIBZE	Q4ir34 gibberella
50	153.5	8.4	244	1	QNO32_HUMAN	Q8ndc0 homo sapien
51	153.5	8.4	244	1	QNO32_PONPY	Q8r623 pongo pygma
52	153.5	8.4	464	1	SF3A2_HUMAN	Q15428 homo sapien
53	153.5	8.4	571	2	Q4V873_XENLA	Q4v873 xenopus lae
54	152.5	8.4	571	2	Q3B8L3_XENLA	Q3b8l3 xenopus lae
55	152.5	8.4	571	2	Q5XHK1_XENLA	Q5xhk1 xenopus lae
56	152.5	8.4	784	2	Q9XKL5_STRCO	Q9xkl5 streptomyce
57	152.5	8.4	1193	2	Q6ING0_ARATH	Q6ing0 arabidopsis
58	152.5	8.4	1492	2	Q3VXS2_9ACTO	Q3vxs2 frankia sp.
59	152.5	8.4	1600	2	Q4VQ79_XENLA	Q4vq79 xenopus lae
60	152.5	8.4	1600	2	Q5MMR9_XENLA	Q5mmr9 xenopus lae
61	152	8.3	604	2	Q9L252_STRCO	Q9l252 streptomyce
62	151.5	8.3	288	2	Q35845_MOUSE	Q35845 mus musculus
63	151.5	8.3	716	2	Q47LM4_THEFY	Q47lm4 thermobifid
64	151.5	8.3	888	2	Q73SS5_MYCPA	Q73ss5 mycobacteri
65	150.5	8.3	255	2	Q8YZQ0_ANASP	Q8yzq0 anabaena sp
66	150.5	8.3	431	1	UL61_HGWA	P16818 human cytom
67	150.5	8.3	1132	2	Q17KL3_AEDAE	Q17kl3 aedes aegyp
68	150.5	8.3	2136	2	Q1D888_MYXXA	Q1d888 myxococcus
69	150	8.2	680	1	COAA1_HUMAN	Q03692 homo sapien
70	150	8.2	903	2	Q82HF3_STRAW	Q82hf3 streptomyce
71	150	8.2	966	1	F1BAl_PETMA	P02674 petromyzon
72	150	8.2	1579	2	Q4TS74_TETNG	Q4ts74 tetraodon n
73	149.5	8.2	446	2	Q55PF7_CRYNE	Q55pf7 cryptococcu
74	149.5	8.2	446	2	Q5KE03_CRYNE	Q5ke03 cryptococcu
75	149.5	8.2	1097	2	Q17BF4_AEDAE	Q17bf4 aedes aegyp
76	149	8.2	664	2	Q6CDQ5_YARLI	Q6cdq5 yarrowia li
77	148.5	8.1	508	2	Q93447_ORYLA	Q93447 oryzias lat
78	148	8.1	562	2	Q803N3_BRARE	Q803n3 brachydanio
79	148	8.1	740	2	Q8NC88_HUMAN	Q8nc88 homo sapien
80	148	8.1	1630	2	Q90753_CHICK	Q90753 gallus gall
81	148	8.1	1683	2	Q4T3E8_TETNG	Q4t3e8 tetraodon n
82	147.5	8.1	278	2	Q9NW25_HUMAN	Q9nw25 homo sapien
83	147.5	8.1	388	1	SSBF3_HUMAN	Q9bwa4 homo sapien
84	147.5	8.1	388	1	SSBF3_MOUSE	Q9bwa4 mus musculus
85	147.5	8.1	388	1	STG51_HUMAN	Q8tg51 homo sapien
86	147.5	8.1	425	2	Q4A3V6_PHYDA	Q4a3v6 physocitre
87	147.5	8.1	926	2	Q9W3G1_DROME	Q9w3g1 drosophila
88	147.5	8.1	1272	2	Q4IQS4_GIBZE	Q4iqs4 gibberella
89	147	8.1	461	2	Q8AX89_FUGRU	Q8ax89 fugu rubrip
90	147	8.1	544	2	Q744Q9_MYCPA	Q744q9 mycobacteri
91	147	8.1	617	2	Q5B4Q0_EMENI	Q5b4q0 emericeila
92	147	8.1	812	2	Q6P181_HUMAN	Q6p181 homo sapien
93	147	8.1	821	2	Q96JM3_HUMAN	Q96jm3 homo sapien
94	146.5	8.0	322	2	Q6P4M2_XENTR	Q6p4m2 xenopus tro
95	146.5	8.0	665	2	Q2KXG4_WAGGR	Q2kxg4 magnaporthe
96	146.5	8.0	1046	1	IF2_STRAM	Q82k53 streptomyce
97	146.5	8.0	1175	2	Q35126_MOUSE	Q35126 mus musculus
98	146	8.0	419	1	LWA_HYD8C	Q50560 hydractinia
99	146	8.0	485	2	Q804G3_BRARE	Q804g3 brachydanio
100	146	8.0	1095	2	Q3WAD4_9ACTO	Q3wad4 frankia sp.
101	146	8.0	1344	2	Q93419_CHICK	Q93419 gallus gall
102	146	8.0	1366	2	Q7Z5S6_HUMAN	Q7z5s6 homo sapien
103	146	8.0	1366	2	Q15177_HUMAN	Q15177 homo sapien
104	146	8.0	1372	1	CO1A2_RAT	P02466 rattus norv

105	145.5	8.0	950	2	Q9VE45_DROME	Q9ve45 drosophila	178	139.5	7.6	1449	2	Q802B5_XENLA	Q802b5 xenopus lae
106	145.5	8.0	1388	1	COFAL1_HUMAN	P39059 homo sapien	179	139.5	7.6	1758	2	Q8CHN9_RAT	Q8chn9 rattus norv
107	145.5	8.0	3157	2	Q5KXK0_CRYNE	Q5knk0 cryptococcu	180	139.5	7.6	1902	2	Q925Q1_MOUSE	Q925q1 mus musculu
108	145	7.9	407	2	Q29NN2_DROPS	Q29nn2 drosophila	181	139.5	7.6	1902	2	Q640Q1_MOUSE	Q640q1 mus musculu
109	145	7.9	885	2	Q2HHC9_CHAGB	Q2hnc9 chaetomium	182	139	7.6	311	2	Q6P2L2_MOUSE	Q6p2l2 mus musculu
110	145	7.9	944	2	Q5XGE8_XENTR	Q5xge8 xenopus tro	183	139	7.6	459	2	Q54TI7_DICDI	Q54ti7 dictyosteli
111	145	7.9	1096	2	Q2GMP5_CHAGB	Q2gmp5 chaetomium	184	139	7.6	551	2	Q2VPQ6_MOUSE	Q2vpq6 mus musculu
112	145	7.9	1353	2	Q5UGI1_CRYNE	Q5ugl1 cryptococcu	185	139	7.6	674	1	COAA1_CHICK	P08125 gallus gall
113	145	7.9	1493	2	Q5KHY3_CRYNE	Q5khy3 cryptococcu	186	139	7.6	714	2	Q5TIU7_HUMAN	Q5tiu7 homo sapien
114	145	7.9	1493	2	Q3E9M3_ARATH	Q3e9m3 arabidopsis	187	139	7.6	748	2	Q3U0V1_MOUSE	Q3u0v1 mus musculu
115	144.5	7.9	540	1	MAVS_HUMAN	Q7z434 h mitochond	188	139	7.6	770	2	Q7WHU6_BORBR	Q7whu6 borderella
116	144.5	7.9	540	2	Q2HWT5_HUMAN	Q2hwt5 homo sapien	189	139	7.6	1361	2	Q4P3V7_USTWA	Q4p3v7 ustilago ma
117	144.5	7.9	540	2	Q2HWT5_NEUCR	Q7sg28 neurospora	190	139	7.6	1366	1	COIA2_CANFA	Q46392 canis fami
118	144.5	7.9	1903	2	Q29FV7_DROPS	Q29fv7 drosophila	191	139	7.6	1701	2	Q61DV2_CAEBR	Q61dv2 caenorhabdi
119	144	7.9	364	2	Q5TS42_ANOGA	Q5ts42 anopheles g	192	139	7.6	2157	1	BAT2_HUMAN	P48634 homo sapien
120	144	7.9	1185	1	ATN1_HUMAN	Q54259 homo sapien	193	138.5	7.6	299	2	Q3U5B9_MOUSE	Q3u5b9 mus musculu
121	144	7.9	1551	2	Q1BCG9_9MYCO	Q1bcg9 mycobacteri	194	138.5	7.6	361	2	Q3B7C9_RAT	Q3b7c9 rattus norv
122	144	7.9	1617	2	Q1T896_9MYCO	Q1t896 mycobacteri	195	138.5	7.6	446	2	Q6PH33_BRARE	Q6ph33 brachydanio
123	143.5	7.9	361	1	SSBP3_RAT	Q9r050 rattus norv	196	138.5	7.6	495	2	Q5SVZ3_HUMAN	Q5svz3 homo sapien
124	143.5	7.9	433	2	Q1EBX4_DROME	Q1ebx4 drosophila	197	138.5	7.6	888	2	Q90796_CHICK	Q90796 gallus gall
125	143.5	7.9	443	2	Q28243_CANFA	Q28243 canis fami	198	138.5	7.6	946	2	Q1U0Y6_9MYCO	Q1u0y6 mycobacteri
126	143.5	7.9	525	2	Q52342_NOCFA	Q5z342 nocardia fa	199	138.5	7.6	977	2	Q4SEP8_TETNG	Q4sep8 tetraodon n
127	143.5	7.9	631	2	Q6ZWK2_HUMAN	Q6zwk2 homo sapien	200	138.5	7.6	1208	2	Q96TA9_HUMAN	Q96ta9 homo sapien
128	143.5	7.9	844	2	Q7Q3C5_ANOGA	Q7q3c5 anopheles g	201	138.5	7.6	1374	2	Q4LE49_HUMAN	Q4le49 homo sapien
129	143.5	7.9	1001	2	Q4S0G2_TETNG	Q4s0g2 tetraodon n	202	138.5	7.6	2285	1	ARIIA1_HUMAN	Q14497 h at-rich i
130	143.5	7.9	1494	2	Q67FY1_HUMAN	Q67fy1 homo sapien	203	138	7.6	387	2	Q7ZX94_XENLA	Q7zx94 xenopus lae
131	143.5	7.9	1499	2	Q86UU0_HUMAN	Q86uu0 homo sapien	204	138	7.6	590	2	Q3VXJ2_XACTO	Q3vxj2 frankia sp.
132	143	7.8	533	2	Q2TWR4_ASPOR	Q2twr4 aspergillus	205	138	7.6	636	2	Q7SE15_NEUCR	Q7se15 neurospora
133	143	7.8	1186	1	ATN1_PANTR	Q5is70 pan troglod	206	138	7.6	641	2	Q17740_CAEBL	Q17740 caenorhabdi
134	143	7.8	1249	2	Q5SP95_CRYNE	Q5sp95 cryptococcu	207	138	7.6	647	2	Q29FK6_DROPS	Q29fk6 drosophila
135	143	7.8	1499	2	Q59IP2_PIG	Q59ip2 sus scrofa	208	138	7.6	727	2	Q35LJ9_9BRAD	Q35lj9 bradyrhizob
136	142.5	7.8	391	2	Q801Q3_XENLA	Q801q3 xenopus lae	209	138	7.6	754	2	Q4HM09_GIBZE	Q4hm09 gibberella
137	142.5	7.8	492	1	FOXD2_MOUSE	Q15392 mus musculu	210	138	7.6	913	2	Q8K291_MOUSE	Q8k291 mus musculu
138	142.5	7.8	873	2	Q59G71_HUMAN	Q59g71 homo sapien	211	138	7.6	934	2	Q8VCD2_MOUSE	Q8vcd2 mus musculu
139	142.5	7.8	1735	2	Q4ZG71_HUMAN	Q4zg71 homo sapien	212	138	7.6	967	1	SPTS_DEBHA	Q6bz90 debaryomyce
140	142	7.8	672	2	Q613K3_CAEBR	Q613k3 caenorhabdi	213	138	7.6	1011	2	Q1IIT3_ACIBL	Q1iit3 acidobacter
141	142	7.8	773	2	Q95TR3_DROME	Q95tr3 drosophila	214	138	7.6	1022	2	Q6IP11_XENLA	Q6ip11 xenopus lae
142	142	7.8	1215	2	Q9W2K4_DROME	Q9w2k4 drosophila	215	138	7.6	1449	2	Q4RY48_TETNG	Q4ry48 tetraodon n
143	142	7.8	1242	2	Q5K561_CRYNE	Q5ke61 cryptococcu	216	138	7.6	2160	1	BAT2_MACMU	Q5tm26 macaca mula
144	142	7.8	1510	2	Q7XWS7_ORYSA	Q7xws7 oryza sativ	217	137.5	7.5	358	2	Q28CH5_XENTR	Q28ch5 xenopus tro
145	141.5	7.8	485	2	Q9UV68_NEOPA	Q9uv68 neocallimas	218	137.5	7.5	388	2	Q2UAI0_ASPOR	Q2uai0 aspergillus
146	141.5	7.8	571	2	Q1L8T6_BRARE	Q1l8t6 brachydanio	219	137.5	7.5	566	2	Q28GA5_XENTR	Q28ga5 xenopus tro
147	141.5	7.8	576	2	Q7SXM3_BRARE	Q7sxm3 brachydanio	220	137.5	7.5	573	2	Q5XGB1_XENTR	Q5xgb1 xenopus tro
148	141.5	7.8	838	2	Q8T5L5_ANOGA	Q8t5l5 anopheles g	221	137.5	7.5	660	1	YHL1_EBV	P03181 epstein-bar
149	141.5	7.8	838	2	Q7PUU9_ANOGA	Q7puu9 anopheles g	222	137.5	7.5	660	2	Q777A3_EBVG	Q777a3 epstein-bar
150	141.5	7.8	1006	2	Q9LWQ1_ARATH	Q9lmq1 arabidopsis	223	137.5	7.5	1270	2	Q172C8_REDAE	Q172c8 ades aegypt
151	141.5	7.8	1627	2	Q7ZSY3_BRARE	Q7zsy3 brachydanio	224	137	7.5	277	2	Q8BM12_MOUSE	Q8bmy2 mus musculu
152	141	7.7	362	2	Q9VC23_DROME	Q9vc23 drosophila	225	137	7.5	368	2	Q5TG50_HUMAN	Q5tg50 homo sapien
153	141	7.7	793	2	Q13876_HUMAN	Q13876 homo sapien	226	137	7.5	450	2	Q801J9_FUGRU	Q801j9 figu rubrip
154	141	7.7	815	1	PYGO_DROME	Q9v9w8 drosophila	227	137	7.5	507	2	Q1RU53_MEDTR	Q1ru53 medicago tr
155	141	7.7	888	2	Q8CCZ8_MOUSE	Q8ccz8 mus musculu	228	137	7.5	805	2	Q6CX81_KLULA	Q6cxe1 kluyveromyc
156	141	7.7	1140	2	Q61434_MOUSE	Q61434 mus musculu	229	137	7.5	936	2	Q8CGZ0_MOUSE	Q8cgz0 mus musculu
157	141	7.7	1191	2	Q86V38_HUMAN	Q86v38 homo sapien	230	137	7.5	1126	2	Q19371_CAEBL	Q19371 caenorhabdi
158	141	7.7	1315	2	Q6PIY4_MOUSE	Q6piy4 mus musculu	231	137	7.5	1688	2	Q597P9_CANFA	Q597p9 canis fami
159	141	7.7	1315	2	Q6ZNK9_MOUSE	Q6znk9 mus musculu	232	136.5	7.5	489	2	Q6PHB5_MOUSE	Q6phb5 mus musculu
160	141	7.7	1366	1	CO1A2_HUMAN	P08123 homo sapien	233	136.5	7.5	920	2	Q1U3A1_9MYCO	Q1u3a1 mycobacteri
161	141	7.7	1774	1	CO1A1_MOUSE	Q18465 hirudo medi	234	136.5	7.5	920	2	Q1TEJ5_9MYCO	Q1tej5 mycobacteri
162	140.5	7.7	889	2	Q9FZNE_STRCO	Q9fzns streptomyce	235	136.5	7.5	920	2	Q1BA94_9MYCO	Q1ba94 mycobacteri
163	140.5	7.7	1033	1	IF2_STRCO	Q8cj38 streptomyce	236	136.5	7.5	1060	2	Q4SK66_TETNG	Q4sk66 tetraodon n
164	140.5	7.7	1333	2	Q4SK58_TETNG	Q4sk58 tetraodon n	237	136.5	7.5	1562	2	Q6GQ87_MOUSE	Q6gq87 mus musculu
165	140.5	7.7	1723	1	TNC68_HUMAN	Q9upg9 homo sapien	238	136.5	7.5	1564	2	Q23T82_TETTH	Q23t82 tetrahymena
166	140.5	7.7	1880	2	O18465_HIRME	Q18465 hirudo medi	239	136.5	7.5	1669	1	CO4A1_MOUSE	P02463 mus musculu
167	140	7.7	293	2	Q5T6S6_HUMAN	Q5t6s6 homo sapien	240	136.5	7.5	1669	2	Q3UJ57_MOUSE	Q3uj57 mus musculu
168	140	7.7	796	2	Q6NRE2_XENLA	Q6nre2 xenopus lae	241	136.5	7.5	1669	2	Q3UHU4_MOUSE	Q3uhj4 m cdna, rik
169	140	7.7	924	2	Q6ZWJ0_HUMAN	Q6zwj0 homo sapien	242	136.5	7.5	2161	1	BAT2_RAT	Q6mj48 rattus norv
170	140	7.7	933	2	Q68F05_XENLA	Q68f05 xenopus lae	243	136	7.5	357	2	Q503T8_BRARE	Q503t8 brachydanio
171	140	7.7	1447	2	Q6P4U1_BRARE	Q6p4u1 brachydanio	244	136	7.5	484	2	Q45V74_RAT	Q45v74 rattus norv
172	140	7.7	1447	2	Q6UIJ5_BRARE	Q6uij5 brachydanio	245	136	7.5	526	2	Q2II58_ANADE	Q2ii58 anaeromyxob
173	139.5	7.6	89	2	Q7KYZ4_HUMAN	Q7kyz4 homo sapien	246	136	7.5	526	2	Q804G4_BRARE	Q804g4 brachydanio
174	139.5	7.6	97	2	Q16409_HUMAN	Q16409 homo sapien	247	136	7.5	623	2	Q2HNRI_CANFA	Q2hnri canis fami
175	139.5	7.6	867	2	Q4I4C1_GIBZE	Q4i4c1 gibberella	248	136	7.5	748	2	Q67W44_ORYSA	Q67w44 oryza sativ
176	139.5	7.6	1088	2	Q4P2J6_USTWA	Q4p2j6 ustilago ma	249	136	7.5	907	2	Q26312_STRPU	Q26312 strongyloce
177	139.5	7.6	1183	1	ATN1_RAT	P54258 rattus norv	250	136	7.5	943	2	Q8BK12_MOUSE	Q8bk12 mus musculu

251	136	7.5	1049	1	CO3A1_BOVIN	P04258	bos taurus	324	133	7.3	1502	2	Q59GR4_HUMAN	Q59gr4	homo sapien
252	136	7.5	1463	1	CO3A1_RAT	P13941	rattus norv	325	133	7.3	1617	2	Q6MGB2_RAT	Q6mgb2	rattus norv
253	136	7.5	1496	1	CO3A2_HUMAN	P05997	homo sapien	326	133	7.3	1690	1	CO4A4_HUMAN	P53420	homo sapien
254	136	7.5	1496	2	Q53WR4_HUMAN	P05997	homo sapien	327	133	7.3	1690	1	CO4A4_HUMAN	Q53wr1	homo sapien
255	136	7.5	1535	2	Q6NVE4_MOUSE	Q6nve4	mus musculus	328	133	7.3	1796	2	Q5DJT4_MOUSE	Q5dtj4	mus musculus
256	136	7.5	1644	2	Q4T2V9_TETNG	Q4t2v9	tetraodon n	329	133	7.3	1860	2	Q8IZC6_HUMAN	Q8izc6	homo sapien
257	136	7.5	1669	2	Q5VWF6_HUMAN	Q5vwf6	homo sapien	330	133	7.3	2158	1	BAT2_MOUSE	Q7tsc1	mus musculus
258	136	7.5	1752	2	Q07265_STRPU	Q07265	strongyloce	331	132.5	7.3	81	2	Q7KYY8_HUMAN	Q7kyy8	homo sapien
259	136	7.5	1884	2	Q7S737_NEUCR	Q7s737	neuropora	332	132.5	7.3	469	2	Q2IKI5_ANADE	Q2iki5	anaeromyxob
260	136	7.5	2030	2	Q860P5_XENLA	Q860p5	xenopus lae	333	132.5	7.3	494	2	Q5F3Q7_CHICK	Q5f3q7	gallus gall
261	135.5	7.4	349	2	Q8TEE4_HUMAN	Q8tee4	homo sapien	334	132.5	7.3	497	1	FOX2_HUMAN	Q60548	homo sapien
262	135.5	7.4	483	2	Q7T391_BRARE	Q7t391	brachydanio	335	132.5	7.3	605	2	Q801J8_SALSA	Q801j8	salmo salar
263	135.5	7.4	497	2	Q5I4J1_PAROL	Q5i4j1	paralichthy	336	132.5	7.3	704	1	SYN1_RAT	P09951	rattus norv
264	135.5	7.4	551	1	EPN1_HUMAN	Q9y613	homo sapien	337	132.5	7.3	731	2	Q1L863_BRARE	Q1l863	brachydanio
265	135.5	7.4	595	2	Q7XJ24_ORYSA	Q7xj24	oryza sativ	338	132.5	7.3	877	2	Q8MR22_DROME	Q8mr22	drosophila
266	135.5	7.4	1069	2	Q69140_EBVG	Q69140	epstein-bar	339	132.5	7.3	1184	2	Q6C414_YARLI	Q6c414	yarrowia li
267	135.5	7.4	1447	2	Q9IB91_XENLA	Q9ib91	xenopus lae	340	132.5	7.3	1204	2	Q8J0E5_YARLI	Q8j0e5	yarrowia li
268	135.5	7.4	2236	1	AR11B_HUMAN	Q8ntd5	homo sapien	341	132.5	7.3	1474	2	Q67FY0_ERARE	Q67fy0	brachydanio
269	135	7.4	172	2	Q5EBP1_MOUSE	Q5ebp1	mus musculus	342	132.5	7.3	2061	2	Q9VUH9_DROME	Q9vuh9	drosophila
270	135	7.4	416	2	Q9VT88_DROME	Q9vt88	drosophila	343	132.5	7.3	2103	2	Q7KUL0_DROME	Q7kul0	drosophila
271	135	7.4	493	2	Q2J6C4_FRASC	Q2j6c4	frankia sp.	344	132.5	7.3	3691	2	Q4S201_TETNG	Q4s201	tetraodon n
272	135	7.4	840	2	Q5U0Y6_DROME	Q5u0y6	drosophila	345	132	7.2	325	2	Q4KXEL_OPEL	Q4kxel	lophopyrum
273	135	7.4	969	1	IF2_NOCPA	Q5y8c6	nocardia fa	346	132	7.2	652	1	GGN_HUMAN	Q86u5	homo sapien
274	135	7.4	969	2	Q4VED6_MOUSE	Q4vdb6	mus musculus	347	132	7.2	689	2	Q6ND96_RHOPA	Q6nd96	rhodopseudo
275	135	7.4	1003	2	Q3TY92_MOUSE	Q3ty92	mus musculus	348	132	7.2	700	2	Q8TG00_ASPFU	Q8tg00	aspergillus
276	135	7.4	1070	2	Q96JG5_HUMAN	Q96jg5	homo sapien	349	132	7.2	788	2	Q7Q6Z2_ANOGA	Q7q6z2	anopheles g
277	135	7.4	1070	2	Q9APM8_MYXXA	Q9apm8	myxococcus	350	132	7.2	1501	2	Q172C7_AEDAE	Q172c7	aedes aegypt
278	135	7.4	1072	2	Q1DAM6_MYXXA	Q1dam6	myxococcus	351	132	7.2	1900	2	Q3UHC0_MOUSE	Q3uhc0	mus musculus
279	134.5	7.4	376	2	Q4SD35_TETNG	Q4sd35	tetraodon n	352	132	7.2	2161	1	SHAN1_HUMAN	Q9y566	homo sapien
280	134.5	7.4	589	2	Q18756_CABEL	Q18756	caenorhabdi	353	131.5	7.2	309	2	Q4VAY3_HUMAN	Q4vay3	homo sapien
281	134.5	7.4	1155	2	Q25U51_MYCVN	Q25u51	mycobacteri	354	131.5	7.2	335	2	Q5SJA5_THET8	Q5sja5	thermus t
282	134.5	7.4	1193	2	Q9VQ94_DROME	Q9vq94	drosophila	355	131.5	7.2	375	2	Q5TMG9_ANOGA	Q5tmg9	anopheles g
283	134.5	7.4	1259	2	Q276L5_MYCFV	Q276l5	mycobacteri	356	131.5	7.2	404	2	Q8SX96_DROME	Q8sx96	drosophila
284	134.5	7.4	1262	1	CO3A1_CHICK	P12105	gallus gall	357	131.5	7.2	531	2	Q8T8Q4_DROME	Q8t8q4	drosophila
285	134.5	7.4	1350	2	Q3UTT4_MOUSE	Q3utt4	mus musculus	358	131.5	7.2	653	2	Q5BCR0_EMENI	Q5bcr0	emeritella
286	134.5	7.4	1477	2	Q3TVR2_MOUSE	Q3tvr2	mus musculus	359	131.5	7.2	690	2	Q7J3T9_MYCPA	Q7j3t9	mycobacteri
287	134.5	7.4	1497	2	Q3UHK7_MOUSE	Q3uhk7	mus musculus	360	131.5	7.2	706	2	Q41972_MHV68	Q41972	murid herpe
288	134.5	7.4	1497	2	Q7TMS0_MOUSE	Q7tms0	mus musculus	361	131.5	7.2	707	1	FUBP2_HUMAN	Q92945	homo sapien
289	134.5	7.4	1497	2	Q3VLJ6_MOUSE	Q3vlj6	mus musculus	362	131.5	7.2	727	2	Q41973_MHV68	Q41973	murid herpe
290	134.5	7.4	1497	2	Q61431_MOUSE	Q61431	mus musculus	363	131.5	7.2	774	2	Q41971_MHV68	Q41971	murid herpe
291	134.5	7.4	1497	2	Q3U962_MOUSE	Q3u962	m bone marr	364	131.5	7.2	869	2	Q2UEV8_ASPOR	Q2uev8	aspergillus
292	134.5	7.4	1740	2	Q6DLU9_PIG	Q6dlu9	sus scrofa	365	131.5	7.2	946	2	Q6COS3_YARLI	Q6cos3	yarrowia li
293	134.5	7.4	1804	1	COBA1_MOUSE	Q61245	mus musculus	366	131.5	7.2	1002	2	Q5KFG1_CRYNE	Q5kfg1	cryptococcu
294	134	7.3	262	2	Q90713_CHICK	Q90713	gallus gall	367	131.5	7.2	1099	2	Q8W362_ORYSA	Q8w362	oryza sativ
295	134	7.3	345	2	Q4REE4_TETNG	Q4ree4	tetraodon n	368	131.5	7.2	1286	2	Q3TST6_MOUSE	Q3tst6	mus musculus
296	134	7.3	368	1	S8BP3_CHICK	Q98948	gallus gall	369	131.5	7.2	1594	2	Q4RXU2_TETNG	Q4rxu2	tetraodon n
297	134	7.3	403	2	P91736_HYDNA	P91736	hydra magni	370	131.5	7.2	1740	2	Q9HCU0_HUMAN	Q9hcj0	homo sapien
298	134	7.3	650	2	FUBP2_ASPOR	Q99pf5	aspergillus	371	131.5	7.2	1804	2	Q8WRQ7_DROME	Q8wrq7	drosophila
299	134	7.3	721	1	FUBP2_RAT	Q3uuu1	mus musculus	372	131.5	7.2	4001	2	Q9VCA8_DROME	Q9vca8	drosophila
300	134	7.3	771	2	Q3UUU1_MOUSE	Q3uuu1	mus musculus	373	131.5	7.2	4001	2	Q866V8_9EUTH	Q866v8	manis sp. p
301	134	7.3	1017	2	Q59HB5_HUMAN	Q59hb5	homo sapien	374	131	7.2	250	2	PRB2_HUMAN	P02812	homo sapien
302	134	7.3	1691	2	Q9RSQ2_MOUSE	Q9rsq2	mus musculus	375	131	7.2	382	1	Q6AXT8_RAT	Q6axt8	rattus norv
303	134	7.3	1691	2	Q63ZW6_MOUSE	Q63zw6	mus musculus	376	131	7.2	471	2	Q77087_9ANNE	Q77087	alvinella p
304	134	7.3	1736	1	COBA2_MOUSE	Q64739	mus musculus	377	131	7.2	890	2	Q77087_9ANNE	Q77087	alvinella p
305	134	7.3	1806	1	COBA1_HUMAN	P12107	homo sapien	378	131	7.2	920	2	Q5JUN9_HUMAN	Q5jun9	homo sapien
306	134	7.3	1806	2	Q5VT31_HUMAN	Q5vt31	homo sapien	379	131	7.2	1044	2	Q40U11_KINRA	Q40u11	kineococcus
307	134	7.3	4027	2	Q512R0_CHLIN	Q5i2r0	chlamydomon	380	131	7.2	1064	2	Q5JSH9_HUMAN	Q5jsh9	homo sapien
308	133.5	7.3	445	1	SM50_STRPU	P11994	strongyloce	381	131	7.2	1067	1	ZIM10_HUMAN	Q9uij6	homo sapien
309	133.5	7.3	447	2	Q323U8_DROPS	Q29u8	drosophila	382	131	7.2	1113	2	Q6WEQ5_ARALY	Q6weq5	arabidopsis
310	133.5	7.3	463	2	Q97640_FELCA	Q97640	felis silve	383	131	7.2	1453	1	CO1A1_CHICK	P02457	gallus gall
311	133.5	7.3	670	2	Q9SIV5_ARATH	Q9siv5	arabidopsis	384	131	7.2	1578	2	Q2KG58_MAGGR	Q2kg58	magnaporthe
312	133.5	7.3	783	2	Q91331_9GAMA	Q91331	cercopithec	385	131	7.2	1693	2	Q5STP6_HUMAN	Q5stp6	homo sapien
313	133.5	7.3	1004	1	IF2_CORGL	Q8np40	corynebacte	386	131	7.2	2966	2	Q29FY0_DROPS	Q29fy0	drosophila
314	133.5	7.3	1078	2	Q337J6_ORYSA	Q337j6	oryza sativ	387	130.5	7.2	475	1	SF3A2_MOUSE	Q62203	mus musculus
315	133.5	7.3	1449	2	Q640B2_XENTR	Q640b2	xenopus tro	388	130.5	7.2	589	2	Q99LL6_MOUSE	Q99ll6	mus musculus
316	133	7.3	241	2	Q29EW1_DROPS	Q29ew1	drosophila	389	130.5	7.2	749	2	Q9BIW6_DROME	Q9biw6	drosophila
317	133	7.3	285	2	Q75942_HUMAN	Q75942	homo sapien	390	130.5	7.2	802	2	Q7PYX1_ANOGA	Q7pyx1	anopheles g
318	133	7.3	529	2	Q2GXZ0_CHAGB	Q2gxz0	chaetomium	391	130.5	7.2	900	2	Q7JFB9_FRASC	Q7jfb9	frankia sp.
319	133	7.3	789	2	Q2HTV2_CHAGB	Q2htv2	chaetomium	392	130.5	7.2	919	1	ANDR_HUMAN	P10275	homo sapien
320	133	7.3	1126	2	Q5YNA3_NOCPA	Q5yna3	nocardia fa	393	130.5	7.2	1002	2	Q5SQQ5_CRYNE	Q5sqqs	cryptococcu
321	133	7.3	1226	2	Q5TX03_ANOGA	Q5tx03	anopheles g	394	130.5	7.2	1086	2	Q172C6_AEDAE	Q172c6	aedes aegypt
322	133	7.3	1324	2	Q53RW9_HUMAN	Q53rw9	homo sapien	395	130.5	7.2	1453	1	CO1A1_MOUSE	P11087	mus musculus
323	133	7.3	1348	2	Q29CP6_DROPS	Q29cp6	drosophila	396	130.5	7.2	1475	2	Q4S5M8_TETNG	Q4s5m8	tetraodon n

397	130.5	7.2	1669	1	CO4A1_HUMAN	P02462	homo sapien	128.5	7.0	906	2	Q9UN21_HUMAN	Q9un21	homo sapien
398	130.5	7.2	1735	1	TEN51_HUMAN	Q9h510	homo sapien	128.5	7.0	922	1	O44367_MYTED	O44367	mytilus edu
399	130.5	7.2	1758	2	Q61315_CAEER	Q61315	caenorhabdi	128.5	7.0	1003	2	MBD6_HUMAN	Q96dn6	homo sapien
400	130.5	7.2	1838	1	CO5A1_MOUSE	Q88207	mus musculus	128.5	7.0	1003	2	Q6P0P0_HUMAN	Q6P0P0	homo sapien
401	130	7.1	417	2	Q52PC7_9DELT	Q52pc7	angilococcus	128.5	7.0	1254	2	Q7SYD5_BRARE	Q7syd5	brachydanio
402	130	7.1	597	2	Q58MY1_9CAUD	Q58my1	cyanophage	128.5	7.0	1415	2	Q9H7M7_HUMAN	Q9h7m7	homo sapien
403	130	7.1	611	2	Q3WIM0_9ACTO	Q3wim0	frankia sp.	128.5	7.0	1797	1	COEA1_MOUSE	Q80x19	mus musculus
404	130	7.1	891	2	Q80VS8_MOUSE	Q80vs8	mus musculus	128.5	7.0	1992	2	Q55BR0_DICDI	Q55br0	dictyosteli
405	130	7.1	935	2	Q6AWJ6_DROME	Q6awj6	drosofila	128	7.0	277	2	Q6SES1_HUMAN	Q6ses1	homo sapien
406	130	7.1	955	1	IF2_THFY	Q47rv1	thermobifid	128	7.0	400	2	Q8JGT1_BRARE	Q8jgt1	brachydanio
407	130	7.1	1414	2	Q26634_STRPU	Q26634	strongyloce	128	7.0	400	2	Q6NWB3_BRARE	Q6nwb3	brachydanio
408	130	7.1	1445	2	Q93251_RANCA	Q93251	rana catesb	128	7.0	400	2	Q97643_LAMGL	Q97643	lama glama
409	130	7.1	1450	2	Q9YIB4_CINPEY	Q9yib4	cynops pyrr	128	7.0	422	2	Q6PIX2_HUMAN	Q6pix2	homo sapien
410	130	7.1	1650	2	Q5JP94_HUMAN	Q5jp94	homo sapien	128	7.0	591	2	Q96HCO_HUMAN	Q96hc0	homo sapien
411	130	7.1	1658	2	Q59GD4_HUMAN	Q59gd4	homo sapien	128	7.0	624	2	Q3AIY3_SYNSC	Q3aiy3	synecococc
412	130	7.1	1693	2	Q5SUI8_HUMAN	Q5sui8	homo sapien	128	7.0	643	2	Q2GP69_CHAGB	Q2gp69	chaetomium
413	130	7.1	1724	2	Q91019_CABEL	P91019	caenorhabdi	128	7.0	674	1	COA21_BOVIN	Q9206	bos taurus
414	130	7.1	1736	1	COBA2_HUMAN	P13942	homo sapien	128	7.0	686	2	Q1LUA9_BRARE	Q1lua9	brachydanio
415	130	7.1	1745	1	CO5A3_HUMAN	P25940	homo sapien	128	7.0	707	1	SFPQ_HUMAN	P23246	h splicing
416	130	7.1	1802	2	Q17163_BRUMA	Q17163	brugia mala	128	7.0	707	2	Q86VG2_HUMAN	Q86vg2	homo sapien
417	130	7.1	1840	2	Q5RGW7_BRARE	Q5rgw7	brachydanio	128	7.0	707	2	Q5SZ71_HUMAN	Q5sz71	homo sapien
418	130	7.1	2157	2	Q4SH46_TETNG	Q4sh46	tetraodon n	128	7.0	782	2	Q1ULM1_9MYCO	Q1ulm1	mycobacteri
419	129.5	7.1	259	1	PRI0_TRIVU	P51780	trichosurus	128	7.0	806	2	Q7TSV1_MOUSE	Q7tsv1	mus musculus
420	129.5	7.1	399	2	Q2H664_CHAGB	Q2h664	chaetomium	128	7.0	895	1	ANDR_PAPHA	Q97960	papio namad
421	129.5	7.1	417	2	Q561H9_CRYNE	Q561h9	cryptococcu	128	7.0	907	1	ANDR_CANFA	Q9tt90	canis famli
422	129.5	7.1	417	2	Q5KQ61_CRYNE	Q5kq61	cryptococcu	128	7.0	1355	1	CO1A2_RANCA	Q42350	rana catesb
423	129.5	7.1	448	2	Q28936_PIG	Q28936	sus scrofa	128	7.0	1423	2	Q172H6_AEDAE	Q172h6	aedes aegyp
424	129.5	7.1	456	2	Q7SH82_NEUCR	Q7sh82	neurospora	128	7.0	1464	2	Q3UH72_MOUSE	Q3uh72	mus musculus
425	129.5	7.1	484	2	Q1T7B1_9MYCO	Q1ttb1	mycobacteri	128	7.0	1669	2	Q9QZ50_MOUSE	Q9qzs0	mus musculus
426	129.5	7.1	558	2	Q9SR80_DROME	Q9sr80	drosofila	128	7.0	1792	2	Q59EE7_HUMAN	Q59ee7	homo sapien
427	129.5	7.1	924	2	Q7ZWT5_XENLA	Q7zwt5	xenopus lae	128	7.0	1838	1	CO5A1_HUMAN	P20908	homo sapien
428	129.5	7.1	1059	2	Q7SOG4_NEUCR	Q7sog4	neurospora	127.5	7.0	320	2	Q6YY27_ORYSA	Q6yy27	oryza sativ
429	129.5	7.1	1155	2	Q9V367_DROME	Q9v367	drosofila	127.5	7.0	338	2	Q29E08_DROPS	Q29e08	drosofila
430	129.5	7.1	1190	2	Q17JW4_AEDAE	Q17jw4	aedes aegyp	127.5	7.0	445	2	Q9VEB9_DROME	Q9veb9	drosofila
431	129.5	7.1	1840	1	CO5A1_CRILLO	Q60467	cricetulus	127.5	7.0	455	2	Q28495_MACMU	Q28495	macaca mula
432	129.5	7.1	2167	1	SHAN1_RAT	Q9mw48	rattus norv	127.5	7.0	745	2	Q1JPC3_BOVIN	Q1jpc3	bos taurus
433	129	7.1	200	2	Q61TM4_CAEER	Q61tm4	caenorhabdi	127.5	7.0	785	2	Q61L47_CAEER	Q61l47	caenorhabdi
434	129	7.1	394	2	Q9J210_9GAMA	Q9j210	rhesus monk	127.5	7.0	884	2	Q00302_HUMAN	Q00302	homo sapien
435	129	7.1	485	2	Q7TN25_MOUSE	Q7tn25	mus musculus	127.5	7.0	884	2	Q8WU30_HUMAN	Q8wu30	homo sapien
436	129	7.1	488	2	Q4R8G0_MACFA	Q4r8g0	macaca fasc	127.5	7.0	916	2	Q8IWX8_HUMAN	Q8iwx8	homo sapien
437	129	7.1	509	2	Q6CEV4_YARLU	Q6cev4	yarrowia li	127.5	7.0	1084	2	Q53RI4_HUMAN	Q53r14	homo sapien
438	129	7.1	683	2	Q3UG94_MOUSE	Q3ug94	mus musculus	127.5	7.0	1109	2	Q7SFA3_NEUCR	Q7sfa3	neurospora
439	129	7.1	694	2	Q5DEV1_SCHUJ	Q5dev1	schistosoma	127.5	7.0	1142	1	ENAM_PIG	Q97939	sus scrofa
440	129	7.1	707	2	Q4WV54_ASFPU	Q4wv54	aspergillus	127.5	7.0	1163	2	Q8N6U4_HUMAN	Q8n6u4	homo sapien
441	129	7.1	835	2	Q1E0Q2_COCIM	Q1e0q2	coccidioid	127.5	7.0	1453	1	CO1A1_RAT	P02454	rattus norv
442	129	7.1	957	2	Q29H84_DROPS	Q29h84	drosofila	127.5	7.0	1466	1	CO3A1_HUMAN	P02461	homo sapien
443	129	7.1	998	2	Q8CFM4_DROPS	Q8cfm4	mus musculus	127.5	7.0	1466	2	Q53S91_HUMAN	Q53s91	homo sapien
444	129	7.1	1097	1	SC24C_ARATH	Q9m291	arabidopsis	127.5	7.0	1466	2	Q541P8_HUMAN	Q541p8	homo sapien
445	129	7.1	1103	2	Q59FN7_HUMAN	Q59fn7	homo sapien	127.5	7.0	1670	1	CO4A3_HUMAN	Q01955	homo sapien
446	129	7.1	1207	2	Q9PVF5_BRARE	Q9pvf5	brachydanio	127	7.0	300	2	Q4KR06_LYCPE	Q4kr06	lycopersico
447	129	7.1	1222	2	Q8K173_MOUSE	Q8k173	mus musculus	127	7.0	430	2	Q3B710_APIME	Q3b710	apis mellif
448	129	7.1	1464	1	CO3A1_MOUSE	P08121	mus musculus	127	7.0	430	2	Q3B709_APIME	Q3b709	apis mellif
449	129	7.1	1464	2	Q7TT32_MOUSE	Q7tt32	mus musculus	127	7.0	516	2	Q17DVO_AEDAE	Q17dvo	aedes aegyp
450	129	7.1	1464	2	Q8BKY2_MOUSE	Q8bkY2	mus musculus	127	7.0	544	2	Q26RY1_XANP2	Q26ry1	xanthobacte
451	129	7.1	1464	2	Q8BLM4_MOUSE	Q8blm4	mus musculus	127	7.0	880	2	Q7Q9S9_ANOGA	Q7q9s9	anopheles g
452	129	7.1	1464	2	Q3TWI5_MOUSE	Q3twi5	m osteoclas	127	7.0	880	2	Q3ULI5_MOUSE	Q3uli5	mus musculus
453	129	7.1	1467	2	Q5DTG2_MOUSE	Q5dtg2	mus musculus	127	7.0	888	1	PPIRA_MOUSE	Q80w00	mus musculus
454	129	7.1	1494	2	Q55ZW9_CRYNE	Q55zw9	cryptococcu	127	7.0	911	1	ANDR_PANTR	Q97775	pan troglod
455	129	7.1	1494	2	Q5KP78_CRYNE	Q5kp78	cryptococcu	127	7.0	1009	2	Q5TUG3_CANFA	Q5tjg3	canis famli
456	129	7.1	1835	2	Q9IAU4_CHICK	Q9iau4	gallus gall	127	7.0	1078	2	Q4NLM4_9MYCC	Q4nlm4	arthrobacte
457	129	7.1	1840	1	CO5A1_RAT	Q9f103	rattus norv	127	7.0	1106	1	GLI1_HUMAN	P08151	homo sapien
458	129	7.1	2715	1	MLL4_HUMAN	Q9um66	homo sapien	127	7.0	1464	2	Q6P9I2_XENLA	Q6p9i2	xenopus lae
459	128.5	7.0	1132	2	Q6E1P8_BOVIN	Q6elp8	bos taurus	127	7.0	1596	2	Q5TJG0_CANFA	Q5tjg0	canis famli
460	128.5	7.0	212	2	Q811W5_CAVFO	Q811w5	cavia porce	127	7.0	1736	1	COBA2_BOVIN	Q32824	bos taurus
461	128.5	7.0	309	2	Q4VAY4_HUMAN	Q4vay4	homo sapien	127	7.0	1840	2	Q59IP3_PIG	Q59ip3	sus scrofa
462	128.5	7.0	316	2	Q53PL2_ORYSA	Q53pl2	oryza sativ	127	6.9	238	2	Q2HGM6_CHAGB	Q2hgm6	chaetomium
463	128.5	7.0	374	2	Q6IHV8_DROME	Q6ihv8	drosofila	126.5	6.9	334	2	Q5ATU9_EWENI	Q5atu9	emericeila
464	128.5	7.0	415	1	SYN1_CANFA	Q62732	canis famli	126.5	6.9	485	2	Q60X57_CAEER	Q60x57	caenorhabdi
465	128.5	7.0	415	2	Q3HKQ0_DROME	Q3hkq0	drosofila	126.5	6.9	502	2	Q66HH6_RAT	Q66hh6	rattus norv
466	128.5	7.0	461	2	Q2MDJ2_DICBI	Q2mdj2	diceros bic	126.5	6.9	548	2	Q3TZI3_MOUSE	Q3tzi3	mus musculus
467	128.5	7.0	521	2	Q9N9G8_9ASCI	Q9n9g8	phallusia m	126.5	6.9	636	2	Q658K5_HUMAN	Q658k5	homo sapien
468	128.5	7.0	751	2	Q3UVS2_MOUSE	Q3uvs2	mus musculus	126.5	6.9	638	1	SF01_HUMAN	Q15637	homo sapien
469	128.5	7.0	768	2	Q5AFN4_CANAL	Q5afn4	candida alb	126.5	6.9	639	2	Q3UI45_MOUSE	Q3ui45	mus musculus

543	126.5	6.9	652	1	SR01_MOUSE	Q64213	mus musculus	616	125	6.9	561	2	Q17D40_AEDAE	Q17d40	aedes aegypti
544	126.5	6.9	705	1	PAU1_NEUCR	Q7sn5	neurospora	617	125	6.9	574	1	WSP1_SCHPO	Q36027	schizosaccharomyces pombe
545	126.5	6.9	745	1	Q6Z125_ORYSA	Q6z125	oryza sativa	618	125	6.9	662	1	PFS2_NEUCR	Q7ry68	neurospora
546	126.5	6.9	788	2	Q29AE6_DROPS	Q29ae6	drosophila	619	125	6.9	745	2	Q16R99_AEDAE	Q16r99	aedes aegypti
547	126.5	6.9	958	2	Q7JXX2_DROME	Q7jxx2	drosophila	620	125	6.9	749	2	Q3U0Q9_MOUSE	Q3u0q9	mus musculus
548	126.5	6.9	1034	2	Q4T233_TETNG	Q4t233	tetradon n	621	125	6.9	845	1	MUCDL_HUMAN	Q9hbb8	homo sapiens
549	126.5	6.9	1040	2	Q8IR84_DROME	Q8ir84	drosophila	622	125	6.9	895	1	ANDR_MACFA	Q97952	macaca fascicularis
550	126.5	6.9	1139	2	Q5PR22_HUMAN	Q5pr22	homo sapiens	623	125	6.9	895	1	ANDR_MACMU	Q6qt55	macaca mulatta
551	126.5	6.9	1301	2	Q6P3M9_XENTR	Q6p3m9	xenopus tropicalis	624	125	6.9	922	2	Q8MW53_MYTGA	Q8mw53	mytilus galloprovincialis
552	126.5	6.9	1347	2	Q96QB3_HUMAN	Q96qb3	homo sapiens	625	125	6.9	1136	2	Q3S053_MOUSE	Q3s053	mus musculus
553	126.5	6.9	1399	2	Q4SB89_TETNG	Q4sb89	tetradon n	626	125	6.9	1449	2	Q6PEI9_BRARE	Q6pei9	brachydanio rerio
554	126.5	6.9	1737	2	Q9J104_RAT	Q9j104	rattus norvegicus	627	125	6.9	1631	2	Q597Q0_CANFA	Q597q0	canis familiaris
555	126	6.9	117	2	Q9WUJ1_CAVPO	Q9wuji1	cavia porcellus	628	125	6.9	1685	1	CO4A5_HUMAN	P29400	homo sapiens
556	126	6.9	230	2	Q5YU13_NOCFA	Q5yuh3	nocardia farcinosa	629	125	6.9	1827	2	Q9NUB7_HUMAN	Q9nub7	homo sapiens
557	126	6.9	300	2	Q4KR02_LYCCI	Q4kr02	lycopersicon esculentum	630	125	6.9	1875	2	Q8UDM5_ORYLA	Q8udm5	oryzias latipes
558	126	6.9	445	2	Q8MZ49_DROME	Q8mz49	drosophila	631	124.5	6.8	264	1	PRIO_BOSTR	Q5ujg7	boselephas
559	126	6.9	473	2	Q3VXV7_9ACTO	Q3vxy7	frankia sp.	632	124.5	6.8	345	2	Q95WV2_MELJA	Q95wv2	meloidogyne incognita
560	126	6.9	576	2	Q2TBG3_BOVIN	Q2tbg2	bos taurus	633	124.5	6.8	401	2	Q89FL1_BRAJA	Q89fl1	bradyrhizobium elkanii
561	126	6.9	577	2	Q2H3E3_CHAGB	Q2h3e3	chaetomium	634	124.5	6.8	414	2	Q8NDG2_HUMAN	Q8ndg2	homo sapiens
562	126	6.9	600	2	Q6C6N4_YARLI	Q6c6n4	yarrowia lipolytica	635	124.5	6.8	596	2	Q3GYQ5_9ACTO	Q3gyq5	nocardioides
563	126	6.9	739	2	Q7PYL4_ANOGA	Q7pyl4	anopheles gambiae	636	124.5	6.8	636	2	Q1X17_DEIGD	Q1x17	deinoceratus
564	126	6.9	743	1	COBAl_MOUSE	Q00780	mus musculus	637	124.5	6.8	690	2	Q3LUD4_RAT	Q3lud4	rattus norvegicus
565	126	6.9	744	2	Q8BGL6_MOUSE	Q8bgl6	m. adult male	638	124.5	6.8	848	2	Q4S270_TETNG	Q4sz70	tetradon n
566	126	6.9	744	2	Q3TWU7_MOUSE	Q3twu7	mus musculus	639	124.5	6.8	857	2	Q6RH33_9HYME	Q6rh33	dinocampus
567	126	6.9	744	2	Q921S8_MOUSE	Q921s8	mus musculus	640	124.5	6.8	992	1	EBNA6_EBV	P03204	epstein-barr virus
568	126	6.9	757	1	CEP68_HUMAN	Q76n32	homo sapiens	641	124.5	6.8	992	2	Q69119_EBVG	Q69119	epstein-barr virus
569	126	6.9	779	1	HCN3_MOUSE	Q88705	mus musculus	642	124.5	6.8	992	2	Q777E7_EBVG	Q777e7	epstein-barr virus
570	126	6.9	812	2	Q5VZ72_NOCFA	Q5vz72	nocardia farcinosa	643	124.5	6.8	1033	2	Q7SAP0_NEUCR	Q7sap0	neurospora
571	126	6.9	981	2	Q8NQ11_DROME	Q8nq11	drosophila	644	124.5	6.8	1307	2	Q8JPF7_XENLA	Q8jpf7	xenopus laevis
572	126	6.9	1069	2	Q6LAN8_HUMAN	Q6lan8	homo sapiens	645	124.5	6.8	1418	1	CO2A1_HUMAN	P02458	homo sapiens
573	126	6.9	1069	2	Q2V3R0_ARATH	Q2v3r0	arabidopsis thaliana	646	124.5	6.8	1487	2	Q1JQ82_HUMAN	Q1jq82	homo sapiens
574	126	6.9	1096	2	Q27GK4_ARATH	Q27gk4	arabidopsis thaliana	647	124.5	6.8	1487	2	Q1JQ82_HUMAN	Q1jq82	homo sapiens
575	126	6.9	1364	1	CO1A2_BOVIN	P02465	bos taurus	648	124.5	6.8	1493	2	Q7PTF3_ANOGA	Q7ptf3	anopheles gambiae
576	126	6.9	1369	2	Q4FYQ8_TETNG	Q4fyq8	tetradon n	649	124.5	6.8	3119	1	COCA1_MOUSE	Q60847	mus musculus
577	126	6.9	1461	2	Q76045_HUMAN	Q76045	homo sapiens	650	124.5	6.8	3530	1	MYO15_HUMAN	Q9ukn7	homo sapiens
578	126	6.9	1464	1	CO1A1_HUMAN	P02452	homo sapiens	651	124	6.8	175	2	Q9D3Y5_MOUSE	Q9d3y5	mus musculus
579	126	6.9	1464	2	Q8N473_HUMAN	Q8n473	homo sapiens	652	124	6.8	225	2	Q866V9_MACCA	Q866v9	macrus callosus
580	126	6.9	1467	2	Q59F64_HUMAN	Q59f64	homo sapiens	653	124	6.8	269	2	Q4NJ99_9MICC	Q4nj99	arthrobacter
581	126	6.9	1849	2	Q1LWX5_BRARE	Q1lwx5	brachydanio rerio	654	124	6.8	304	2	Q9SRR0_ARATH	Q9srr0	arabidopsis thaliana
582	126	6.9	2308	2	Q9W2U7_DROME	Q9w2u7	drosophila	655	124	6.8	340	2	Q3M0Y6_9ACTO	Q3w0y6	frankia sp.
583	125.5	6.9	164	2	Q3XSP9_9PROT	Q3xsp9	magnetococcus	656	124	6.8	463	2	Q6IRJ7_RAT	Q6irj7	rattus norvegicus
584	125.5	6.9	254	2	Q866W8_TUPTA	Q866w8	tupaia tupaia	657	124	6.8	463	2	Q8VIN2_RAT	Q8vin2	rattus norvegicus
585	125.5	6.9	331	2	Q5JU46_HUMAN	Q5ju46	homo sapiens	658	124	6.8	506	2	Q5I4J0_LATJA	Q5i4j0	lateolabrax
586	125.5	6.9	508	2	Q3VXW7_9ACTO	Q3vwx7	frankia sp.	659	124	6.8	521	2	Q7U303_MYCBO	Q7u303	mycobacterium
587	125.5	6.9	588	2	Q1EBD6_COCIM	Q1ebd6	coccidioides immitis	660	124	6.8	585	2	Q8OV57_MOUSE	Q8ov57	mus musculus
588	125.5	6.9	589	2	Q2S8V1_XANP2	Q2sbv1	xanthobacter	661	124	6.8	593	2	Q4QA28_LEIMA	Q4qa28	leishmania
589	125.5	6.9	710	2	Q8MWJ2_BOVIN	Q8mwj2	bos taurus	662	124	6.8	675	2	Q9N178_FIG	Q9n178	sus scrofa
590	125.5	6.9	724	2	Q5JU46_HUMAN	Q5ju46	homo sapiens	663	124	6.8	735	2	Q5TNP5_ANOGA	Q5tnp5	anopheles gambiae
591	125.5	6.9	730	2	Q26052_PARLI	Q26052	paracentrotus	664	124	6.8	744	1	CO8A1_RABIT	P14282	oryctolagus cuniculus
592	125.5	6.9	744	1	CO8A1_HUMAN	P27658	homo sapiens	665	124	6.8	744	2	Q7LZR2_CHICK	Q7lzz2	gallus gallus
593	125.5	6.9	744	2	Q53X16_HUMAN	Q53x16	homo sapiens	666	124	6.8	811	2	Q25UC0_MYCVN	Q25uc0	mycobacterium
594	125.5	6.9	752	2	Q93NY7_ANAPH	Q93ny7	anaplasma phagocytophilum	667	124	6.8	881	2	Q68EM7_HUMAN	Q68em7	homo sapiens
595	125.5	6.9	860	2	Q02290_NEOPA	Q02290	neocallimastix	668	124	6.8	940	1	Q2L610_HUMAN	Q2l610	homo sapiens
596	125.5	6.9	881	2	Q4S1X8_TETNG	Q4s1x8	tetradon n	669	124	6.8	940	2	PF1RA_HUMAN	Q9eqc0	homo sapiens
597	125.5	6.9	916	1	IF2_LETXX	Q6a4q9	leifsonia xanthodans	670	124	6.8	1048	1	SFR15_RAT	Q63627	rattus norvegicus
598	125.5	6.9	993	2	Q9V731_DROME	Q9v731	drosophila	671	124	6.8	1069	1	SC24B_ARATH	Q9m081	arabidopsis thaliana
599	125.5	6.9	1026	2	Q4SZ73_TETNG	Q4sz73	tetradon n	672	124	6.8	1072	1	ZIM10_MOUSE	Q6pie1	mus musculus
600	125.5	6.9	1032	2	Q9JUG3_MOUSE	Q9jjg3	mus musculus	673	124	6.8	1142	1	ENAM_HUMAN	Q9nrm1	homo sapiens
601	125.5	6.9	1043	2	Q6NXX1_MOUSE	Q6nxx1	mus musculus	674	124	6.8	1142	2	Q8IWP4_HUMAN	Q8iwp4	homo sapiens
602	125.5	6.9	1098	2	Q69Z85_MOUSE	Q69z85	mus musculus	675	124	6.8	1142	2	Q17R15_HUMAN	Q17r15	homo sapiens
603	125.5	6.9	1418	2	Q9W7R9_CYNPY	Q9w7r9	cynops pyrrhonorhynchus	676	124	6.8	1222	2	Q4TC61_TETNG	Q4tc61	tetradon n
604	125.5	6.9	1457	2	Q641L9_MOUSE	Q641l9	mus musculus	677	124	6.8	1272	2	Q6URC4_HUMAN	Q6urc4	homo sapiens
605	125.5	6.9	1463	1	CO1A1_BOVIN	P02453	bos taurus	678	124	6.8	1287	1	TCGAP_HUMAN	O14559	homo sapiens
606	125.5	6.9	1494	2	Q67FY2_MOUSE	Q67fy2	mus musculus	679	124	6.8	1299	2	Q59FH8_HUMAN	Q59fh8	homo sapiens
607	125.5	6.9	1494	2	Q617B5_MOUSE	Q617b5	mus musculus	680	124	6.8	1336	2	Q6RZ41_HUMAN	Q6rzz41	homo sapiens
608	125.5	6.9	1758	1	CO4A2_CABEL	P17140	caenorhabditis elegans	681	124	6.8	1336	2	Q58EX6_HUMAN	Q58ex6	homo sapiens
609	125.5	6.9	1927	2	Q2LZG1_DROPS	Q2lzz1	drosophila	682	124	6.8	1486	2	Q7ZT16_XENLA	Q7zt16	xenopus laevis
610	125.5	6.9	1958	2	Q7Q532_ANOGA	Q7q532	anopheles gambiae	683	124	6.8	1516	2	Q6RZ39_HUMAN	Q6rzz39	homo sapiens
611	125.5	6.9	2488	2	Q4VXL0_HUMAN	Q4vxl0	homo sapiens	684	124	6.8	1738	2	Q2M075_DROPS	Q2m075	drosophila
612	125.5	6.9	2948	2	Q86WG6_HUMAN	Q86wg6	homo sapiens	685	124	6.8	1739	2	Q9JLI2_MOUSE	Q9jli2	mus musculus
613	125	6.9	233	2	Q86GW4_9EUTH	Q86gw4	hymenys	686	124	6.8	1751	2	Q6RZ40_HUMAN	Q6rzz40	homo sapiens
614	125	6.9	276	1	PRB4L_HUMAN	P10162	homo sapiens	687	124	6.8	1827	2	Q589R0_ORYLA	Q589r0	oryzias latipes
615	125	6.9	484	2	Q704P7_9HEM1	Q704p7	lethocercus	688	124	6.8	1962	1	TNR6A_HUMAN	Q8ndv7	homo sapiens

689	124	6.8	2365	1	TARA HUMAN	Q9h2d6 homo sapien	762	122	6.7	254	2	Q8BYA8_MOUSE	Q8bya8 mus musculus
690	123.5	6.8	435	2	Q72152_CABEL	Q72152 caenorhabdi	763	122	6.7	260	2	Q86GW6_TALEU	Q86gw6 talpa europ
691	123.5	6.8	488	1	ANXA7 HUMAN	P20073 homo sapien	764	122	6.7	317	1	COCAL1_RAT	P70560 rattus norv
692	123.5	6.8	494	2	Q9L1T2_STRCO	Q9L1t2 streptomyc	765	122	6.7	323	1	JUND1_CHICK	P27921 gallus gall
693	123.5	6.8	501	2	Q55762_SYNV3	Q55762 streptocyst	766	122	6.7	396	2	Q7UGP9_RHOBA	P70929 rhodopirell
694	123.5	6.8	571	2	Q5M7R7_XENTR	Q5m7r7 xenopus tro	767	122	6.7	445	2	Q99JR3_MOUSE	Q99jr3 mus musculus
695	123.5	6.8	582	2	Q2RV13_RHOSP	Q2rv13 rhodospiril	768	122	6.7	463	2	Q50190_MYCLE	Q50190 mycobacteri
696	123.5	6.8	623	2	Q86BN3_DROME	Q86bn3 drosophila	769	122	6.7	482	1	IRX5_HUMAN	P78411 homo sapien
697	123.5	6.8	663	1	DUS8_MOUSE	Q09112 mus musculu	770	122	6.7	488	2	Q3UCD4_MYCLE	Q3ucd4 mycobacteri
698	123.5	6.8	664	1	Q1S4F8_MEDTR	Q1s4f8 medicago tr	771	122	6.7	500	2	Q3U045_MOUSE	Q3u045 m 15 days e
699	123.5	6.8	665	2	Q7TSZ9_MOUSE	Q7tsz9 mus musculu	772	122	6.7	567	2	Q50388_BRARE	Q50388 brachydanio
700	123.5	6.8	706	1	SYN1_MOUSE	Q88935 mus musculu	773	122	6.7	575	1	EPN1_RAT	Q88339 rattus norv
701	123.5	6.8	730	2	Q13771_HUMAN	Q13771 homo sapien	774	122	6.7	627	2	Q8BXM6_MOUSE	Q8bxm6 mus musculu
702	123.5	6.8	799	2	Q8BNS7_MOUSE	Q8bns7 mus musculu	775	122	6.7	722	2	Q55PY1_CRYNE	Q55py1 cryptococcu
703	123.5	6.8	809	2	Q28396_HORSE	Q28396 equus cabal	776	122	6.7	727	2	Q3UUG8_MOUSE	Q3uug8 mus musculu
704	123.5	6.8	816	2	Q8N4S4_HUMAN	Q8n4s4 homo sapien	777	122	6.7	777	2	Q3TU06_MOUSE	Q3tu06 mus musculu
705	123.5	6.8	925	1	PP1RA_PIG	Q8n4s4 homo sapien	778	122	6.7	783	2	Q9XA11_STRCO	Q9xai1 streptomyc
706	123.5	6.8	1026	2	Q7RYP7_NEUCR	Q7ryp7 neurospora	779	122	6.7	829	2	Q7ZYG1_XENLA	Q7zyg1 xenopus lae
707	123.5	6.8	1054	2	Q4SAN6_TETNG	Q4san6 tetraodon n	780	122	6.7	940	1	PP1RA_PANTR	Q7yr38 pan troglod
708	123.5	6.8	1418	2	Q28396_HORSE	Q28396 equus cabal	781	122	6.7	940	1	Q1XHY0_PANTR	Q1xhy0 pan troglod
709	123.5	6.8	1449	2	Q910C0_ONCWY	Q910c0 oncorhynch	782	122	6.7	1038	1	SC24A_ARATH	Q9sfu0 arabidopsis
710	123.5	6.8	1516	1	CO1A1_HUMAN	P39060 homo sapien	783	122	6.7	1153	2	Q8MOW5_DROME	Q8mqw5 drosophila
711	123.5	6.8	1625	2	Q6MVD4_NEUCR	Q6mvd4 neurospora	784	122	6.7	1191	2	Q6PCK7_XENLA	Q6pck7 xenopus lae
712	123	6.7	237	2	Q866U8_TENEC	Q866u8 tenrec ecau	785	122	6.7	1223	2	Q4JSA7_AZOVI	Q4jsa7 azotobacter
713	123	6.7	323	2	Q9XVY1_CABEL	Q9xvy1 caenorhabdi	786	122	6.7	1310	2	Q6DFR4_XENTR	Q6dfr4 xenopus tro
714	123	6.7	356	2	Q9Q0B8_HHV2	Q9q0b8 human herpe	787	122	6.7	1368	2	Q6V5B9_CARAS	Q6v5b9 cardaminops
715	123	6.7	356	2	Q9Q0B7_HHV2	Q9q0b7 human herpe	788	122	6.7	1447	2	Q5NT96_PAROL	Q5nt96 paralichthy
716	123	6.7	399	2	Q47T40_THERFY	Q47t40 thermobifid	789	122	6.7	1487	2	Q77J53_CANFA	Q77j53 canis fami
717	123	6.7	437	2	Q5Z7Y6_ORYSA	Q5z7y6 oryza sativ	790	122	6.7	1492	2	Q6P4Z2_XENTR	Q6p4z2 xenopus tro
718	123	6.7	464	2	Q25SAU9_DAUMA	Q25sau9 daubenton	791	122	6.7	1884	2	Q4RWK6_TETNG	Q4rwk6 tetraodon n
719	123	6.7	475	2	Q1D1N9_COCIM	Q1d1n9 coccidioide	792	122	6.7	1888	1	COEAL1_CHICK	P32018 gallus gall
720	123	6.7	481	2	Q97641_HORSE	Q97641 equus cabal	793	122	6.7	1896	2	Q3UHK8_MOUSE	Q3uhk8 mus musculu
721	123	6.7	486	2	Q9U1W1_CABEL	Q9u1w1 caenorhabdi	794	122	6.7	1966	2	Q9NHX6_DROME	Q9nhx6 drosophila
722	123	6.7	533	2	Q8R5A5_MOUSE	Q8r5a5 mus musculu	795	122	6.7	1966	2	Q8IQA6_DROME	Q8lqa6 drosophila
723	123	6.7	533	2	Q8BHM2_MOUSE	Q8bhm2 m adult mal	796	122	6.7	1985	2	Q8T9N4_DROME	Q8tcn4 drosophila
724	123	6.7	638	2	Q7PM40_ANOGA	Q7pm40 anopheles g	797	122	6.7	1985	2	Q7KUW8_DROME	Q7kuw8 drosophila
725	123	6.7	670	2	Q8NGW7_HUMAN	Q8ngw7 homo sapien	798	122	6.7	1985	2	Q9VSK5_DROME	Q9vsk5 drosophila
726	123	6.7	682	2	Q9VKG4_DROME	Q9vkg4 drosophila	799	122	6.7	1988	2	Q86BH2_DROME	Q86bh2 drosophila
727	123	6.7	718	2	Q96OH2_HUMAN	Q96oh2 homo sapien	800	121.5	6.7	361	2	Q29H14_DROPS	Q29h14 drosophila
728	123	6.7	750	2	Q9VZG4_DROME	Q9vzg4 drosophila	801	121.5	6.7	363	2	Q3B7L7_BOVIN	Q3b7l7 bos taurus
729	123	6.7	795	2	Q2UPM4_ASPOR	Q2upm4 aspergillus	802	121.5	6.7	397	2	Q5Q0D0_ARATH	Q5qcd0 arabidopsis
730	123	6.7	800	2	Q61Q09_CABER	Q61q09 caenorhabdi	803	121.5	6.7	405	2	Q8OV76_MOUSE	Q8ov76 mus musculu
731	123	6.7	937	2	Q9QVR2_9MURI	Q9qvr2 rattus sp.	804	121.5	6.7	457	2	Q961D0_DROME	Q961d0 drosophila
732	123	6.7	1037	2	Q4T8U2_TETNG	Q4t8u2 tetraodon n	805	121.5	6.7	469	2	Q7M2X0_BOVIN	Q7m2x0 bos taurus
733	123	6.7	1323	1	NMD54_MOUSE	Q03391 mus musculu	806	121.5	6.7	566	1	EPN1_MOUSE	Q80vp1 mus musculu
734	123	6.7	1325	1	UBP42_HUMAN	Q9h9j4 homo sapien	807	121.5	6.7	575	2	Q6NX78_MOUSE	Q6nx78 mus musculu
735	123	6.7	1770	2	Q7Q1Y4_ANOGA	Q7q1y4 anopheles g	808	121.5	6.7	615	1	FIBA_BOVIN	P02672 bos taurus
736	123	6.7	3124	1	COCAL1_CHICK	P13944 gallus gall	809	121.5	6.7	650	2	Q7XIQ4_ORYSA	Q7xliq4 oryza sativ
737	123	6.7	3400	2	Q55285_CRYNE	Q55285 cryptococcu	810	121.5	6.7	653	2	Q29MX9_DROPS	Q29mx9 drosophila
738	122.5	6.7	264	1	PRIO_AILME	Q6eh52 ailuropoda	811	121.5	6.7	670	2	Q24K74_RAT	Q24k74 rattus norv
739	122.5	6.7	309	1	PRB3_HUMAN	Q04118 homo sapien	812	121.5	6.7	684	2	P90679_AREMA	P90679 arenicola m
740	122.5	6.7	338	2	Q86YA1_HUMAN	Q86ya1 homo sapien	813	121.5	6.7	730	2	Q7SDP6_NEUCR	Q7sdf6 neurospora
741	122.5	6.7	392	1	PRP1_HUMAN	P04280 homo sapien	814	121.5	6.7	749	2	Q9W384_DROME	Q9w384 drosophila
742	122.5	6.7	418	2	Q01662_CABEL	Q01662 caenorhabdi	815	121.5	6.7	837	2	Q2GKP4_ANAPZ	Q2gkp4 anaplasm p
743	122.5	6.7	420	1	Q670R1_NEUCR	Q670r1 neurospora	816	121.5	6.7	895	2	Q4T021_TETNG	Q4t021 tetraodon n
744	122.5	6.7	623	1	CO4A4_RABIT	P55787 oryctolagus	817	121.5	6.7	990	2	Q7RSN4_GIALA	Q7r5n4 giardia lam
745	122.5	6.7	677	2	Q5KD10_CRYNE	Q5kd10 cryptococcu	818	121.5	6.7	1002	1	EBM12_MOUSE	Q8r4x3 mus musculu
746	122.5	6.7	687	2	Q4G0U1_HUMAN	Q4gou1 homo sapien	819	121.5	6.7	1002	1	EBM12_MOUSE	Q8r4x3 mus musculu
747	122.5	6.7	699	1	CO8A2_MOUSE	P25318 mus musculu	820	121.5	6.7	1389	2	Q7T2Z7_CHICK	Q7t2z7 gallus gall
748	122.5	6.7	746	2	Q2JCD7_FRASC	Q2jcd7 frankia sp.	821	121.5	6.7	1629	2	Q414C4_GIBZE	Q414c4 gibberella
749	122.5	6.7	884	1	ANDR_EULFC	Q97776 eulemur ful	822	121	6.6	193	2	Q9YQ08_CAEEL	Q9yhc9 neurospora
750	122.5	6.7	1024	2	Q3MZL0_9DELT	Q3mzl0 syntrophoba	823	121	6.6	204	2	Q9TSI7_9CETA	Q9tsi7 odocoileus
751	122.5	6.7	1168	1	MYSC_AACA	P10569 acanthamoeb	824	121	6.6	216	2	Q9BT57_HUMAN	Q9bt57 homo sapien
752	122.5	6.7	1178	2	Q8CB68_MOUSE	Q8cb68 mus musculu	825	121	6.6	256	2	Q9MZU8_9CETA	Q9mzu8 odocoileus
753	122.5	6.7	1186	2	Q61080_ACACA	Q61080 acanthamoeb	826	121	6.6	256	2	Q5XM84_CEREL	Q5xm84 cervus elap
754	122.5	6.7	1262	2	Q17RN4_HUMAN	Q17rn4 homo sapien	827	121	6.6	405	2	Q89M75_BRAJA	Q89m75 bradyrhizob
755	122.5	6.7	1315	2	Q55151_CRYNE	Q55151 cryptococcu	828	121	6.6	417	2	Q17MW1_AEDAE	Q17mw1 aedes aegyp
756	122.5	6.7	1360	2	Q5K7N8_CRYNE	Q5k7n8 cryptococcu	829	121	6.6	567	2	Q5K4F8_BRARE	Q5k4f8 brachydanio
757	122.5	6.7	1420	2	Q90W37_CHICK	Q90w37 gallus gall	830	121	6.6	591	2	Q6PUJ3_HUMAN	Q6puj3 homo sapien
758	122.5	6.7	1473	2	Q23JZ2_TETTH	Q23jz2 tetrahymena	831	121	6.6	592	2	Q8TPM9_STMTH	Q8tpm9 symbiobacte
759	122.5	6.7	1480	2	Q96Q04_HUMAN	Q96q04 homo sapien	832	121	6.6	597	2	Q8STP5_ENCCO	Q8stp5 encephalito
760	122.5	6.7	1855	2	Q80ZF0_RAT	Q80zf0 rattus norv	833	121	6.6	615	2	Q5YNH6_NOCFA	Q5ynh6 nocardia fa
761	122.5	6.7	1860	2	Q4A666_9CHON	Q4a666 raja kenoje	834	121	6.6	623	2	Q353F4_9GAMM	Q353f4 alkalilimni

835	121	6.6	634	2	Q7RWB0	neurospora
836	121	6.6	637	2	Q32MK1	homo sapien
837	121	6.6	645	2	Q2JF54	frankia sp.
838	121	6.6	651	2	Q2TB40	homo sapien
839	121	6.6	654	1	TRE2	HUMAN
840	121	6.6	658	2	Q2TB39	homo sapien
841	121	6.6	694	2	Q6YXK3	ORYZA
842	121	6.6	748	1	RAVR1	MOUSE
843	121	6.6	759	2	Q82IJ7	STRAW
844	121	6.6	776	2	Q17MK0	AEDAE
845	121	6.6	871	2	Q96S23	HUMAN
846	121	6.6	878	2	Q8BNF0	MOUSE
847	121	6.6	949	2	Q7S4X4	neurospora
848	121	6.6	1125	2	Q2UY09	homo sapien
849	121	6.6	1220	2	Q6NS79	MOUSE
850	121	6.6	1255	1	DIAP1	MOUSE
851	121	6.6	1285	2	Q5DTQ1	MOUSE
852	121	6.6	1378	2	Q97405	HALDI
853	121	6.6	1379	2	Q8SWX1	DROME
854	121	6.6	1403	2	Q4RKG5	TETNG
855	121	6.6	1419	1	CO2A1	RAT
856	121	6.6	1470	1	COHAI1	MOUSE
857	121	6.6	1486	2	Q91717	XENLA
858	121	6.6	1884	2	Q9W2Y5	DROME
859	121	6.6	2249	2	Q9NHW4	NEPCL
860	121	6.6	2280	2	Q9V8E6	DROME
861	121	6.6	2302	2	Q9N693	DROME
862	121	6.6	2310	2	Q9CRA9	DROME
863	120.5	6.6	251	2	Q86GV4	PHYCA
864	120.5	6.6	441	2	Q2HG22	CHAGB
865	120.5	6.6	531	2	Q9BZG5	HUMAN
866	120.5	6.6	539	2	Q9NUA2	HUMAN
867	120.5	6.6	542	2	Q9BZG6	HUMAN
868	120.5	6.6	561	2	Q3N6S1	DEBELT
869	120.5	6.6	631	2	Q6BL65	DESHA
870	120.5	6.6	652	2	Q9VSH4	DROME
871	120.5	6.6	657	2	Q4VAP9	HUMAN
872	120.5	6.6	703	1	CO8A2	HUMAN
873	120.5	6.6	703	2	Q5JV31	HUMAN
874	120.5	6.6	717	2	Q6C9B8	YARLI
875	120.5	6.6	763	2	Q4RZL2	TETNG
876	120.5	6.6	795	2	Q9G6V1	HUMAN
877	120.5	6.6	812	2	Q06452	EPHUM
878	120.5	6.6	819	2	Q32MK0	HUMAN
879	120.5	6.6	933	2	Q7S583	NEUCR
880	120.5	6.6	1016	1	MAML1	HUMAN
881	120.5	6.6	1100	2	Q2PBM9	BRARE
882	120.5	6.6	1134	2	Q2PEM8	BRARE
883	120.5	6.6	1255	2	Q2GZN9	CHAGB
884	120.5	6.6	1315	2	Q8QHL9	XENLA
885	120.5	6.6	1338	1	IRS2	HUMAN
886	120.5	6.6	1338	2	Q96RG4	HUMAN
887	120.5	6.6	1339	2	Q96RG5	HUMAN
888	120.5	6.6	1384	2	Q4FXR7	LEIMA
889	120.5	6.6	1396	2	Q2PBM7	BRARE
890	120.5	6.6	1706	2	Q5VZA9	HUMAN
891	120.5	6.6	1712	1	CO4A2	HUMAN
892	120.5	6.6	1715	1	TENS1	BOVIN
893	120.5	6.6	1747	2	Q26640	STRPU
894	120.5	6.6	3164	1	TEGU	HRV1
895	120.5	6.6	5262	1	MLL2	HUMAN
896	120	6.6	256	2	Q8G3E9	9CETA
897	120	6.6	263	1	M1SS	MOUSE
898	120	6.6	265	2	Q9PW56	BOTJA
899	120	6.6	309	2	Q18751	CAEEL
900	120	6.6	334	2	Q9VY61	DROME
901	120	6.6	430	2	Q98Q42	MYCPU
902	120	6.6	483	2	Q267B9	MYCVN
903	120	6.6	544	2	Q9BZG7	HUMAN
904	120	6.6	547	2	Q3WDR2	9ACTO
905	120	6.6	616	2	Q3WDZ7	frankia sp.
906	120	6.6	661	2	Q4T0A9	TETNG
907	120	6.6	774	2	Q6ZPG8	MOUSE

908	120	6.6	789	2	Q5SRP3	CRYNE
909	120	6.6	789	2	Q5KG47	CRYNE
910	120	6.6	819	2	Q5RDG7	PONPY
911	120	6.6	923	2	Q8R4U3	MOUSE
912	120	6.6	931	1	SEM6C	MOUSE
913	120	6.6	932	1	RBW12	HUMAN
914	120	6.6	932	1	RBW12	MACMU
915	120	6.6	932	2	Q5RBM8	PONPY
916	120	6.6	954	2	Q69YJ7	HUMAN
917	120	6.6	963	2	Q91Y36	MOUSE
918	120	6.6	1213	1	SMRC2	MOUSE
919	120	6.6	1213	1	Q801M5	XENLA
920	120	6.6	1346	2	Q8UUJ3	ONCKE
921	120	6.6	1370	2	Q6C3B8	YARLI
922	120	6.6	1380	2	Q21PF9	ANADE
923	120	6.6	1419	2	Q80VY3	MOUSE
924	120	6.6	1419	2	Q80X38	MOUSE
925	120	6.6	1487	2	Q641K3	MOUSE
926	120	6.6	1648	2	Q419Y3	GIBZEL
927	120	6.6	1733	2	Q9NPF26	CAEEL
928	120	6.6	1733	2	Q30D77	MOUSE
929	119.5	6.6	262	2	Q6ZNM4	HUMAN
930	119.5	6.6	264	2	Q5UJH4	BOSJA
931	119.5	6.6	390	2	Q8BIR3	MOUSE
932	119.5	6.6	445	2	Q16GB0	AEDAE
933	119.5	6.6	493	1	WASIP	MOUSE
934	119.5	6.6	496	2	Q2PZB0	SPAAU
935	119.5	6.6	639	2	Q3UK67	MOUSE
936	119.5	6.6	640	2	Q5TNL6	ANOCA
937	119.5	6.6	705	2	Q4S2U5	TETNG
938	119.5	6.6	725	2	Q6R0H6	MOUSE
939	119.5	6.6	728	1	PALI	YARLI
940	119.5	6.6	747	2	Q6NW57	BRARE
941	119.5	6.6	790	2	Q4R3G8	MACFA
942	119.5	6.6	894	2	Q8MW54	MYTGA
943	119.5	6.6	910	2	Q874V3	PODAN
944	119.5	6.6	914	2	Q3TKT7	MOUSE
945	119.5	6.6	950	2	Q7S4P3	NEUCR
946	119.5	6.6	992	2	Q7TT14	MOUSE
947	119.5	6.6	1109	2	Q3YQM8	PAPTE
948	119.5	6.6	1121	2	Q59FV5	HUMAN
949	119.5	6.6	1187	2	Q4HXA6	GIBZE
950	119.5	6.6	1258	1	GLI2	HUMAN
951	119.5	6.6	1375	2	Q5S477	CRYNE
952	119.5	6.6	1449	2	Q6NZ15	BRARE
953	119.5	6.6	1487	2	Q68E09	HUMAN
954	119.5	6.6	1510	2	Q8N3D4	HUMAN
955	119.5	6.6	1586	2	Q4JHT4	HUMAN
956	119.5	6.6	1603	1	COGAI	HUMAN
957	119.5	6.6	1651	2	Q6ZML7	HUMAN
958	119.5	6.6	2659	2	Q5BLQ2	HUMAN
959	119.5	6.6	3201	2	Q2QBE0	9ALPH
960	119	6.5	143	2	Q9MZ17	SHEEP
961	119	6.5	185	2	Q97694	CERNI
962	119	6.5	204	2	Q9TSI8	9CETA
963	119	6.5	204	2	Q97629	9CETA
964	119	6.5	220	2	Q02825	ODOHE
965	119	6.5	220	2	Q7JJ72	ODOHE
966	119	6.5	223	2	Q97910	HIPNIP
967	119	6.5	244	2	Q6B506	CEREL
968	119	6.5	245	2	Q9MZU7	9CETA
969	119	6.5	254	2	Q9TSF8	RABIT
970	119	6.5	255	1	PRI0	CANFA
971	119	6.5	256	1	PRI0	CEREL
972	119	6.5	256	1	PRI0	CEREN
973	119	6.5	256	1	PRI0	MOSCH
974	119	6.5	256	1	PRI0	ODOHE
975	119	6.5	256	2	Q3Y673	RANTA
976	119	6.5	256	2	Q5XM82	CEREL
977	119	6.5	256	2	Q6VS46	ODOHE
978	119	6.5	256	2	Q8SPV4	CAPHI
979	119	6.5	256	2	Q3Y667	9CETA
980	119	6.5	256	2	Q3Y668	9CETA

Q55RP3	cryptococcus
Q5KG47	cryptococcus
Q5RDG7	pongo pygma
Q8R4U3	mus musculus
Q9WT33	mus musculus
Q9T26	homo sapien
Q8SQ27	macaca mula
Q8SBM8	pongo pygma
Q69YJ7	homo sapien
Q91Y36	mus musculus
Q6PDG5	mus musculus
Q801M5	xenopus lae
Q8UUJ3	oncorhynchus
Q6C3B8	yarrowia li
Q21PF9	anaeromyxob
Q80VY3	mus musculus
Q80X38	mus musculus
Q641K3	mus musculus
Q419Y3	gibberella
Q9NPF26	caenorhabdi
Q30D77	mus musculus
Q6ZNM4	homo sapien
Q5UJH4	bos javanic
Q8BIR3	mus musculus
Q16GB0	aedes aegypt
Q8K117	mus musculus
Q2PZB0	sparus aura
Q3UK67	mus musculus
Q5TNL6	anopheles g
Q4S2U5	tetradodon n
Q6R0H6	mus musculus
Q7Z8T5	yarrowia li
Q6NW57	brachydanio
Q4R3G8	macaca fasc
Q8MW54	mytilus gal
Q874V3	podospira a
Q3TKT7	mus musculus
Q7S4P3	neurospora
Q7TT14	mus musculus
Q3YQM8	paramecium
Q59FV5	homo sapien
Q4HXA6	gibberella
P10070	homo sapien
GLI2	homo sapien
Q5S477	cryptococcus
Q6NZ15	brachydanio
Q68E09	homo sapien
Q8N3D4	homo sapien
Q4JHT4	homo sapien
Q07092	homo sapien
Q6ZML7	homo sapien
Q5BLQ2	homo sapien
Q2QBE0	cercopithec
Q9MZ17	ovis aries
Q97694	cervus nipp
Q9TSI8	odocoileus
Q97629	odocoileus
Q02825	odocoileus
Q7JJ72	odocoileus
Q97910	hippotragus
Q6B506	cervus elap
Q9MZU7	odocoileus
Q9TSF8	oryctolagus
Q46501	canis fami
P67987	cervus elap
P67895	cervus elap
Q88995	moschus chr
P47852	odocoileus
Q3Y673	rangifer ta
Q5XM82	cervus elap
Q8SPV4	capra hircu
Q3Y667	alces alces
Q3Y668	alces alces

981	119	6.5	256	2	Q3Y670_RANTA	Q3Y670	rangifer ta	1054	118.5	6.5	763	2	Q4PCR2_USTWA	Q4PCR2	ustilago ma
982	119	6.5	256	2	Q3Y671_RANTA	Q3Y671	rangifer ta	1055	118.5	6.5	773	2	Q1DQ81_COCIM	Q1DQ81	coccidioid
983	119	6.5	256	2	Q5XM83_CEREL	Q5XM83	cervus elap	1056	118.5	6.5	826	2	Q8K0N6_MOUSE	Q8K0N6	mus musculu
984	119	6.5	256	2	Q693S2_ALCAA	Q693s2	alces alces	1057	118.5	6.5	886	2	Q8CEf7_MOUSE	Q8CEf7	mus musculu
985	119	6.5	256	2	Q693S4_RANTA	Q693s4	rangifer ta	1058	118.5	6.5	921	1	CO9A1_HUMAN	P20849	homo sapien
986	119	6.5	256	2	Q6V656_SHEEP	Q6V656	ovis aries	1059	118.5	6.5	940	1	PP1RA_MACMU	P5tm61	macaca mula
987	119	6.5	256	2	Q863E8_9CETA	Q863e8	odocoileus	1060	118.5	6.5	1041	2	Q66S51_OIKDI	Q66S51	oikopleura
988	119	6.5	256	2	Q865Z5_9CETA	Q865z5	alces alces	1061	118.5	6.5	1042	1	SPT5_GIBZE	Q41514	gibberella
989	119	6.5	256	2	Q865Z6_9CETA	Q865z6	alces alces	1062	118.5	6.5	1075	2	Q86X41_HUMAN	Q86X41	homo sapien
990	119	6.5	256	2	Q5UAF3_RANTA	Q5uaf3	rangifer ta	1063	118.5	6.5	1228	2	Q1D282_COCIM	Q1d282	coccidioid
991	119	6.5	256	2	Q693S1_CAPCA	Q693s1	capreolus c	1064	118.5	6.5	1312	2	Q55RV4_CRYNE	Q55rv4	cryptococu
992	119	6.5	256	2	Q6B507_CERNI	Q6b507	cervus nipp	1065	118.5	6.5	1323	1	NND54_RAT	Q82645	rattus norv
993	119	6.5	256	2	Q6DN38_CERNI	Q6dn38	cervus nipp	1066	118.5	6.5	1599	2	Q55139_CRYNE	Q55139	cryptococu
994	119	6.5	256	2	Q7YJQ1_9CETA	Q7yjq1	odocoileus	1067	118.5	6.5	1599	2	Q5K7M6_CRYNE	Q5K7m6	cryptococu
995	119	6.5	256	2	Q7Y5F3_DAMDA	Q7y5f3	dama dama (1068	118.5	6.5	1608	1	CIC_HUMAN	Q66rk0	homo sapien
996	119	6.5	256	2	Q549D4_CEREN	Q549d4	cervus elap	1069	118	6.5	104	2	Q6EIQ1_BOVIN	Q6Eiq1	bos taurus
997	119	6.5	256	2	Q62670_CEREN	Q62670	cervus elap	1070	118	6.5	105	2	Q97697_MUNMU	Q97697	muntiacus m
998	119	6.5	256	2	Q02841_ODOHE	Q02841	odocoileus	1071	118	6.5	133	2	Q6EIQ7_BOVIN	Q6Eiq7	bos taurus
999	119	6.5	265	2	Q8Q691_BOTIN	Q8q691	bothrops in	1072	118	6.5	133	2	Q6EIQ6_BOVIN	Q6Eiq6	bos taurus
1000	119	6.5	301	2	Q97923_HYLLA	Q97923	hylobates l	1073	118	6.5	181	2	Q97911_BUDTA	Q97911	budorcas ta
1001	119	6.5	332	2	Q8QGD9_CHICK	Q8qgd9	gallus gall	1074	118	6.5	197	2	Q6RV14_SHEEP	Q6rv14	ovis aries
1002	119	6.5	356	2	Q9Q0B9_HHV2	Q9q0b9	human herpe	1075	118	6.5	197	2	Q6RV12_SHEEP	Q6rv12	ovis aries
1003	119	6.5	414	2	Q3N646_9DELT	Q3n646	syntrophoba	1076	118	6.5	197	2	Q6RV13_SHEEP	Q6rv13	ovis aries
1004	119	6.5	446	2	Q5ZIL5_NOCPA	Q5zil5	nocardia fa	1077	118	6.5	197	2	Q6RV15_SHEEP	Q6rv15	ovis aries
1005	119	6.5	457	2	Q5XIR5_RAT	Q5xir5	rattus norv	1078	118	6.5	197	2	Q6RV16_SHEEP	Q6rv16	ovis aries
1006	119	6.5	472	2	Q4TA88_TETNG	Q4ta88	tetraodon n	1079	118	6.5	197	2	Q6RYR6_SHEEP	Q6ryr6	ovis aries
1007	119	6.5	503	2	Q53TA9_HUMAN	Q53ta9	homo sapien	1080	118	6.5	202	2	Q97908_CAPNU	Q97908	capra nubia
1008	119	6.5	511	2	Q5TNP4_ANOGA	Q5tnp4	anopheles g	1081	118	6.5	215	2	Q97904_BOSJA	Q97904	bos javanic
1009	119	6.5	569	2	Q17208_BOMMO	Q17208	bombyx mori	1082	118	6.5	235	2	Q97695_GIRCA	Q97695	giraffa cam
1010	119	6.5	608	2	Q6ZUS4_HUMAN	Q6zus4	homo sapien	1083	118	6.5	254	2	Q9Z0T4_PRODE	Q9Z0t4	sigmodon fu
1011	119	6.5	629	2	Q3VXY1_9ACTO	Q3vxy1	frankia sp.	1084	118	6.5	256	1	PRIO_BUDTA	PRIO_BUDTA	budorcas ta
1012	119	6.5	659	2	Q6CQ78_YARLI	Q6cq78	yarrowia li	1085	118	6.5	256	1	PRIO_CAPHI	P52113	capra hircu
1013	119	6.5	712	2	Q4S272_TETNG	Q4s272	tetraodon n	1086	118	6.5	256	1	PRIO_FELCA	Q818754	felis silve
1014	119	6.5	731	2	Q9ZUE0_ARATH	Q9zue0	arabidopsis	1087	118	6.5	256	1	PRIO_OVICA	Q7jh13	ovis canad
1015	119	6.5	752	2	Q9LQC5_ARATH	Q9lqc5	arabidopsis	1088	118	6.5	256	1	PRIO_OVIMO	Q7jiy2	ovibos mosc
1016	119	6.5	767	2	Q9U234_CABEL	Q9u234	caenorhabdi	1089	118	6.5	256	1	PRIO_RUPRU	Q7jk02	ovis orient
1017	119	6.5	817	2	Q5K7C2_CRYNE	Q5k7c2	cryptococu	1090	118	6.5	256	1	PRIO_OVIMO	Q5xvm4	rupicapra r
1018	119	6.5	845	2	Q7S4M4_NEUCR	Q7s4m4	neurospora	1091	118	6.5	256	1	PRIO_SHEEP	P23907	ovis aries
1019	119	6.5	1005	2	Q55KA7_CRYNE	Q55ka7	cryptococu	1092	118	6.5	256	1	Q712V9_SHEEP	Q712v9	ovis aries
1020	119	6.5	1096	2	Q4RPJ2_TETNG	Q4rpj2	tetraodon n	1093	118	6.5	256	2	Q5UAF2_OVICA	Q5uaf2	ovis canad
1021	119	6.5	1108	2	Q1DNW4_COCIM	Q1dnw4	coccidioid	1094	118	6.5	256	2	Q70KZ9_SHEEP	Q70kz9	ovis aries
1022	119	6.5	1159	2	Q9IMX8_9GAMA	Q9imx8	cercopithe	1095	118	6.5	256	2	Q712M4_SHEEP	Q712m4	ovis aries
1023	119	6.5	1240	2	Q9DWH8_RCMVM	Q9dwh8	rat cytomeg	1096	118	6.5	256	2	Q7YRQ6_SHEEP	Q7Yrq6	ovis aries
1024	119	6.5	1256	2	Q873A1_NEUCR	Q873a1	neurospora	1097	118	6.5	256	2	Q9TV01_CAPHI	Q9tv01	capra hircu
1025	119	6.5	1374	2	Q9VSU0_DROME	Q9vsu0	drosophila	1098	118	6.5	256	2	Q5ECG4_SHEEP	Q5ecg4	ovis aries
1026	119	6.5	1441	2	Q9CEFL1_LACLA	Q9cfl1	lactococcus	1099	118	6.5	256	2	Q5ECG5_SHEEP	Q5ecg5	ovis aries
1027	119	6.5	1442	2	Q62033_MOUSE	Q62033	mus musculu	1100	118	6.5	256	2	Q68G93_SHEEP	Q68g93	ovis aries
1028	119	6.5	1442	2	Q62031_MOUSE	Q62031	mus musculu	1101	118	6.5	256	2	Q68G94_SHEEP	Q68g94	ovis aries
1029	119	6.5	1450	2	Q81Q88_DROME	Q81q88	drosophila	1102	118	6.5	256	2	Q8SPV6_CAPHI	Q8spv6	capra hircu
1030	119	6.5	1459	1	CO2A1_MOUSE	P28481	mus musculu	1103	118	6.5	256	2	Q95N12_SHEEP	Q95n12	ovis aries
1031	119	6.5	1459	2	Q62032_MOUSE	Q62032	mus musculu	1104	118	6.5	256	2	Q9TTU5_SHEEP	Q9ttu5	ovis aries
1032	119	6.5	1460	1	CO1A1_CANFA	Q9xsj7	canis famil	1105	118	6.5	256	2	Q9TU07_SHEEP	Q9tu07	ovis aries
1033	119	6.5	1554	2	Q621K0_CABER	Q621k0	caenorhabdi	1106	118	6.5	256	2	Q46648_CAPHI	Q46648	capra hircu
1034	119	6.5	1690	2	Q5JYH8_HUMAN	Q5jyh8	homo sapien	1107	118	6.5	256	2	Q5UJH3_BOSJA	Q5ujh3	bos javanic
1035	119	6.5	1691	1	CO4A6_HUMAN	Q14031	homo sapien	1108	118	6.5	256	2	Q68G89_CAPHI	Q68g89	capra hircu
1036	119	6.5	1746	2	Q17A79_AEDA	Q17a79	aedes aegyp	1109	118	6.5	256	2	Q68G91_CAPHI	Q68g91	capra hircu
1037	119	6.5	1880	2	Q7RZX6_NEUCR	Q7rxz6	neurospora	1110	118	6.5	256	2	Q6V643_SHEEP	Q6v643	ovis aries
1038	119	6.5	286	2	Q9VSU2_DROME	Q9vsu2	drosophila	1111	118	6.5	256	2	Q6V652_SHEEP	Q6v652	ovis aries
1039	119	6.5	2968	2	Q4TBM7_TETNG	Q4tbm7	tetraodon n	1112	118	6.5	256	2	Q1L4F2_SHEEP	Q1l4f2	ovis aries
1040	118.5	6.5	125	2	Q6EIQ8_BUBBU	Q6eiq8	bubalus bub	1113	118	6.5	256	2	Q6V649_SHEEP	Q6v649	ovis aries
1041	118.5	6.5	247	2	Q811W7_SCIVU	Q811w7	sciuurus vul	1114	118	6.5	256	2	Q866V2_TRIMA	Q866v2	trichechus
1042	118.5	6.5	248	2	Q866V0_ORYAF	Q866v0	oryctopus	1115	118	6.5	256	2	Q4U480_CAPHI	Q4u480	capra hircu
1043	118.5	6.5	264	1	PRIO_BUBBU	Q5ujh8	bubalus bub	1116	118	6.5	256	2	Q712W1_SHEEP	Q712w1	ovis aries
1044	118.5	6.5	264	2	Q5UJH9_EURDE	Q5ujh9	bubalus dep	1117	118	6.5	256	2	Q2HZ93_HYDIN	Q2hz93	hydropotes
1045	118.5	6.5	264	2	Q5UJH0_EURDE	Q5ujh0	bubalus dep	1118	118	6.5	256	2	Q2L9A5_CAPHI	Q2l9a5	capra hircu
1046	118.5	6.5	314	2	Q9P038_HUMAN	Q9p038	homo sapien	1119	118	6.5	256	2	Q2L9A4_CAPHI	Q2l9a4	capra hircu
1047	118.5	6.5	370	2	Q5SKG1_THET8	Q5skg1	thermus the	1120	118	6.5	256	2	Q1AFW6_SHEEP	Q1afw6	ovis aries
1048	118.5	6.5	483	2	Q4SHT3_TETNG	Q4sht3	tetraodon n	1121	118	6.5	256	2	Q1AFL5_SHEEP	Q1afl5	ovis aries
1049	118.5	6.5	485	2	Q3UYL7_MOUSE	Q3uy17	mus musculu	1122	118	6.5	256	2	Q712W0_SHEEP	Q712w0	ovis aries
1050	118.5	6.5	498	2	Q5KGJ5_CRYNE	Q5kgj5	cryptococu	1123	118	6.5	256	2	Q5ECG8_SHEEP	Q5ecg8	ovis aries
1051	118.5	6.5	699	1	VGLG_HHV2H	P13290	human herpe	1124	118	6.5	256	2	Q27H92_SHEEP	Q27h92	ovis aries
1052	118.5	6.5	710	2	Q5U4P6_HUMAN	Q5u4p6	homo sapien	1125	118	6.5	256	2	Q212K7_SHEEP	Q212k7	ovis aries
1053	118.5	6.5	748	1	RAVR1_RAT	Q5x128	rattus norv	1126	118	6.5	256	2	Q70L02_SHEEP	Q70l02	ovis aries

1127	118	6.5	256	2	Q1AFH1_SHEEP	Q1afh1 ovis aries	1200	117.5	6.4	264	2	Q5UJG5_TRAST	Q5ujg5 tragelaphus
1128	118	6.5	256	2	Q6SG92_SHEEP	Q6sg92 ovis aries	1201	117.5	6.4	310	2	Q90612_CHICK	Q90612 gallus gall
1129	118	6.5	256	2	Q1AFG2_SHEEP	Q1afg2 ovis aries	1202	117.5	6.4	355	2	Q84T97_ORYZA	Q84t97 oryza sativ
1130	118	6.5	256	2	Q1AFH2_SHEEP	Q1afh2 ovis aries	1203	117.5	6.4	481	2	Q32PT5_BRARE	Q32pt5 brachydanio
1131	118	6.5	263	2	Q68G99_CAMEBA	Q68g99 camelus bac	1204	117.5	6.4	482	2	Q5M5M6_STRT2	Q5m5m6 streptococc
1132	118	6.5	264	1	PRIO_BISBI	Q5uaf1 bison bison	1205	117.5	6.4	496	2	Q7U8L8_SYNPX	Q7u8l8 synechococc
1133	118	6.5	264	1	PRIO_BOSGA	Q5ujh0 bos gaurus	1206	117.5	6.4	571	2	Q2DYX2_ACICE	Q2dyx2 acidothermu
1134	118	6.5	264	1	PRIO_BOSIN	Q5ujj1 bos indicus	1207	117.5	6.4	609	2	Q3XT84_MOUSE	Q3xt84 mus musculu
1135	118	6.5	264	1	PRIO_BOVIN	P10279 bos taurus	1208	117.5	6.4	636	1	EPN3_MOUSE	Q91w69 mus musculu
1136	118	6.5	264	2	Q5UJH2_BISBI	Q5ujh2 bison bison	1209	117.5	6.4	671	1	LZTS2_MOUSE	Q91w6 mus musculu
1137	118	6.5	264	2	Q5UJH6_BOSJA	Q5ujh6 bos javanic	1210	117.5	6.4	687	2	Q2H6H3_CHAGB	Q2h6h3 chaetomium
1138	118	6.5	264	2	Q68G98_CAMEBA	Q68g98 camelus bac	1211	117.5	6.4	696	2	Q8MJX3_BOVIN	Q8mjx3 bos taurus
1139	118	6.5	264	2	Q6UL09_BOSMU	Q6ul09 bos mutus g	1212	117.5	6.4	708	2	Q7ZWN8_XENLA	Q7zwn8 xenopus lae
1140	118	6.5	264	2	Q864M0_BOVIN	Q864m0 bos taurus	1213	117.5	6.4	772	2	Q4SRQ5_TETNG	Q4srq5 tetraodon n
1141	118	6.5	264	2	Q5UJR9_9CETA	Q5ujr9 bos taurus	1214	117.5	6.4	781	2	Q5ARJ3_EMENI	Q5arj3 emericeella
1142	118	6.5	264	2	Q5UK70_BOSIN	Q5uk70 bos indicus	1215	117.5	6.4	792	2	Q5ICCS_EMENI	Q5iccs emericeella
1143	118	6.5	264	2	Q6UL07_BOSMU	Q6ul07 bos mutus g	1216	117.5	6.4	841	2	Q64542_ARATH	Q64542 arabidopsis
1144	118	6.5	264	2	Q2LDZ4_BOVIN	Q2ldz4 bos taurus	1217	117.5	6.4	976	2	Q5KA53_CRYNE	Q5ka53 cryptococcu
1145	118	6.5	344	2	Q270J1_MYCFV	Q270j1 mycobacteri	1218	117.5	6.4	976	2	Q55LD5_CRYNE	Q55ld5 cryptococcu
1146	118	6.5	356	2	Q900B2_HHV2	Q9q0b2 human herpe	1219	117.5	6.4	1015	2	Q7S698_NEUCR	Q7s698 neurospora
1147	118	6.5	356	2	Q900B6_HHV2	Q9q0b6 human herpe	1220	117.5	6.4	1049	2	Q5BGU4_EMENI	Q5bgu4 emericeella
1148	118	6.5	356	2	Q900B4_HHV2	Q9q0b4 human herpe	1221	117.5	6.4	1072	1	MAP4_BOVIN	P36225 bos taurus
1149	118	6.5	356	2	Q900B3_HHV2	Q9q0b3 human herpe	1222	117.5	6.4	1308	2	Q5XUX5_BRARE	Q5xux5 brachydanio
1150	118	6.5	398	2	Q1HR40_AEDAE	Q1hr40 aedes aegyp	1223	117.5	6.4	1318	2	P90493_HHV2	Q587j1 human herpe
1151	118	6.5	442	2	Q1TMC4_9MYCO	Q1tmc4 mycobacteri	1224	117.5	6.4	1336	2	Q587J1_HUMAN	Q7Q9V5 anopheles g
1152	118	6.5	468	2	Q6ZRW4_HUMAN	Q6zrw4 homo sapien	1225	117.5	6.4	1402	2	Q7Q9V5_ANOGA	Q5xjv6 mus musculu
1153	118	6.5	514	1	LWA_ANTEL	Q16992 anthopleura	1226	117.5	6.4	1424	2	Q5XJV6_MOUSE	Q52kf1 mus musculu
1154	118	6.5	583	2	Q218X9_PETMA	Q218x9 petromyzon	1227	117.5	6.4	1424	2	Q5XJV6_MOUSE	Q505d3 mus musculu
1155	118	6.5	589	2	Q7TSJ1_MOUSE	Q7tsj1 mus musculu	1228	117.5	6.4	1578	2	Q505D3_MOUSE	Q9qzr9 mus musculu
1156	118	6.5	615	2	Q7VIL7_DROME	Q7vyl7 drosophila	1229	117.5	6.4	1682	2	Q9QYR9_MOUSE	Q8hycl canis famil
1157	118	6.5	695	2	Q49AM6_HUMAN	Q49am6 homo sapien	1230	117.5	6.4	1691	1	CO4A5_CANFA	Q28247 canis famil
1158	118	6.5	734	2	Q4HZ13_GIBZE	Q4hz13 gibberella	1231	117.5	6.4	1796	1	COEAL_HUMAN	Q05707 homo sapien
1159	118	6.5	747	1	CO2A1_BOVIN	P02459 bos taurus	1232	117.5	6.4	2061	2	Q4S2C2_TETNG	Q4s2c2 tetraodon n
1160	118	6.5	749	2	Q55TS2_CRYNE	Q55ts2 cryptococcu	1233	117.5	6.4	2183	2	Q6CEV2_YARLI	Q6cev2 yarrowia li
1161	118	6.5	749	2	Q5KIL5_CRYNE	Q5kil5 cryptococcu	1234	117.5	6.4	227	2	Q97906_EQUPR	Q97906 equus cabal
1162	118	6.5	751	1	CEP68_PONPY	Q5rcq2 pongo pygma	1235	117.5	6.4	227	2	Q97964_HORSE	Q97964 equus cabal
1163	118	6.5	753	2	Q93107_ACACA	Q93107 acanthamoeb	1236	117	6.4	248	2	Q866V6_DICBI	Q866v6 diceros bic
1164	118	6.5	761	2	Q4RN84_TETNG	Q4rn84 tetraodon n	1237	117	6.4	269	2	Q7QCG4_ANOGA	Q7qcg4 anopheles g
1165	118	6.5	771	2	Q1B7N1_9MYCO	Q1b7n1 mycobacteri	1238	117	6.4	406	2	Q5R6N5_PONPY	Q5r6n5 pongo pygma
1166	118	6.5	780	1	HCN3_RAT	Q9jka8 rattus norv	1239	117	6.4	410	2	Q59FT6_HUMAN	Q59ft6 homo sapien
1167	118	6.5	780	1	T22D2_HUMAN	Q75157 homo sapien	1240	117	6.4	432	2	Q5B8U8_EMENI	Q5b8u8 emericeella
1168	118	6.5	864	2	Q4FYD4_LEITMA	Q4fyd4 leishmania	1241	117	6.4	443	2	Q54NF8_DICDI	Q54nf8 dictyosteli
1169	118	6.5	871	2	Q5CZV2_BRARE	Q5czv2 brachydanio	1242	117	6.4	481	2	Q82CH7_STRAW	Q82ch7 streptomyce
1170	118	6.5	897	2	Q3CEC6_ARATH	Q3cec6 arabidopsis	1243	117	6.4	484	1	IRX5_MOUSE	Q9ikn3 rattus norv
1171	118	6.5	914	2	Q6GV09_MYCAV	Q6gv09 mycobacteri	1244	117	6.4	487	1	WASIP_RAT	Q6in36 rattus norv
1172	118	6.5	1005	2	Q5X995_CRYNE	Q5x995 cryptococcu	1245	117	6.4	523	2	Q4PE18_USTWA	Q4pe18 ustilago ma
1173	118	6.5	1024	2	Q5DU15_PARTE	Q5du15 paramecium	1246	117	6.4	524	2	Q71E72_HUMAN	Q71e72 homo sapien
1174	118	6.5	1098	2	Q2BNS3_JANSC	Q2bns3 jannaschia	1247	117	6.4	545	2	Q8NDH8_HUMAN	Q8ndh8 homo sapien
1175	118	6.5	1192	1	CENG1_HUMAN	Q99490 homo sapien	1248	117	6.4	553	2	Q6DN78_LOLPR	Q6dn78 lolium pere
1176	118	6.5	1245	2	Q5RD55_PONPY	Q5rd55 pongo pygma	1249	117	6.4	566	2	Q4WEK1_ASPPU	Q4wek1 aspergillus
1177	118	6.5	1248	1	DIAP1_HUMAN	Q60510 homo sapien	1250	117	6.4	603	2	Q68U18_CHLRE	Q68u18 chlamydomon
1178	118	6.5	1263	2	Q4SV50_TETNG	Q4sv50 tetraodon n	1251	117	6.4	615	2	Q8MS22_DROME	Q8ms22 drosophila
1179	118	6.5	1305	1	TCGAP_MOUSE	Q80yif9 mus musculu	1252	117	6.4	692	2	Q38ES8_9TRYP	Q38es8 trypanosoma
1180	118	6.5	1324	2	Q3UQS4_MOUSE	Q3uqs4 mus musculu	1253	117	6.4	788	2	Q414K5_KINRA	Q414k5 kineococcus
1181	118	6.5	1641	2	Q5NCY0_MOUSE	Q5ncy0 mus musculu	1254	117	6.4	872	1	PP1BA_RAT	Q55000 rattus norv
1182	118	6.5	1929	2	Q4PCA3_USTMA	Q4pca3 ustilago ma	1255	117	6.4	882	2	Q4IB27_GIBZE	Q4ib27 gibberella
1183	118	6.5	2346	2	Q94LG9_ORYSA	Q94lg9 oryza sativ	1256	117	6.4	892	1	HICI_MOUSE	Q9riy5 mus musculu
1184	118	6.5	2435	2	Q2U8X6_ASPOR	Q2u8x6 aspergillus	1257	117	6.4	892	1	Q5NCQ8_MOUSE	Q5ncq8 mus musculu
1185	117.5	6.4	195	2	Q6H4Q0_ORYSA	Q6h4q0 oryza sativ	1258	117	6.4	925	1	IF2_MYCPA	Q73vv4 mycobacteri
1186	117.5	6.4	211	2	Q77787_ANTAM	Q77787 antilocapra	1259	117	6.4	980	1	SPT5_YARLI	Q6cc84 yarrowia li
1187	117.5	6.4	219	2	Q5BBX9_EMENI	Q5bbx9 emericeella	1260	117	6.4	1003	2	Q6FNM2_CANGA	Q6fnm2 candida gla
1188	117.5	6.4	256	2	Q8SPV7_CAPHI	Q8spv7 capra hircu	1261	117	6.4	1157	2	Q4PAN2_USTWA	Q4pan2 ustilago ma
1189	117.5	6.4	256	2	Q8SPV5_CAPHI	Q8spv5 capra hircu	1262	117	6.4	1191	2	Q4S4D3_TETNG	Q4s4d3 tetraodon n
1190	117.5	6.4	264	1	PRIOT_TRAST	P40242 tragelaphus	1263	117	6.4	1227	2	Q1E1H4_COCIM	Q1e1h4 coccidioid
1191	117.5	6.4	264	1	PRIOT_ANTCE	Q5ujg1 antilope ce	1264	117	6.4	1253	2	Q9DEH3_CHICK	Q9deh3 gallus gall
1192	117.5	6.4	264	1	PRIOT_TRAIM	Q5ujg3 tragelaphus	1265	117	6.4	1362	1	CO1A2_CHICK	P02467 gallus gall
1193	117.5	6.4	264	2	Q5UAX7_BUBBU	Q5uax7 bubalus bub	1266	117	6.4	1412	2	Q8MUF5_HYDAT	Q8muf5 hydra atten
1194	117.5	6.4	264	2	Q5UJ11_SYNCA	Q5uj11 syncerus ca	1267	117	6.4	1438	2	Q4S012_TETNG	Q4s012 tetraodon n
1195	117.5	6.4	264	2	Q5UAX8_BUBBU	Q5uax8 bubalus bub	1268	117	6.4	1495	2	Q1E577_COCIM	Q1e577 coccidioid
1196	117.5	6.4	264	2	Q5UJ12_SYNCA	Q5uj12 syncerus ca	1269	117	6.4	1540	2	Q4TIP0_TETNG	Q4tip0 tetraodon n
1197	117.5	6.4	264	2	Q5UJ13_SYNCA	Q5uj13 syncerus ca	1270	117	6.4	1622	2	Q411K9_KINRA	Q411k9 kineococcus
1198	117.5	6.4	264	2	Q5UJ14_SYNCA	Q5uj14 syncerus ca	1271	117	6.4				
1199	117.5	6.4	264	2	Q9MZU6_ANTAM	Q9mzu6 antilocapra	1272	117	6.4				

1273	117	6.4	1310	2	Q7P834_ANOGA	Q7P834	anopheles g
1274	117	6.4	2966	2	Q4RMT7_TETNG	Q4Rmt7	tetraodon n
1275	117	6.4	3455	2	Q6R5A9_TENNO	Q6r5a9	tetrahio mo
1276	116.5	6.4	273	2	Q5ENX3_9VIRU	Q5enx3	torque teno
1277	116.5	6.4	291	2	Q9NAG3_CAREL	Q9nag3	caenorhabdi
1278	116.5	6.4	305	2	Q3OGY4_9SOLN	Q3og74	solanum och
1279	116.5	6.4	326	2	Q22514_9MAGN	Q22514	santalum al
1280	116.5	6.4	361	1	SSBP4_HUMAN	P81877	homo sapien
1281	116.5	6.4	361	2	Q3KWH3_BOVIN	Q3khw3	bos sapien
1282	116.5	6.4	396	2	Q1DI52_COCIM	Q1di52	coccidioid
1283	116.5	6.4	424	1	SP3B4_HUMAN	Q15427	homo sapien
1284	116.5	6.4	424	2	Q53PG6_HUMAN	Q53f66	homo sapien
1285	116.5	6.4	424	2	Q5S263_HUMAN	Q5s263	homo sapien
1286	116.5	6.4	447	2	Q1JPF8_BOVIN	Q1jpf8	bos sapien
1287	116.5	6.4	449	2	Q82DCl_STRAW	Q82dcl1	streptomyce
1288	116.5	6.4	451	2	Q2SAV3_EULFU	Q2sav3	eulemur ful
1289	116.5	6.4	499	2	Q7EXJ1_ORYSA	Q7exj1	oryza sativ
1290	116.5	6.4	562	2	Q9RMR8_KLEPN	Q9rmr8	klebsiella
1291	116.5	6.4	572	2	Q2GVA3_CHAGB	Q2gva3	chaetomium
1292	116.5	6.4	586	2	Q54T87_DICDI	Q54t87	dictyosteli
1293	116.5	6.4	608	2	Q9Q5K9_CHV12	Q9q5k9	cercopithe
1294	116.5	6.4	652	2	Q7XIX3_ORYSA	Q7xix3	oryza sativ
1295	116.5	6.4	657	2	Q8WQ99_DROME	Q8wqp9	drosophila
1296	116.5	6.4	682	2	Q2H7P7_CHAGB	Q2h7p7	chaetomium
1297	116.5	6.4	682	2	Q2YQK2_BOVIN	Q2yqk2	bos taurus
1298	116.5	6.4	713	2	Q2GT05_CHAGB	Q2gt05	chaetomium
1299	116.5	6.4	725	2	Q7YOK1_BOVIN	Q7yok1	bos taurus
1300	116.5	6.4	822	2	Q9VJ77_DROME	Q9vj77	drosophila
1301	116.5	6.4	830	2	Q4IN92_GIBZE	Q4in92	giberella
1302	116.5	6.4	878	2	Q4SSLS_TETNG	Q4ssl5	tetraodon n
1303	116.5	6.4	927	1	PALF_NEUCR	Q7sgz5	neurospora
1304	116.5	6.4	1036	1	ACK1_HUMAN	Q79912	homo sapien
1305	116.5	6.4	1057	2	Q4RTQ1_TETNG	Q4rtq1	tetraodon n
1306	116.5	6.4	1083	2	Q2QSF9_ORYSA	Q2qsf9	oryza sativ
1307	116.5	6.4	1095	2	Q5RA00_PONPY	Q5ra00	pongo pygma
1308	116.5	6.4	1129	1	LATS1_MOUSE	Q8byr2	mus musculus
1309	116.5	6.4	1171	2	Q4SWC4_TETNG	Q4swc4	tetraodon n
1310	116.5	6.4	1439	2	Q97406_HALDI	Q97406	haliotis di
1311	116.5	6.4	1442	2	Q42066_9ALPH	Q42066	quail herpe
1312	116.5	6.4	1449	2	Q9U1I2_DROME	Q9u1i2	drosophila
1313	116.5	6.4	1458	2	Q910B9_ONCMY	Q910b9	oncornynch
1314	116.5	6.4	1759	1	CO4A1_CABEL	P71319	caenorhabdi
1315	116.5	6.4	1835	2	Q4S914_TETNG	Q4s914	tetraodon n
1316	116.5	6.4	2103	2	Q17PB6_AEDAE	Q17pb6	aedes aegypt
1317	116.5	6.4	2409	2	Q960G6_DROME	Q960g6	drosophila
1318	116.5	6.4	2795	2	Q708L5_PARLI	Q708l5	paracentrot
1319	116.5	6.4	3288	2	Q7TSD9_CHV1	Q7t5d9	cercopithe
1320	116	6.4	247	2	Q5T5U5_ANOGA	Q5t5u5	anopheles g
1321	116	6.4	248	2	Q866W1_CYNSP	Q866w1	cynopterus
1322	116	6.4	255	1	PRIO_CAMDR	P79141	camelus dro
1323	116	6.4	255	2	Q68G96_CAMBA	Q68g96	camelus bac
1324	116	6.4	385	1	SSBP4_HUMAN	Q9bwg4	homo sapien
1325	116	6.4	501	2	Q8TEE9_HUMAN	Q8tee9	homo sapien
1326	116	6.4	521	2	Q8VKT1_MYCTU	Q8vkt1	mycobacteri
1327	116	6.4	533	1	LCP2_HUMAN	Q13094	homo sapien
1328	116	6.4	533	2	Q53XV4_HUMAN	Q53xv4	homo sapien
1329	116	6.4	551	1	ERF_MOUSE	P70459	mus musculus
1330	116	6.4	551	2	Q6P544_MOUSE	Q6p544	mus musculus
1331	116	6.4	551	2	Q3TXK4_MOUSE	Q3txk4	mus musculus
1332	116	6.4	571	2	Q7ZWT3_XENLA	Q7zwt3	xenopus lae
1333	116	6.4	605	2	Q307M9_METAN	Q307m9	metarhizium
1334	116	6.4	829	2	Q6NSQ1_RHOPA	Q6nsq1	rhodopsuod
1335	116	6.4	907	2	Q44359_NEPCL	Q44359	nephila cla
1336	116	6.4	920	1	CO9A1_CHICK	P12106	gallus gall
1337	116	6.4	959	1	SPTS_ASHGO	Q759t6	ashya goss
1338	116	6.4	1081	2	Q69ZT7_MOUSE	Q69zt7	mus musculus
1339	116	6.4	1124	2	Q5B7C9_EMENI	Q5b7c9	emericeila
1340	116	6.4	1200	2	Q4IJY6_GIBZE	Q4ijy6	giberella
1341	116	6.4	1233	1	SYGPI_FAT	Q9quh6	rattus norv
1342	116	6.4	1352	2	Q50TJ00_BRARE	Q50tj0	brachydanio
1343	116	6.4	1352	2	Q5NT95_PAROL	Q5nt95	paralichthy
1344	116	6.4	1356	2	Q6V5H0_CARAS	Q6v5h0	cardaminops
1345	116	6.4	1431	1	COHA1_MESAU	Q9jmb4	mesocricetu

Q46jv1	prochloroco	1543	2	Q46JV1_PROMT	Q46jv1	prochloroco
Q5j104	mus musculu	1567	1	FMN2_MOUSE	Q5j104	mus musculu
Q5bdw2	emericella	1844	2	Q5BDW2_EMENI	Q5bdw2	emericella
P04925	mus musculu	254	1	PRIO_MOUSE	P04925	mus musculu
Q0gyt9	mus musculu	254	2	Q0QVT9_MOUSE	Q0gyt9	mus musculu
Q3ug89	mus musculu	254	2	Q3UG89_MOUSE	Q3ug89	mus musculu
Q3uf68	mus musculu	254	2	Q3UF68_MOUSE	Q3uf68	mus musculu
Q4uf68	mus musculu	254	2	Q3UBH0_MOUSE	Q4uf68	mus musculu
Q4fjg7	h prnp prot	254	2	Q4FJG7_MOUSE	Q4fjg7	h prnp prot
Q9Q0C7	human herpe	357	2	Q9Q0C7_HHV2	Q9Q0C7	human herpe
Q9Q0C8	human herpe	357	2	Q9Q0C8_HHV2	Q9Q0C8	human herpe
Q410q3	giberella	422	2	Q410Q3_GIBZE	Q410q3	giberella
Q73wv8	mycobacteri	454	2	Q73WV8_MYCPA	Q73wv8	mycobacteri
Q8ci61	mus musculu	457	1	BAG4_MOUSE	Q8ci61	mus musculu
Q8C4Z4	mus musculu	470	2	Q8C4Z4_MOUSE	Q8C4Z4	mus musculu
Q7m4L6	homo sapien	480	2	Q7M4L6_HUMAN	Q7m4L6	homo sapien
P49455	drosophila	518	1	TPM4_DROME	P49455	drosophila
Q5YrG4	nocardia fa	522	2	Q5YRG4_NOCFA	Q5YrG4	nocardia fa
Q3wh39	frankia sp.	630	2	Q3WH39_9ACTO	Q3wh39	frankia sp.
Q6azq8	xenopus lae	681	2	Q6AZQ8_XENLA	Q6azq8	xenopus lae
Q82ev6	streptomyce	701	2	Q82EV6_STRAW	Q82ev6	streptomyce
Q6mi66	bdellovibri	717	2	Q6MI66_BDEBA	Q6mi66	bdellovibri
Q9H8U5	homo sapien	726	2	Q9H8U5_HUMAN	Q9H8U5	homo sapien
Q96ss8	homo sapien	803	2	Q96SS8_HUMAN	Q96ss8	homo sapien
Q8cd02	mus musculu	820	2	Q8CD02_MOUSE	Q8cd02	mus musculu
Q17A80	aedes aegypt	840	2	Q17A80_AEDAE	Q17A80	aedes aegypt
Q171T5	aedes aegypt	982	2	Q171T5_AEDAE	Q171T5	aedes aegypt
Q3ph67	paracoccus	1096	2	Q3PH67_PARDE	Q3ph67	paracoccus
Q4t711	tetraodon n	1140	2	Q4T711_TETNG	Q4t711	tetraodon n
Q1r177	clona intes	1142	2	Q1RL77_CIOIN	Q1r177	clona intes
Q28X10	drosophila	1150	2	Q28X10_DROPS	Q28X10	drosophila
Q4Qgw6	leishmania	1158	2	Q4QGW6_LEIMA	Q4Qgw6	leishmania
Q4Q3E4	usilago ma	1293	2	Q4Q3E4_USTWA	Q4Q3E4	usilago ma
Q8X4p0	mus musculu	1330	2	Q8X4P0_MOUSE	Q8X4p0	mus musculu
Q4R1V6	tetraodon n	1388	2	Q4R1V6_TETNG	Q4R1V6	tetraodon n
Q21dAl	brachydanio	1491	2	Q2LDAl_BRARE	Q21dAl	brachydanio
Q9nc37	neurospora	1578	2	Q9NC37_NEUCR	Q9nc37	neurospora
Q9nx53	homo sapien	252	2	Q9NX53_HUMAN	Q9nx53	homo sapien
Q21zm3	drosophila	254	2	Q21ZM3_DROPS	Q21zm3	drosophila
Q6uuw8	odocoleus	256	2	Q6UW8_9CETA	Q6uuw8	odocoleus
Q6uuw7	odocoleus	256	2	Q6UW7_ODOHE	Q6uuw7	odocoleus
Q2uqb9	aspergillus	291	2	Q2UQB9_ASPOR	Q2uqb9	aspergillus
Q4KR08	lycopersico	302	2	Q4KR08_LYCPE	Q4KR08	lycopersico
Q4KR07	lycopersico	302	2	Q4KR07_LYCPE	Q4KR07	lycopersico
Q1T717	mycobacteri	308	2	Q1T717_MYCO	Q1T717	mycobacteri
Q73wg6	mycobacteri	351	2	Q73WG6_MYCPA	Q73wg6	mycobacteri
Q6AY89	rattus norv	364	2	Q6AY89_RAT	Q6AY89	rattus norv
P23548	paenibacill	397	1	GUN_PAEP0	P23548	paenibacill
Q17mv2	aedes aegypt	407	2	Q17MV2_AEDAE	Q17mv2	aedes aegypt
Q72kp2	thermus the	414	2	Q72KP2_THET2	Q72kp2	thermus the
Q6c831	yarrowia li	420	2	Q6C831_YARLI	Q6c831	yarrowia li
Q7qgv7	anopheles g	429	2	Q7QGV7_ANOGA	Q7qgv7	anopheles g
Q95429	homo sapien	437	1	BAG4_HUMAN	Q95429	homo sapien
Q53hm8	homo sapien	466	2	Q53HM8_HUMAN	Q53hm8	homo sapien
Q5T0M6	homo sapien	466	2	Q5T0M6_HUMAN	Q5T0M6	homo sapien
Q2Jei9	frankia sp.	494	2	Q2JET9_FRASC	Q2Jei9	frankia sp.
Q9Zw78	arabidopsis	504	2	Q9ZW78_ARATH	Q9Zw78	arabidopsis
Q93j30	streptomyce	519	2	Q93J30_STRCO	Q93j30	streptomyce
Q5rgw5	brachydanio	526	2	Q5RGW5_BRARE	Q5rgw5	brachydanio
P50548	homo sapien	548	1	ERF_HUMAN	P50548	homo sapien
Q59g38	homo sapien	561	2	Q59G38_HUMAN	Q59g38	homo sapien
Q66043	cercopithe	589	2	Q66043_9GAMA	Q66043	cercopithe
Q9df69	gallus gall	594	1	CSPG5_CHICK	Q9df69	gallus gall
Q9nhw1	nephila ina	626	2	Q9NHW1_9ARAC	Q9nhw1	nephila ina
Q4J454	azotobacter	628	2	Q4J454_AZOV1	Q4J454	azotobacter
Q1SS78	medicago tr	644	2	Q1SS78_MEDTR	Q1SS78	medicago tr
Q2hgj3	chaetomium	712	2	Q2HGJ3_CHAGB	Q2hgj3	chaetomium
P79832	oncornynch	723	1	ARNT_ONCMY	P79832	oncornynch
P08393	human herpe	775	1	ICP0_HHV11	P08393	human herpe
Q985X8	rhizobium l	789	2	Q985X8_RHILO	Q985X8	rhizobium l
Q94A14	arabidopsis	895	2	Q94A14_ARATH	Q94A14	arabidopsis
Q67Y19	arabidopsis	895	2	Q67Y19_ARATH	Q67Y19	arabidopsis

1419	115	6.3	895	2	Q570B8	ARATH	1492	114	6.2	130	2	Q6EIQ4	BOVIN	06eig4	bos taurus
1420	115	6.3	901	2	Q3WHQ0	9ACTO	1493	114	6.2	130	2	Q6EIQ3	BOVIN	Q6eig3	bos taurus
1421	115	6.3	912	2	Q651Q0	ORYZA	1494	114	6.2	200	2	Q50HW7	OVIDA	Q50hw7	ovis dalli
1422	115	6.3	923	2	Q60424	HUMAN	1495	114	6.2	204	2	Q8R051	MOUSE	P8R051	mus musculus
1423	115	6.3	1094	1	SC24C	HUMAN	1496	114	6.2	225	2	P78440	HUMAN	P78440	homo sapien
1424	115	6.3	1209	2	Q6PF00	MOUSE	1497	114	6.2	226	2	O97907	GAZSU	O97907	gazella sub
1425	115	6.3	1329	2	Q1LW91	BRARE	1498	114	6.2	238	1	PRB4M	HUMAN	P10161	homo sapien
1426	115	6.3	1352	2	Q6LXQ2	BRARE	1499	114	6.2	254	1	PRIO	SIGHI	Q920C3	sigmodon hi
1427	115	6.3	1415	2	Q5JV36	HUMAN	1500	114	6.2	254	2	Q8VHV6	APOSY	Q8vHV6	apodemus sy
1428	115	6.3	1497	1	COH41	HUMAN									
1429	115	6.3	1536	2	Q76L82	HUMAN									
1430	115	6.3	1541	1	ASXL1	HUMAN									
1431	115	6.3	1575	1	SYNJ1	HUMAN									
1432	115	6.3	1884	2	Q9NHW2	9ARAC									
1433	115	6.3	2048	2	Q3VZV9	9ACTO									
1434	115	6.3	2398	2	Q4Q3E5	LEIMA									
1435	115	6.3	2442	1	CBP	HUMAN									
1436	115	6.3	2472	2	Q4LE28	HUMAN									
1437	114.5	6.3	144	2	Q5F2H3	HUMAN									
1438	114.5	6.3	220	2	Q866W7	OCHPR									
1439	114.5	6.3	238	2	Q4WQM6	ASPFU									
1440	114.5	6.3	249	2	Q866W2	CYNXP									
1441	114.5	6.3	257	2	Q58F50	TURTR									
1442	114.5	6.3	257	2	Q4SKP3	TURTR									
1443	114.5	6.3	289	2	Q5JCS5	9GAMA									
1444	114.5	6.3	323	2	Q7XD95	ORYZA									
1445	114.5	6.3	323	2	Q8W368	ORYZA									
1446	114.5	6.3	333	2	Q6CA41	YARLI									
1447	114.5	6.3	361	1	SBP2	MOUSE									
1448	114.5	6.3	361	2	Q540I3	MOUSE									
1449	114.5	6.3	369	2	Q754Z9	NEUCR									
1450	114.5	6.3	377	2	Q8N3K4	HUMAN									
1451	114.5	6.3	410	2	Q9BR76	MOUSE									
1452	114.5	6.3	445	2	Q21414	CAEEL									
1453	114.5	6.3	456	2	Q297C6	DROPS									
1454	114.5	6.3	461	2	Q6C2Y6	YARLI									
1455	114.5	6.3	467	2	Q3W0R6	9ACTO									
1456	114.5	6.3	477	2	Q3UQEO	MOUSE									
1457	114.5	6.3	488	1	ANXA7	MACFA									
1458	114.5	6.3	488	2	Q5T0M7	HUMAN									
1459	114.5	6.3	495	2	Q1S8H3	MEDTR									
1460	114.5	6.3	506	2	Q4XG36	PLASCH									
1461	114.5	6.3	517	2	Q2GSM9	CHAGB									
1462	114.5	6.3	520	2	Q2QSH7	BOVIN									
1463	114.5	6.3	524	2	Q2GVN1	CHAGB									
1464	114.5	6.3	561	2	Q5YJK4	BRARE									
1465	114.5	6.3	565	2	Q8K036	MOUSE									
1466	114.5	6.3	570	2	Q1D0E9	CAEBR									
1467	114.5	6.3	570	2	Q1DD82	MYXXA									
1468	114.5	6.3	587	2	Q74555	SCHPO									
1469	114.5	6.3	658	2	Q4X874	PLACH									
1470	114.5	6.3	688	2	Q171U1	AEDAE									
1471	114.5	6.3	698	2	Q44447	CAEBL									
1472	114.5	6.3	700	2	Q6BMU3	DEBHA									
1473	114.5	6.3	706	1	SYN1	BOVIN									
1474	114.5	6.3	707	1	Q5TGC2	HUMAN									
1475	114.5	6.3	717	1	PRD13	HUMAN									
1476	114.5	6.3	807	2	Q5ASG5	EMENI									
1477	114.5	6.3	816	2	Q1TJY5	9MYCO									
1478	114.5	6.3	816	2	Q1BC44	MYCO									
1479	114.5	6.3	964	2	Q7TS70	MOUSE									
1480	114.5	6.3	975	2	Q6FUW3	CANGA									
1481	114.5	6.3	1009	2	Q3KST0	EBVG									
1482	114.5	6.3	1053	2	Q7Q3D3	ANOAG									
1483	114.5	6.3	1067	2	Q747N2	GEOSL									
1484	114.5	6.3	1095	2	Q5R5N0	PONPY									
1485	114.5	6.3	1125	1	Q5B3C8	EMENI									
1486	114.5	6.3	1208	1	RECQ4	HUMAN									
1487	114.5	6.3	1209	2	Q4WNF8	ASPFU									
1488	114.5	6.3	1606	1	C1C	MOUSE									
1489	114.5	6.3	1682	2	Q15054	HUMAN									
1490	114.5	6.3	1748	2	Q591P1	PIG									
1491	114.5	6.3	3326	2	Q7T591	CHV1									

ALIGNMENTS

RESULT 1

AC0015	HUMAN	STANDARD;	PRT;	325	AA.	
ID	CF015	HUMAN	STANDARD;	PRT;	325	AA.
AC	Q6UXA7	Q5SQ81	Q86Z05	Q9UIG3		
DT	19-JUL-2005	integrated into UniProtKB/Swiss-Prot.				
DT	19-JUL-2005	sequence version 2.				
DT	27-JUN-2006	entry version 19.				
DE	Protein C6orf15 precursor (Protein STG).					
GN	Name=C6orf15; Synonyms=STG; ORFNames=UNQ1840/PRO3566;					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;					
OC	Catarrhini; Hominiidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE [MRNA], AND VARIANT ALA-83.					
RC	TISSUE=Keratinocyte;					
RX	MEDLINE=20014706; PubMed=10545595; DOI=10.1093/hmg/8.12.2165;					
RA	Oka A., Tamiya G., Tomizawa M., Ota M., Katsuyama Y., Makino S.,					
RA	Shina T., Yoshitome M., Lizuka M., Sasao Y., Iwashita K.,					
RA	Kawakubo Y., Sugai J., Ozawa A., Ohkido M., Kimura M., Bahram S.,					
RA	Inoko H.;					
RT	"Association analysis using refined microsatellite markers localizes a					
RT	susceptibility locus for psoriasis-vulgaris within a 11kb segment					
RT	telomeric to the HLA-C gene";					
RL	Hum. Mol. Genet. 8:2165-2170(1999).					
RN	[2]					
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT PHE-40.					
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;					
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,					
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,					
RA	Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,					
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,					
RA	Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,					
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,					
RA	Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,					
RA	Yanura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,					
RA	Wood W.I., Godowski P.J., Gray A.M.;					
RT	"The secreted protein discovery initiative (SPDI), a large-scale					
RT	effort to identify novel human secreted and transmembrane proteins: a					
RT	bioinformatics assessment.";					
RL	Genome Res. 13:2265-2270(2003).					
RN	[3]					
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA], AND VARIANTS ALA-83 AND					
RP	LYS-165.					
RA	Shina T., Ota M., Katsuyama Y., Hashimoto N., Inoko H.;					
RT	"Genome diversity in HLA: a new strategy for detection of genetic					
RT	polymorphisms in expressed genes within the HLA class III and class I					
RT	regions.";					
RL	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.					
RN	[4]					
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA], AND VARIANTS PHE-40;					
RP	ASP-43; ALA-83 AND LYS-165.					
RX	MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;					
RA	Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,					
RA	Wilming L.J., Jones M.C., Horton R., Hunt S.E., Scott C.E.,					
RA	Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,					
RA	Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,					
RA	Babbage A.K., Bagguley C.L., Bailey J., Banerjee R., Barker D.J.,					

RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
RA Blakey S.E., Bray-Allien S., Brook J., Brown A.J., Brown J.Y.,
RA Burford D.C., Burrill W., Burton C., Carder C., Carter N.P.,
RA Chapman J.C., Clark S.Y., Clark G., Clegg S., Cobley V.,
RA Collier R.E., Collins J.B., Colman L.K., Corby N.R., Coville G.J.,
RA Cullley K.M., Dhani P., Davies J., Dunn M., Earthrowl M.E.,
RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,
RA Frankland J., French L., Garner P., Garnett J., Ghori M.J.,
RA Gilby L.M., Gillson C.J., Githero R.J., Graham D.V., Grant M.,
RA Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S.,
RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcote R.,
RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,
RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,
RA Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McLay K.,
RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,
RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,
RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,
RA Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Seale S.M.,
RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggan L.,
RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,
RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,
RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L.,
RA Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,
RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
RA Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.,
RT "The DNA sequence and analysis of human chromosome 6";
RL Nature 425:805-811(2003).
CC -!- SUBCELLULAR LOCATION: Secreted protein (Potential).
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC
DR EMBL; AB031481; BAA88132.1; -; mRNA.
DR EMBL; AY358438; AAQ88804.1; -; mRNA.
DR EMBL; AB088114; BAC54947.1; -; Genomic DNA.
DR EMBL; AL662867; CAI17718.1; -; Genomic DNA.
DR EMBL; AL662844; CAI18322.1; -; Genomic DNA.
DR EMBL; AL773544; CAI18478.1; -; Genomic DNA.
DR Ensembl; ENSG00000137327; Homo sapiens.
DR HGNC; HGNC:13927; C6orf15.
DR RZPD-ProteExp; U0765; -;
KW Polymorphism; Signal.
FT SIGNAL 1 26
FT CHAIN 27 325
FT
FT COMPBIAS 219 284
FT COMPBIAS 290 320
FT VARIANT 40 40
FT
FT VARIANT 43 43
FT
FT VARIANT 83 83
FT
FT VARIANT 165 165
FT
FT SEQUENCE 325 AA; 34222 MW; 42222FIED62C CRC64;
SQ
Query Match 99.7%; Score 1818; DB 1; Length 325;
Best Local Similarity 99.7%; Pred. No. 7.7e-103;
Matches 324; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGRVAGSCAPLGLLVCLHLVCLFARSIQVVEKVSQNFQTNLPQLGQPSSTGPSNSEH 60
DB 1 MGRVAGSCAPLGLLVCLHLVCLFARSIQVVEKVSQNLGLNLPQLGQPSSTGPSNSEH 60
QY 61 POPALDPRNDLARPVLKLSVPPSDGFPFAGGSVAVQRPWPSWGLPAMDSPDPQWMA 120
DB 61 POPALDPRNDLARPVLKLSVPPSDGFPFAGGSVAVQRPWPSWGLPAMDSPDPQWMA 120
QY 121 AAEDRLGEALPEELSYLSAAALPGSGPLPGESSPDATGLSPASLLHQDSRRLLPR 180
RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
RA Blakey S.E., Bray-Allien S., Brook J., Brown A.J., Brown J.Y.,
RA Burford D.C., Burrill W., Burton C., Carder C., Carter N.P.,
RA Chapman J.C., Clark S.Y., Clark G., Clegg S., Cobley V.,
RA Collier R.E., Collins J.B., Colman L.K., Corby N.R., Coville G.J.,
RA Cullley K.M., Dhani P., Davies J., Dunn M., Earthrowl M.E.,
RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,
RA Frankland J., French L., Garner P., Garnett J., Ghori M.J.,
RA Gilby L.M., Gillson C.J., Githero R.J., Graham D.V., Grant M.,
RA Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S.,
RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcote R.,
RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,
RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,
RA Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McLay K.,
RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,
RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,
RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,
RA Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Seale S.M.,
RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggan L.,
RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,
RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,
RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L.,
RA Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,
RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
RA Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.,
RT "The DNA sequence and analysis of human chromosome 6";
RL Nature 425:805-811(2003).
CC -!- SUBCELLULAR LOCATION: Secreted protein (Potential).
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC
DR EMBL; AB031481; BAA88132.1; -; mRNA.
DR EMBL; AY358438; AAQ88804.1; -; mRNA.
DR EMBL; AB088114; BAC54947.1; -; Genomic DNA.
DR EMBL; AL662867; CAI17718.1; -; Genomic DNA.
DR EMBL; AL662844; CAI18322.1; -; Genomic DNA.
DR EMBL; AL773544; CAI18478.1; -; Genomic DNA.
DR Ensembl; ENSG00000137327; Homo sapiens.
DR HGNC; HGNC:13927; C6orf15.
DR RZPD-ProteExp; U0765; -;
KW Polymorphism; Signal.
FT SIGNAL 1 26
FT CHAIN 27 325
FT
FT COMPBIAS 219 284
FT COMPBIAS 290 320
FT VARIANT 40 40
FT
FT VARIANT 43 43
FT
FT VARIANT 83 83
FT
FT VARIANT 165 165
FT
FT SEQUENCE 325 AA; 34222 MW; 42222FIED62C CRC64;
SQ
Query Match 99.7%; Score 1818; DB 1; Length 325;
Best Local Similarity 99.7%; Pred. No. 7.7e-103;
Matches 324; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGRVAGSCAPLGLLVCLHLVCLFARSIQVVEKVSQNFQTNLPQLGQPSSTGPSNSEH 60
DB 1 MGRVAGSCAPLGLLVCLHLVCLFARSIQVVEKVSQNLGLNLPQLGQPSSTGPSNSEH 60
QY 61 POPALDPRNDLARPVLKLSVPPSDGFPFAGGSVAVQRPWPSWGLPAMDSPDPQWMA 120
DB 61 POPALDPRNDLARPVLKLSVPPSDGFPFAGGSVAVQRPWPSWGLPAMDSPDPQWMA 120
QY 121 AAEDRLGEALPEELSYLSAAALPGSGPLPGESSPDATGLSPASLLHQDSRRLLPR 180

not 1-26

```

QY 301 LRPPGSSWNIPAGFPNPPSPRLQW 325
DB 301 LRPPGSSWNIPAGFPNPPSPRLQW 325

RESULT 3
QX113_PANTR
ID QX113_PANTR PRELIMINARY; PRT; 347 AA.
AC QX113;
DT 02-MAY-2006, integrated into UniProtKB/TrEMBL.
DT 02-WAY-2006, sequence version 1.
DT 27-JUN-2006, entry version 2.
DE STG protein.
GN Name=STG;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN NUCLEOTIDE SEQUENCE.
RA Shiina T., Ota M., Katsuyama Y., Hashimoto N., Yanagiya K., Ikeo K.,
RA Tokunaga K., Kulski J.Y., Gojobori T., Inoko H., Bahram S.;
RT "Rapid MHC-I evolution generates new disease alleles via hitch-hiking
RT diversity.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB210148; BAE92757.1; -; Genomic DNA.
DR EMBL; AB210147; BAE92753.1; -; Genomic DNA.
DR InterPro; IPR008165; XGLTT domain.
DR ProDom; PD003992; XGLTT domain; 1.
DR SEQUENCE 347 AA; 36686 MW; 7B8647FDD2D1E0CA CRC64;
SQ
Query Match 98.1%; Score 1789; DB 2; Length 347;
Best Local Similarity 92.8%; Pred. No. 4.8e-101;
Matches 322; Conservative 0; Mismatches 3; Indels 22; Gaps 1;

QY 1 MGRVAGSCAPGLLLVCLHLPGLFARSIGVVEEKVSQNFNTNLPOLGQPSSTGSPNSEH 60
DB 1 MGRVAGSCAPGLLLVCLHLPGLFARSIGVVEEKVSQNFNTNLPOLGQPSSTGSPNSEH 60
QY 61 POPALDPRNSDLARVPLKLSVPPSDGFPAGGSVQVRWPPSGCLPAMDSWPPDPQWMA 120
DB 61 POPALDPRNSDLARVPLKLSVPPSDGFPAGGSVQVRWPPSGCLPAMDSWPPDPQWMA 120
QY 121 AAAEDRLGEALPEELSYLSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSERRLLPR 180
DB 121 AAAEDRLGEALPEELSYLSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSERRLLPR 180
QY 181 SNSLAGGKILSQRPWLSLHRLVLPDHPWGTLNPSVSGGGGPGTGWTRPMPHPEGIWG 240
DB 181 SNSLAGGKILSQRPWLSLHRLVLPDHPWGTLNPSVSGGGGPGTGWTRPMPHPEGIWG 240
QY 241 INNQPCTSWGNI-----NRYPGSGWGNINRYPGSGWGNINRY 278
DB 241 INNQPCTSWGNI-----NRYPGSGWGNINRYPGSGWGNINRYPGSGWGNINRY 300
QY 279 PGSGWGNHLYPGINNPPPGVLRPPGSSWNIPAGFPNPPSPRLQW 325
DB 301 PGSGWGNHLYPGINNPPPGVLRPPGSSWNIPAGFPNPPSPRLQW 347

RESULT 4
CF015_MACMU
ID CF015_MACMU STANDARD; PRT; 314 AA.
AC Q9BLG5;
DT 19-JUL-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2001, sequence version 1.
DT 18-APR-2006, entry version 15.
DE Protein C6orf15 homolog precursor (rmSTG).

```

```

GN Name=STG;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP TISSUE=Taste bud;
RC MEDLINE=21030747; PubMed=11178745; DOI=10.1007/s003350010227;
RA Neira M., Danilova V., Hellekant G., Azen E.A.;
RT "A new gene (rmSTG) specific for taste buds is found by laser capture
RT microdissection.";
RL Mamm. Genome 12:60-66 (2001).
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP PubMed=15269276; DOI=10.1093/molbev/msh216;
RA Kulski J.K., Anzai T., Shiina T., Inoko H.;
RT "Rhesus macaque class I duplication structures, organization, and
RT evolution within the alpha block of the major histocompatibility
RT complex.";
RL Mol. Biol. Evol. 21:2079-2091 (2004).
CC -!- SUBCELLULAR LOCATION: Secreted protein (Potential).
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF245204; AAK09263.1; -; Genomic DNA.
DR EMBL; AB128049; BAD69750.1; -; Genomic DNA.
KW Signal.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 314 Protein C6orf15 homolog.
FT FTID=PRO_0000019542.
FT COMEBIAS 219 273 Gly-rich.
FT COMEBIAS 279 309 Pro-rich.
FT SEQUENCE 314 AA; 32985 MW; 2E79766470229D4B CRC64;
SQ
Query Match 87.3%; Score 1591.5; DB 1; Length 314;
Best Local Similarity 89.8%; Pred. No. 4.6e-89;
Matches 292; Conservative 2; Mismatches 20; Indels 11; Gaps 1;

QY 1 MGRVAGSCAPGLLLVCLHLPGLFARSIGVVEEKVSQNFNTNLPOLGQPSSTGSPNSEH 60
DB 1 MGRVAGSCAPGLLLVCLHLPGLFARSIGVVEEKVSQNFNTNLPOLGQPSSTGSPNSEH 60
QY 61 POPALDPRNSDLARVPLKLSVPPSDGFPAGGSVQVRWPPSGCLPAMDSWPPDPQWMA 120
DB 61 POPALDPRNSDLARVPLKLSVPPSDGFPAGGSVQVRWPPSGCLPAMDSWPPDPQWMA 120
QY 121 AAAEDRLGEALPEELSYLSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSERRLLPR 180
DB 121 AAAEDRLGEALPEELSYLSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSERRLLPR 180
QY 181 SNSLAGGKILSQRPWLSLHRLVLPDHPWGTLNPSVSGGGGPGTGWTRPMPHPEGIWG 240
DB 181 SNSLAGGKILSQRPWLSLHRLVLPDHPWGTLNPSVSGGGGPGTGWTRPMPHPEGIWG 240
QY 241 INNQPCTSWGNI-----NRYPGSGWGNINRYPGSGWGNINRYPGSGWGNINRY 300
DB 241 INNQPCTSWGNI-----NRYPGSGWGNINRYPGSGWGNINRYPGSGWGNINRY 289
QY 301 LRPPGSSWNIPAGFPNPPSPRLQW 325
DB 290 LRPPGSSWNIPAGFPNPPSPRLQW 314

RESULT 5
Q76M7_PIG
ID Q76M7_PIG PRELIMINARY; PRT; 240 AA.
AC Q76M7;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.

```

DE Hypothetical protein STG.
GN Name-STG;
OS Sus scrofa (Pig).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=large white;
RX PubMed=14673549; DOI=10.1007/s00251-003-0627-0;
RA Shigenati A., Ando A., Renard C., Chardon P., Shiina T., Kulski J.K.,
RA Yasue H., Inoko H.;
RT "Nucleotide sequencing analysis of the swine 433-kb genomic segment
located between the non-classical and classical SLA class I gene
clusters.";
RL Immunogenetics 55:695-705(2004).
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB113354; BAD08422.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 25066 MW; AC37EAF2D8ED80B4 CRC64;

Query Match 46.1%; Score 841; DB 2; Length 240;
Best Local Similarity 68.0%; Pred. No. 1.7e-43;
Matches 166; Conservative 16; Mismatches 54; Indels 8; Gaps 2;

QY 1 MGRVAGSCAPLGLLLVCLHPLGLFARISGVVEKVSQNFNTNLPQLGQPSSTGSPNSEH 60
DB 1 MQGLAGSWAPLGLLLVCLHPLGLFARISGVVEKVSQNFNTNLPQLGQPSSTGSPNSEH 60

QY 61 POPALDPRSNLDARVPLKLSVPPSDGFPFAGGSVAQVQRPWGLPAMDSPDPQWMA 120
DB 61 PPKPDLGNLDLAKASPKDPASFSFSLLAGSGVQVQRPWGLPAMDSPDPQWMA 120

QY 121 AAEDRLGEALPEELSYLSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSERRLPR 180
DB 121 AAEDHVGVELPEELSYLSGGFALPRGGGVPP---PHSADPSAEASLLHQDSERRLPR 176

QY 181 SNSLGGAGKILSORPPWMSLIHRV-----LPDHPGNTLNPSVSGGGGPGTGTRMPHPDE 236
DB 177 SNVLGARGELARHLPLWSLINRIRPLPGYMGNLSPSVSGGGGPGTGTRMPHPYV 236

QY 237 GIWG 240
DB 237 GSWG 240

RESULT 6
Q3KNI3_MOUSE
ID Q3KNI3_MOUSE PRELIMINARY; PRT; 349 AA.
AC Q3KNI3;
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 08-NOV-2005, sequence version 1.
DT 27-JUN-2006, entry version 6.
DE Hypothetical protein 2300002M23rik.
GN Name=2300002M23rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH WGC Project;
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BC107266; AA107267.1; -; mRNA.
DR MGI; MGI:1916792; 2300002M23rik.
DR GO; GO:0005615; C:extracellular space; RCA.
DR InterPro; IPR008165; XGLTT domain.
DR ProDom; PD003992; XGLTT_domain; 1.
KW Hypothetical protein.
SQ SEQUENCE 349 AA; 36664 MW; EE61B6D99E5AB0B CRC64;

Query Match 37.4%; Score 681.5; DB 2; Length 349;
Best Local Similarity 44.6%; Pred. No. 1.3e-32;
Matches 160; Conservative 20; Mismatches 124; Indels 55; Gaps 10;

QY 1 MGRVAGSCAPLGLLLVCLHPLGLFARISGVVEKVSQNFNTNLPQLGQPSSTGSPNSEH 60
DB 1 MQSHAGSRAPLGLLLVCLHPLGLFARISGVVEKVSQNFNTNLPQLGQPSSTGSPNSEH 53

QY 61 POPALDPRSNLDARVPLKLSVPPSDGFPFAGGSVAQVQRPWGLPAMDSPDPQWMA 120
DB 54 PPKPDLGNLDLAKASPKDPASFSFSLLAGSGVQVQRPWGLPAMDSPDPQWMA 113

QY 121 AAEDRLGEALPEELSYLSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSERRLPR 180
DB 114 AVAEDQLQMLPEALPYLSR-----GRLPEASSAWLQPSPAAS-YPQDSAGLQPG 165

QY 181 SNSLGGAGKILSORPPWMSLIHRVLPDHPGNTLNPSVSGGGGPGTGTRMPHPDEGIWG 240
DB 166 SSSLETEAEAFARSPFWFLIKLLPGSSGRILRPGTSWGGGAGCTGTRMPYPGSIWG 225

QY 241 INNQPFGTS-----WGNINRY-----PGSGWGNINRYPG-GSWGNIN 276
DB 226 SNGLVSGTSLGGRGYPVRIWGRNGWYPLRLILGNGRYPYPVGTWGGYQYPPVPGWGYG 285

QY 277 RYPG-GSWGNILYLP-----GINNPPPGVLRP-----PGSSW-----NIPAGFNPDS 319
DB 286 QYPPVPGWGYGYPVGTWGANQYPPAGRRRNCRYPAGSWGTKGNRLPPGAKRPGS 344

RESULT 7.
Q8BM15_MOUSE
ID Q8BM15_MOUSE PRELIMINARY; PRT; 349 AA.
AC Q8BM15;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 27-JUN-2006, entry version 19.
DE Adult female vagina cDNA, RIKEN full-length enriched library,
GN clone:9930102M7 product:weakly similar to TASTE BUD-SPECIFIC PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OX Muroidea; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodius R., Shimokawa K.,
 RA Baic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Humineik L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McLintz S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Mattisuzzo S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakaguchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Sempke C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugura K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., Van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamashiki H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=22354683; PubMed=1246851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia K., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozaki-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume Y., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavani T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsuke S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT

```

RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitho H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AK037046; BAC29684.1; -; mRNA.
DR UniGene; Mm.265291; -.
DR Ensembl; ENSMUSG00000039269; Mus musculus.
DR MGI; MGI:1916792; 2300002M23Rik.
DR GO; GO:0005615; C:extracellular space; RCA.
DR InterPro; IPR008165; XGLTT domain.
DR ProDom; PD003992; XGLTT domain; 1.
SQ SEQUENCE 349 AA; 36654 MW; 4EE56EC6197B254F CRC64;

Query Match 37.0%; Score 675.5; DB 2; Length 349;
Best Local Similarity 44.3%; Pred. No. 3e-33;
Matches 159; Conservative 21; Mismatches 124; Indels 55; Gaps 10;

QY 1 MCGRVAGSCAPGLGLVCLHLPGLFARSIGVVEKYSQNGTGLPQLGQPSSTGPSNSEH 60
DB 1 MQSHAGSGRAPLGLLLICLLGLFARSTGAPEKAS-----PHSGQPSFTSLNPGQ 53
QY 61 PQAPLPRNSDLARVPLKLSVPSDGFPPAGGSAGVQRPWSGLPAMDSPDPQWMA 120
DB 54 PQKPPDPVNNELGLVLPRLSESPQDGLPFGSEVNGPFFWGPMPHESPSEDPOQMA 113
QY 121 AAEDRLGEALPELSYLSAAALPGSGLPPESSPDATGLSPESALHLDSESRRLPR 180
DB 114 AVAEDQLQMLPEALPYLSR-----GGRLEPASSARLRQPSLAAS-YPQDSEAGLQPG 165
QY 181 SNLSGAGGKILSRPPNSLHRLVDPHPWGTGLNPSVSWGGGGGTGCTGTPMPHPEGIW 240
DB 166 SSSLETEAEAFARSPFWLHKLLPGSSGRLRPGTSGWGGGAGTGTGTPMPYPSGIW 225
QY 241 INNQPPTS-----WGNINRY-----PGSGWGNINRYPG-GSWGNIN 276
DB 226 SNGLVSTSLGCRGPPVRIWGRNGWYPLRLGNGRYPVPVGTWGGYQYPPVGTWGGY 285
QY 277 RYPG-GSWGNIHLYP-----GINNPPPPGVLRP-----PGSSW-----NIPAGFPNPPS 319
DB 286 QYPPVPGWGGYQYPPVGTWGANCOYPAQSRNCRYPAGSWGKTKGNRLPPGAKRPGS 344

RESULT 8
Q3KN14 MOUSE
ID Q3KN14 MOUSE PRELIMINARY; PRT; 250 AA.
AC Q3KN14;
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 08-NOV-2005, sequence version 1.
DT 27-JUN-2006, entry version 6.
DE 2300002M23Rik protein.
GN Name=2300002M23Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner C.M., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

```

```

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Casapiente M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalun D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BC107265; AA107266.1; -; mRNA.
DR MGI; MGI:1916792; 2300002M23Rik.
DR GO; GO:0005615; C:extracellular space; RCA.
DR InterPro; IPR008165; XGLTT domain.
DR ProDom; PD003992; XGLTT domain; 1.
SQ SEQUENCE 250 AA; 26507 MW; 2F4A12CB42BB7278 CRC64;

Query Match 23.5%; Score 428; DB 2; Length 250;
Best Local Similarity 40.7%; Pred. No. 2.5e-18;
Matches 103; Conservative 17; Mismatches 85; Indels 48; Gaps 9;

QY 107 MDSWPPDPQWMAAAEDRLGEALPELSYLSAAALPGSGLPPESSPDATGLSPEA 166
DB 1 MESWSPDPQWMAAAEDRLGEALPELSYLSAAALPGSGLPPESSPDATGLSPEA 53
QY 167 SLHLDSESRRLPRNSLHRLVDPHPWGTGLNPSVSWGGGGGTG 226
DB 54 S-YPQDSEAGLQPGSSSLETEAEAFARSPFWLHKLLPGSSGRLRPGTSGWGGGAGTG 112
QY 227 WGTTPMPHPEGIWGINNQPPTS-----WGNINRY-----PGSGWGN 263
DB 113 WGTTPMPYPSGIWGSNGLVSTSLGCRGPPVRIWGRNGWYPLRLGNGRYPVPVGTWGG 172
QY 264 INRYPG-GSWGNINRYPG-GSWGNIHLYP-----GINNPPPPGVLRP-----PGSSW----- 308
DB 173 YQYPPVGTWGGYQYPPVPGWGGYQYPPVGTWGANCOYPAQSRNCRYPAGSWGKTKG 232
QY 309 --NIPAGFPNPPS 319
DB 233 QNRLPPGAKRPGS 245

RESULT 9.
Q9VR13 DROME
ID Q9VR13 DROME PRELIMINARY; PRT; 1118 AA.
AC Q9VR13;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 3.
DT 04-APR-2006, entry version 28.
DE CG15635-PA.
GN ORFNames=CG15635, Dmel CG15635;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]

```

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale S., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA De Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zeng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT *melanogaster* euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";

Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
[5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: AS003575; AAF50995.3; -; Genomic_DNA.
DR UniGene; Dm.26729; -. CG15635.
DR FlyBase; FBgn0031617; CG15635.
DR InterPro; IPR002951; Atrophin.
DR InterPro; IPR002052; N6_Mtase.
DR PRINTS; PR01222; ATROPHIN.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 1118 AA; 112437 MW; CAC4F9FB2E26C96D CRC64;
Query Match 10.5%; Score 192; DB 2; Length 1118;
Best Local Similarity 28.0%; Pred. No. 0.0028;
Matches 98; Conservative 24; Mismatches 154; Indels 74; Gaps 20;
QY 3 GRVAGSCAPLGLLVCLHPLGLFARSGVVEEVKVSQNFGLNLPQLGQPSSTGP-SNSEHP 61
Db 609 GLPPGSIPLPGSPNQIGHPPG-----SQKPPNVGIYPPSTGWIPPSGLTQSGHP 658
QY 62 QPALDPRSDNDLARVPLKLSVPPSDGPPFAGGSVQRWPPSWGL-PAMDSW-PPEDPWQMM 119
Db 659 PGSLPPNTGLPPGSIPLRPPRPNQGGHPGSGK---PPNVGIYPPSTGWIPPSGP--- 710
QY 120 AAAAEDRLGEALPELSYLSAAALAPGS---GPLPGESSPDATGLSPASLLHQDSES 175
Db 711 LTQGGHPPGSLPPNTGT-LPGSIPPLPGSPNQIGHPPGSKPPNSGIYPPS-----T 761
QY 176 RRLPRNSLCAGGKILSQRPWMSLI--HRLVPD-----HPWGTLPNSVSWGG 220
Db 762 GSIPPSGLTQGG-----HPPGSLPPNTGLPGSIPPLPGSPNQIGHPPGSKPPNS-GI 815
QY 221 GPGTGWGTRMPHPHPEGINGINNPPTGTSNGINRVPGSGWGNINRVPGSGWGNINRVPG 280
Db 816 YPSTGW---IP-PSGLTQGGHPPGSLPPNTGLPPGSGIS-----PLGSPNQIGHPPG 865
QY 281 GSW-GNIHLYPGINNFPPGVLPFGSSWNIPAGFPNPPS-----PRLQW 324
Db 866 SQKPPNVGIYPPSTGSIIPP--LRPNQGGH-PFGSQKPPNVGIYPPSTGW 912
RESULT 10
Q61SL3 CAEBR ID Q61SL3 CAEBR PRELIMINARY; PRT; 1159 AA.
AC Q61SL3;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 13-JUN-2006, entry version 12.
DE Hypothetical protein CBG06129.
GN Names=CBG06129;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AF16;
RX PubMed=14624247; DOI=10.1371/journal.pbio.0000045;

RA Stein L.D., Bao Z., Blasiar D., Blumenthal T., Brent M.R., Chen N.,
 RA Chinwalla A., Clarke L., Clee C., Coghlan A., Coulson A.,
 RA D'Eustachio P., Fitch D.H.A., Fulton L.A., Fulton R.E.,
 RA Griffiths-Jones S., Harris T.W., Hillier L.W., Kamath R.,
 RA Kuwabara P.E., Mardis E.R., Marra M.A., Miner T.L., Minx P.,
 RA Mullikin J.C., Plumb R.W., Rogers J., Schein J.E., Schramm M.,
 RA Spiech J., Stajich J.B., Wei C., Willey D., Wilson R.K., Durbin R.,
 RA Waterston R.H.,
 RT "The genome sequence of *Caenorhabditis briggsae*: a platform for
 RT comparative genomics.",
 RL PLOS Biol. 1:166-192(2003).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----
 CC Copyrighted by the Uniprot Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; CAAC01000028; CAE62099.1; -; Genomic DNA.
 DR GO; GO:0030127; C:COPII vesicle coat; IEA.
 DR GO; GO:0003779; F:actin binding; IEA.
 DR GO; GO:0005515; F:protein binding; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0006888; P:ER to Golgi vesicle-mediated transport; IEA.
 DR GO; GO:0006886; P:intracellular protein transport; IEA.
 DR InterPro; IPR007112; Gelsolin.
 DR InterPro; IPR001290; Sec23 24 beta S.
 DR InterPro; IPR006900; Sec23_helical.
 DR InterPro; IPR006896; Sec23_trunk.
 DR InterPro; IPR006895; Znf_Sec23_Sec24.
 DR Pfam; PF00626; Gelsolin; 1.
 DR Pfam; PF08033; Sec23_BS; 1.
 DR Pfam; PF04815; Sec23_helical; 1.
 DR Pfam; PF04811; Sec23_trunk; 1.
 DR Pfam; PF04810; zf-Sec23_Sec24; 1.
 DR Complete proteome; Hypothetical protein.
 SQ SEQUENCE 1159 AA; 124569 MW; 7367D400D5EAA4D5 CRC64;
 Query Match 10.5%; Score 191; DB 2; Length 1159;
 Best Local Similarity 24.0%; Pred. No. 0.0033;
 Matches 82; Conservative 30; Mismatches 135; Indels 94; Gaps 16;
 QY 45 POLGQPSSTGSPNSERHPQPALDP-----RSNDLARVPLKLSVPSDGFPP-----89
 DB 6 PQYGP-----PGN---PQQFNQOQNGFPQPGQCKTVQAPGGFPVQVQQPNGG 58
 QY 90 -----AGGSVQRWPP-----SWGLPAMDSWPPDPWQMAAAAEADRLGEALPELSY 137
 DB 59 FYQNGAANGTQSYAQPFGVPVQLTQSVQSMGLGRASP-----APQLGQPAQQMGY 110
 QY 138 LSSAALAPGSGPLPGESSPDATGLSPASLLHQDSESRRLP-----SNSLGAGGKIL 191
 DB 111 PGAPTAVPP-QAOPGQQTQFNGFPQNASQISQAPPSNTAQQAPFVQNSTSSGSSV- 168
 QY 192 SQRPPLSLIHRVLDHPWGLTNPVSVSGGGGPGTGWTRMPHPEGIW-----GI 241
 DB 169 NQNP-----TAPSFHGGPPQTGVCGPGGAGAPQPHQIQPASPRLPQAPGYPAPGV 221
 QY 242 NNOPPT--SWGNINRYPGSGWGNINRYPGSGWGNINRYPGSGWGNIHLYPGIN-----293
 DB 222 PNFQPGVAPSPQTPNNYPMPQPTPGNYPCAPAGLQOQPGGN-----YFGAQPATQQG 275
 QY 294 -----NPPFPGVLRP-PGSSWNIIPAGFN-----PPSPR 321
 DB 276 APRGFPPGSPGAPFPVPGAPSNFFPFGPAMFCAFPAPQ 316
 RESULT 11
 Q3BDW0_BRARE
 ID Q3BDW0_BRARE PRELIMINARY; PRT; 606 AA.
 AC Q3BDW0;
 DT 22-NOV-2005, integrated into UniprotKB/TrEMBL.

DT 22-NOV-2005, sequence version 1.
 DT 27-JUN-2006, entry version 8.
 DE Prion protein 1.
 GN Name=prnrs1; Synonyms=prp1;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed:16352647;
 RA Rivera-Milla E., Oidtman B., Panagiotidis C.H., Baier M.,
 RA Sklavadias T., Hoffmann R., Zhou Y., Solis G.P., Stuermer C.A.O.,
 RA Malaga-Trillo E.,
 RT "Disparate evolution of prion protein domains and the distinct origin
 RT of Doppel- and prion-related loci revealed by fish-to-mammal
 RT comparisons.",
 RL FASEB J. 20:317-319(2006).
 CC -----
 CC Copyrighted by the Uniprot Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AY438683; AAS00159.1; -; mRNA.
 DR UniGene; Dr.37983; -.
 DR ZFIN; ZDB-GENE-041221-2; prnrs1.
 DR InterPro; IPR000817; Prion.
 DR InterPro; IPR008165; XGLTT domain.
 DR ProDom; PD003992; XGLTT_domain; 1.
 DR SMART; SM00157; PRP; 1.
 KW Prion.
 SQ SEQUENCE 606 AA; 62806 MW; 1FE4FD4E3FBA494 CRC64;
 Query Match 9.6%; Score 176; DB 2; Length 606;
 Best Local Similarity 27.1%; Pred. No. 0.014;
 Matches 92; Conservative 24; Mismatches 97; Indels 126; Gaps 22;
 QY 34 EKVSQNGT--NLPLQGGPSTGSPS-----NSBHP-----QPALDPRSNDLARVPLKLS 80
 DB 39 EKTSGTKTQPNYPR--QPSNPGAGSNPGYNQYFGRGSSPSGYPNQ-----86
 QY 81 VPPSDGPPFAGGSVAVQWPP--PSWGLPAMDSWPPDPWQMAAAAEADRLGEALPELSYLS 139
 DB 87 --PGAGSYPAAGS---VPYPRGSGSPGGYPNQ-----115
 QY 140 SAAALAPGSGPLP-GESSPDATGLSPASLLHQDSESRRLPNSLGGAGKILSORPPWS 198
 DB 116 -----PGAGSYPGGSPYSAGG-----NPNQYFGRGYNPGG--YPNQNG-- 154
 QY 199 LIHRVLDHPWGLTNPVSVSGGGG---PGTGWTRMPHPEGIWGINNQPPGTW---250
 DB 155 -----AGSYPAAGSYPS---AGGNPNQYFGRG-GTSPAGYNQNPAGSYPAAGSYPSAG 205
 QY 251 GNINRYPGSGWGNINRYP-----GGSW-----GNINRYP--GGS--WGNIHLYPG 291
 DB 206 GNPQYFGRGSGNPGGYPNQNPAGSYPAAGSYPAAGSYPAAGSNQYFGRGSSPGGNPNQNG 265
 QY 292 IN-----NPPFPG---VLRPGSSWNIIPAGFPNPS 319
 DB 266 AGTYAGGYPNQYFGRGSGSNQNPGRSGYSPGGYPGAGS 304
 RESULT 12
 Q5KOE1_BRARE
 ID Q5KOE1_BRARE PRELIMINARY; PRT; 606 AA.
 AC Q5KOE1;
 DT 15-FEB-2005, integrated into UniprotKB/TrEMBL.
 DT 15-FEB-2005, sequence version 1.
 DT 27-JUN-2006, entry version 11.
 DE Prion protein 1 precursor.
 GN Name=prnrs1;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


```
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Olfactory epithelium;
RG NIH MGC Project;
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BC108050; AAI08051.1; -; mRNA.
DR ZFIN; ZDB-GENE-041221-2; zrnprsl.
DR InterPro; IPR008165; XGLTT_domain.
DR ProDom; PD003992; XGLTT_domain; 1.
KW Hypothetical protein.
SQ SEQUENCE 606 AA; 62929 MW; 59129C0B636FA7CD CRC64;
Query Match 9.6%; Score 175; DB 2; Length 606;
Best Local Similarity 27.1%; Pred. No. 0.016;
Matches 92; Conservative 24; Mismatches 97; Indels 126; Gaps 22;
Qy 34 EKVSQFQGT--NLPLQGPSTGTPS-----NSEHP-----QPALDPRSNLDARVPLKLS 80
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 81 VPPSDGFPFAGGSVAVQWKP-PSWGLPAMDSWPPDPWQMMAAAEDRLGEALPELSYLS 139
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 140 SAAALAPGSGPLP-GESSPDATGLSPASLLHQDSERRLPRNSLGGAGKILSORPPWS 198
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 116 -----PGAGSYSGGSGYPAGG-----NPNQYPRGSGYPPGG-YPNQNPAG 156
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 199 LIHRVLPDHPWGTLPNSVWGGGG-----PGTGWCTRPMPHPEGIWNINPPGTSW--- 250
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 157 F-----YAGGSYPS-----AGGNPNQYPRG-GTSPAGYPNQNPAGSYPSAG 205
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 251 GNINRYPGSGWGNINRYP-----GGSW-----GNINRYP--GGS--WGNHLYPG 291
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 206 GNPQYPRGSGNSPGGYPNQNPAGSYPSAGSYPSAGSNQYPRGSGSPGGNPNQNPAG 265
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 292 IN-----NPPPPG---VLRPPGSSWNIPAGFPNPPS 319
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 266 AGTVAGGYPNQYPGGGYSNQNPGRSGFSGYPGAGS 304
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
RESULT 15
ID Q8K1P7_RAT PRELIMINARY; PRT; 1613 AA.
AC Q8K1P7;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 24.
DE Brahma-related protein 1 (fragment).
GN Name=brg-1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wistar; TISSUE=Hippocampus;
RL Hirsch O. Almeida O.F.X.;
RA Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
CC -!- INTERACTION:
CC Q4KLI0:Smarcb1_predicted; NbExp1; IntAct=EBI-689301, EBI-689316;
CC -----
```

```
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AJ504723; CAD43278.1; -; mRNA.
DR IntAct; Q8K1P7; -
DR Ensembl; ENSRNOC0000009271; Rattus norvegicus.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR006576; BRK.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR011545; DEAD/DEAH N.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR008562; HSA.
DR InterPro; IPR000330; SNF2_N.
DR Pfam; PF00439; Bromodomain; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF07529; HSA; 1.
DR Pfam; PF00176; SNF2_N; 1.
DR Pfam; PF07533; TCH; 1.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00592; BRK; 1.
DR SMART; SM00487; BROMO; 1.
DR SMART; SM00490; HELIC_C; 1.
DR SMART; SM00573; HSA; 1.
DR PROSITE; PS00633; BROMODOMAIN_1; 1.
DR PROSITE; PS0014; BROMODOMAIN_2; 1.
FT NON_TER 1
FT NON_TER 1613
SQ SEQUENCE 1613 AA; 191427 MW; 7E5F1B04D4C26C87 CRC64;
Query Match 9.5%; Score 174; DB 2; Length 1613;
Best Local Similarity 25.6%; Pred. No. 0.051;
Matches 95; Conservative 22; Mismatches 124; Indels 130; Gaps 20;
Qy 45 POLQGPSTGSEHQPALDPRSNLDARVPLKLSVPPSPGFPFAGGSVAVQWKP-----P 99
Db 6 PPLGTPRPGSPGPGSPG-----AMLGSPG--PSPGSAHMMGPGSPG 49
Qy 100 PSWGLPAMDSWP---PEDPQMMAAAEDRLGEALPELSY-----LSSAALAPGSGPL 151
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 50 PSAGHPMTQGGYPGGYPDQNMHQMHPESMEHKGMPDDPRYNQMKGMGRGSAHTGMGPP 109
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 152 PGESSPDATGL-SPEASLLHQDSERRLPRSN-----SLGAGGKILSORPPWSL---- 199
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 110 PSPMDQHSQGYPSPLGGSEHASP---VPASGSPSSGPGMSSGPGAPLDGSDPQALGQON 166
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 200 -----IHRV-----LPDH-----PMGTLN-----PSVS 217
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 167 RGPTFFNQNLHQLRAQIMAYKMLARGQLPDHLQMAVQGRKPMPMQOQMPTLPPPSVS 226
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 218 WGGGGPGTGWGTRPMP-----HPSGIWGINNQPPGTSW---GNINRYPGSGWGNINR 266
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 227 ATGPGPGPGPGPGPGAPPNNYSRPHGMGPNMPPPGSPGVPPGMPQPPGG----- 279
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 267 YPGSGWGNINRYPGSGWGNI-----HLYP-----GINNFPFPGVLRPPGSSWNIP--- 311
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 280 -PPKPW-----PSGPMANAAAPTSTPKLIPPTGTGRSPAPPAV--PPAASPTWPPQT 330
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 312 --AGFPNPPSP 320
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 331 QSPGQPAQPAP 341
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Search completed: July 30, 2007, 16:46:13
Job time : 288 secs
```

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 30, 2007, 16:39:49 ; Search time 40 Seconds
(without alignments)
781.761 Million cell updates/sec

Title: US-10-063-569-64

Perfect score: 1824

Sequence: 1 MGRVAGSCAPLGLLVCLH.....SSWNIPAGFPNPPSPRLQWG 325

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	165.5	9.1	2715	T13049	eyelid - fruit fly
2	163	8.9	1647	S45252	SNR2beta protein -
3	157	8.6	1373	A43291	collagen alpha 2(I
4	156.5	8.6	1613	S39059	protein BRG1 - hum
5	156	8.6	1366	CGHU28	collagen alpha 2(I
6	153.5	8.4	464	A47655	spliceosome-associ
7	150.5	8.3	255	AF1857	hypothetical prote
8	150.5	8.3	431	S09824	hypothetical prote
9	150	8.2	680	1 CGHU1D	collagen alpha 1(X
10	150	8.2	966	2 A33626	fibrinogen alpha c
11	145.5	8.0	1388	2 A53317	collagen alpha 1(X
12	144	7.9	1184	2 G01763	atrophin-1 - human
13	142	7.8	1184	2 S08332	atrophin-1 - human
14	141.5	7.8	1006	2 G86292	hypothetical prote
15	141	7.7	1315	2 A56101	collagen alpha 1(X
16	141	7.7	1774	2 B56101	collagen alpha 1(X
17	140.5	7.7	1880	2 T18531	tractin - medicina
18	138.5	7.6	888	2 S28791	collagen alpha 1(X
19	138	7.6	641	2 T30076	hypothetical prote
20	137.5	7.5	660	1 Q9BE3	BHLF1 protein - hu
21	137	7.5	1126	2 T20801	hypothetical prote
22	136.5	7.5	1669	1 CGMS4B	collagen alpha 1(I
23	136	7.5	1049	1 CGS07S	collagen alpha 1(I
24	136	7.5	1496	1 CGHU2V	collagen alpha 2(I
25	136	7.5	1752	2 A45407	collagen alpha 3(I
26	135.5	7.4	674	2 S23297	collagen alpha 1(X
27	135.5	7.4	1069	2 S27922	nuclear antigen BB
28	134.5	7.4	589	2 T29299	hypothetical prote
29	134.5	7.4	886	2 I50694	collagen alpha 1(I

30	134.5	7.4	1497	2	I49607	procollagen type V
31	134	7.3	1806	1	CGHU1E	collagen alpha 1(X
32	133.5	7.3	445	2	A27263	50K spicule matrix
33	133.5	7.3	670	1	FG4540	hypothetical prote
34	133.5	7.3	779	1	CGBO1S	collagen alpha 1(I
35	133	7.3	1142	2	T00022	B120 protein - hum
36	133	7.3	1690	1	CGHU1B	collagen alpha 4(I
37	132.5	7.3	310	1	PIHUSD	salivary proline-r
38	132.5	7.3	704	2	A30411	synapsin Ia - rat
39	131	7.2	1042	1	CGCH1S	collagen alpha 1(I
40	131	7.2	1546	1	CGHU2E	collagen alpha 2(X
41	130.5	7.2	919	2	A39248	androgen receptor
42	130.5	7.2	1453	2	S21626	collagen alpha 1(I
43	130.5	7.2	1869	1	CGHU4B	hypothetical prote
44	130	7.1	1357	2	T29265	hypothetical prote
45	130	7.1	1414	1	S23809	collagen alpha 2(I
46	129.5	7.1	1843	2	S18803	collagen alpha 1(V
47	129	7.1	1464	2	S59856	collagen alpha 1(I
48	128.5	7.0	910	2	A34721	androgen receptor
49	128.5	7.0	911	2	B34721	androgen receptor
50	128	7.0	674	2	S13301	collagen alpha 1(X
51	128	7.0	707	2	A46302	PTB-associated spl
52	128	7.0	1838	1	CGHU1V	collagen alpha 1(V
53	127.5	7.0	1142	2	T37455	enamelin precursor
54	127.5	7.0	1466	1	CGHU7L	collagen alpha 1(I
55	127.5	7.0	1670	1	CGHU3B	collagen alpha 3(I
56	127	7.0	754	2	A55267	collagen alpha 5(I
57	127	7.0	1106	1	TVHUGL	transforming prote
58	126.5	6.9	548	2	S52735	CW17R protein - mo
59	126.5	6.9	639	2	G02919	transcription fact
60	126	6.9	743	1	S23779	collagen alpha 1(V
61	126	6.9	1122	2	T47424	hypothetical prote
62	126	6.9	1464	1	CGHU1S	collagen alpha 1(I
63	125.5	6.9	582	2	S10099	transcription fact
64	125.5	6.9	730	2	A36226	collagen alpha 1 c
65	125.5	6.9	860	2	S43846	xylanase B - rumen
66	125.5	6.9	1758	2	T29350	hypothetical prote
67	125	6.9	574	2	T38819	wiskott-aldrich sy
68	125	6.9	636	2	S41067	collagen alpha 1(I
69	125	6.9	940	2	JE0291	FB19 protein - hum
70	125	6.9	1691	1	S22917	collagen alpha 5(I
71	125	6.9	1759	2	T29351	collagen alpha 2(I
72	124.5	6.8	872	2	S33015	hypothetical prote
73	124.5	6.8	992	2	A31666	hypothetical prote
74	124.5	6.8	1487	1	CGHU6C	collagen alpha 1(I
75	124.5	6.8	3530	2	A59266	unconventional myo
76	124	6.8	744	1	A34246	collagen alpha 1(V
77	124	6.8	744	1	S23298	collagen alpha 1(V
78	124	6.8	903	2	T00705	N-chimerin homolog
79	124	6.8	1008	2	T04462	hypothetical prote
80	124	6.8	1048	2	T31425	C-terminal domain-
81	124	6.8	1069	2	D85383	hypothetical prote
82	123.5	6.8	435	2	T15143	hypothetical prote
83	123.5	6.8	501	2	S76563	hypothetical prote
84	123.5	6.8	1418	2	T45467	collagen alpha 1(I
85	123	6.7	323	2	T27450	hypothetical prote
86	123	6.7	744	2	S15435	collagen alpha 1(V
87	123	6.7	2142	2	B35098	MHC class III hist
88	123	6.7	3124	2	A40020	collagen alpha 1(X
89	122.5	6.7	309	2	S10889	proline-rich prote
90	122.5	6.7	392	1	PIHUB6	salivary proline-r
91	122.5	6.7	418	2	T15142	hypothetical prote
92	122.5	6.7	623	2	A45137	collagen alpha 4(I
93	122.5	6.7	1168	1	MWAXIC	myosin heavy chain
94	122	6.7	323	2	S20099	transforming prote
95	122	6.7	463	2	T10015	hypothetical prote
96	122	6.7	488	2	F86911	conserved hypoteth
97	122	6.7	574	2	T43556	Wiskott-Aldrich sy
98	122	6.7	783	2	T35389	probable serine-th
99	122	6.7	1857	2	S31212	collagen alpha 1(X
100	122	6.7	1888	2	S78476	collagen alpha 1(X
101	121.5	6.7	469	2	A24450	collagen alpha 2(V
102	121	6.6	654	2	A34734	transcription fact

103	121	6.6	673	1	CG806C	collagen alpha 1(I	176	114	6.2	548	2	S59133	ETS2 repressor fac
104	121	6.6	742	4	B34734	transcription fact	177	114	6.2	680	2	S31216	collagen alpha 1(X
105	121	6.6	825	4	B34734	transcription fact	178	114	6.2	1024	2	S18251	protein F54D8.1 (i
106	121	6.6	862	2	T46289	hypothetical prote	179	114	6.2	1120	2	H88449	probable DNA-direc
107	121	6.6	1255	2	T31065	diaphanous protein	180	113.5	6.2	337	2	T49627	transcription fact
108	121	6.6	1433	2	A46053	bullous pemphigoid	181	113.5	6.2	444	1	A39794	synapsin Ia - bovi
109	121	6.6	1486	1	B40338	collagen alpha 1(I	182	113.5	6.2	706	2	E30411	initiation factor
110	120.5	6.6	212	2	B36298	proline-rich prote	183	113.5	6.2	924	2	F87103	hypothetical prote
111	120.5	6.6	812	2	S31521	collagen COLF1 - f	184	113.5	6.2	1007	2	T01437	collagen, cornea-s
112	120.5	6.6	1712	1	CGHU2B	collagen alpha 2(I	185	113.5	6.2	1146	2	A38587	hypothetical prote
113	120.5	6.6	1747	2	A54121	collagen alpha-4 c	186	113.5	6.2	1621	2	T15264	transcription adap
114	120.5	6.6	1747	2	A54974	collagen alpha 1(X	187	113.5	6.2	2414	2	A54277	unconventional myo
115	120.5	6.6	3164	1	WMBEH6	UL36 protein - hum	188	113.5	6.2	3511	2	A59295	major prion PrP-Sc
116	120.5	6.6	4957	2	T03455	ALR protein - huma	189	113	6.2	252	2	JC6175	major prion PrP-Sc
117	120.5	6.6	5262	2	T03454	hypothetical prote	190	113	6.2	254	1	UJHYIH	prion protein - Gh
118	120	6.6	309	2	T29293	lipoprotein vsaG l	191	113	6.2	254	2	B34759	major prion protei
119	120	6.6	430	2	G90577	collagen alpha 1(I	192	113	6.2	257	2	JQ1900	major prion PrP27-
120	120	6.6	1419	2	A41182	collagen alpha 1(I	193	113	6.2	257	2	A23545	hypothetical prote
121	120	6.6	1487	2	B41182	collagen alpha 1(X	194	113	6.2	403	2	S52796	fibronin-3 related
122	119.5	6.6	1603	2	S23810	collagen - silkwor	195	113	6.2	527	2	T49510	interleukin-3 rece
123	119	6.5	569	2	S42886	collagen alpha 2(V	196	113	6.2	670	2	T49510	basal transcrip
124	119	6.5	635	2	A57131	hypothetical prote	197	113	6.2	896	2	I56563	MEGF1 protein - ra
125	119	6.5	731	2	B86369	hypothetical prote	198	113	6.2	1469	2	T09219	major prion protei
126	119	6.5	1441	2	B86807	hypothetical prote	199	113	6.2	4351	2	T00252	collagen, cuticula
127	119	6.5	1691	1	CGHU6B	collagen alpha 6(I	200	112.5	6.2	286	2	S34665	synovial sarcoma t
128	118.5	6.5	699	2	A43674	US4 protein - huma	201	112.5	6.2	294	2	A53892	annexin VII - mous
129	118.5	6.5	931	2	S33580	collagen alpha 1(I	202	112.5	6.2	1334	2	T50568	cloacin Df13 prote
130	118.5	6.5	964	1	CGCH2S	collagen alpha 2(I	203	112.5	6.2	1638	2	A42091	probable integr
131	118.5	6.5	1323	2	T78557	N-methyl-D-asparta	204	112.5	6.2	1744	2	S40391	probable transcrip
132	118.5	6.5	1356	1	C45219	N-methyl-D-asparta	205	112.5	6.2	226	2	A54849	probable multi-dom
133	118.5	6.5	1870	2	S37671	MHC class III hist	206	112.5	6.2	2944	2	A53892	transcription acti
134	118.5	6.5	1872	2	S36152	MHC class III hist	207	112.5	6.2	1334	2	T50568	collagen alpha 1(I
135	118	6.5	256	2	JU0268	major prion protei	208	112.5	6.2	1638	2	A42091	collagen alpha 1(V
136	118	6.5	256	2	S37149	prion protein - go	209	112.5	6.2	226	2	A53892	prion-related prot
137	118	6.5	256	2	A54281	major prion protei	210	112.5	6.2	2944	2	A53892	major prion protei
138	118	6.5	264	2	A54330	major prion protei	211	112.5	6.2	1334	2	T50568	DNA-binding regula
139	118	6.5	780	2	T00366	hypothetical prote	212	112	6.1	502	2	S71048	collagen alpha 1 c
140	117.5	6.4	264	2	S37137	prion protein - gr	213	112	6.1	241	2	A48679	collagen alpha 3(I
141	117.5	6.4	310	2	I50696	collagen alpha 1(I	214	112	6.1	616	2	I38155	hypothetical prote
142	117.5	6.4	671	1	CGHT1S	collagen alpha 1(I	215	112	6.1	632	2	S42731	collagen alpha 1(X
143	117.5	6.4	691	2	A25704	synapsin I - rat	216	112	6.1	684	2	A53019	helix-destabiliz
144	117.5	6.4	841	2	T01046	hypothetical prote	217	112	6.1	1492	2	A40333	collagen alpha 1'
145	117.5	6.4	1072	2	A37127	microtubule-associ	218	112	6.1	1504	2	T49896	glycine/proline-ri
146	117	6.4	760	2	T16726	hypothetical prote	219	112	6.1	253	1	UJHU	major prion protei
147	116.5	6.4	291	2	T31592	hypothetical prote	220	111.5	6.1	253	2	S53617	major prion protei
148	116.5	6.4	424	2	A54964	spliceosome-associ	221	111.5	6.1	253	2	S53635	major prion protei
149	116.5	6.4	488	2	A27353	collagen alpha 1(I	222	111.5	6.1	253	2	I37032	major prion protei
150	116.5	6.4	1091	2	S33596	protein-tyrosine k	223	111.5	6.1	618	2	S02436	major prion protei
151	116.5	6.4	1442	2	T42607	transcription acti	224	111	6.1	825	1	EDBXD	immediate-early pr
152	116	6.4	432	2	T23561	hypothetical prote	225	111	6.1	839	2	T04859	collagen alpha 1(I
153	116	6.4	533	2	A56110	tyrosine phosphor	226	111	6.1	921	2	S40495	collagen alpha 2(I
154	116	6.4	920	2	B34493	collagen alpha 1(I	227	111	6.1	1707	2	A33526	collagen alpha 2(I
155	116	6.4	1166	2	T13958	synGAP-bi protein	228	111	6.1	2027	2	S60123	hypothetical prote
156	116	6.4	1249	2	T14270	Ras-GTPase activat	229	111	6.1	2056	2	G88564	protein R10E11.1 (
157	116	6.4	1293	2	T14259	ras GTPase-activat	230	111	6.1	1215	2	T32734	myosin-IA - Acanth
158	116	6.4	1341	2	T17285	hypothetical prote	231	111	6.1	1549	2	I48103	type VII collagen
159	115.5	6.3	254	2	A23544	major prion protei	232	111	6.1	236	2	T21070	hypothetical prote
160	115.5	6.3	358	1	WMBE38	infected cell prot	233	111	6.1	356	2	T26449	hypothetical prote
161	115.5	6.3	480	2	JC7552	Shb-like adapter p	234	111	6.1	375	2	JS0427	S-antigen precursor
162	115.5	6.3	803	2	F59433	RhoGAP protein [im	235	111	6.1	615	2	A05269	collagen alpha 1(I
163	115.5	6.3	1323	2	S27224	N-methyl-D-asparta	236	111	6.1	618	2	S32436	collagen alpha 2(I
164	115	6.3	397	2	A35136	cellulase (EC 3.2.	237	111	6.1	825	1	EDBXD	immediate-early pr
165	115	6.3	504	2	H84862	hypothetical prote	238	111	6.1	839	2	T04859	collagen alpha 1(I
166	115	6.3	516	2	C44479	collagen alpha 1(X	239	111	6.1	921	2	S40495	collagen alpha 2(I
167	115	6.3	662	2	T17339	hypothetical prote	240	111	6.1	1707	2	A33526	collagen alpha 2(I
168	115	6.3	705	2	A35363	synapsin I splice	241	111	6.1	2027	2	S60123	hypothetical prote
169	115	6.3	775	1	EDBE11	immediate-early pr	242	111	6.1	2056	2	G88564	protein R10E11.1 (
170	115	6.3	1532	2	A61262	collagen alpha 1(X	243	110.5	6.1	1215	2	T32734	myosin-IA - Acanth
171	114.5	6.3	361	2	T12470	hypothetical prote	244	110.5	6.1	1549	2	I48103	type VII collagen
172	114.5	6.3	488	1	LHU07	annexin VII, long	245	110	6.0	236	2	T21070	hypothetical prote
173	114.5	6.3	587	2	T41653	probable transcrip	246	110	6.0	356	2	A96826	T8K14.10 [imported
174	114.5	6.3	698	2	T32594	hypothetical prote	247	110	6.0	512	2	S70644	annexin VII - Afri
175	114	6.2	402	1	CG802S	collagen alpha 2(I	248	110	6.0	532	2	S74453	hypothetical prote

249	110	6.0	571	2	T43456	hypothetical prote	322	106	5.8	1596	2	A33106	neurogenic locus m
250	110	6.0	708	1	QBEB8	U80 protein - hum	323	106	5.8	4180	2	G83559	hypothetical prote
251	110	6.0	751	1	Q87B89	protein C34G6.2 (l	324	105.5	5.8	136	2	T29282	hypothetical prote
252	110	6.0	1201	2	G86441	unknown protein (l	325	105.5	5.8	312	2	T25048	hypothetical prote
253	109.5	6.0	433	2	S20963	homeotic protein H	326	105.5	5.8	325	2	T32248	hypothetical prote
254	109.5	6.0	760	2	F86387	probable Pro kinas	327	105.5	5.8	572	2	JC7833	kumamolysin precu
255	109.5	6.0	818	2	A59433	KIAA0672 protein (l	328	105.5	5.8	751	2	T15230	hypothetical prote
256	109.5	6.0	1684	2	T02367	hypothetical prote	329	105.5	5.8	899	2	A35895	androgen receptor
257	109.5	6.0	2774	2	A43359	microtubule-associ	330	105.5	5.8	1240	2	JC5209	insulin receptor s
258	109.5	6.0	3198	2	A43426	collagen alpha 2 f	331	105.5	5.8	1274	2	T37193	enamelin matrix pr
259	109	6.0	317	2	T19143	hypothetical prote	332	105.5	5.8	2588	2	T14342	NSD1 protein - mou
260	109	6.0	460	2	T33110	hypothetical prote	333	105	5.8	505	2	A53152	annexin XI - human
261	109	6.0	921	2	S42617	collagen alpha 1(l	334	105	5.8	530	2	A45690	transactivator EBN
262	109	6.0	1039	2	T35878	hypothetical prote	335	105	5.8	533	2	S37781	retinoid X recepto
263	109	6.0	1106	2	T31742	hypothetical prote	336	105	5.8	558	2	JC2004	nuclear factor-kap
264	109	6.0	1125	2	B41206	microtubule-associ	337	105	5.8	772	2	T13078	KIAA0992 protein -
265	108.5	5.9	241	2	S71056	major prion protei	338	105	5.8	953	2	A86351	hypothetical prote
266	108.5	5.9	253	2	S53624	major prion protei	339	105	5.8	1027	2	S28774	collagen alpha cha
267	108.5	5.9	253	2	S53623	major prion protei	340	105	5.8	1249	2	T14150	vesicle associated
268	108.5	5.9	253	2	S53620	major prion protei	341	105	5.8	1420	2	T37781	probable cytoskele
269	108.5	5.9	253	2	S53625	major prion protei	342	105	5.8	1446	1	A45344	immediate-early pr
270	108.5	5.9	253	2	I84423	major prion protei	343	105	5.8	1487	1	EDB8F6	155K transcription
271	108.5	5.9	253	2	S71055	major prion protei	344	105	5.8	3176	2	CGHU3A	collagen alpha 3(V
272	108.5	5.9	309	2	T28708	hypothetical prote	345	105	5.8	3190	2	T13828	CREB-binding prote
273	108.5	5.9	317	2	A28996	proline-rich prote	346	104.5	5.7	227	2	C29149	proline-rich prote
274	108.5	5.9	326	2	T29810	hypothetical prote	347	104.5	5.7	252	2	S53634	major prion protei
275	108.5	5.9	326	2	J50169	collagen col-14 -	348	104.5	5.7	260	2	S22373	proline-rich prote
276	108.5	5.9	656	1	A49358	RNA-binding protei	349	104.5	5.7	330	2	S46657	collagen alpha 1(X
277	108.5	5.9	959	2	S32605	collagen alpha 3(V	350	104.5	5.7	431	1	KJHU2G	homeotic protein H
278	108	5.9	242	2	JC4300	galectin-3 - rabbi	351	104.5	5.7	561	2	T16148	hypothetical prote
279	108	5.9	283	2	T19732	hypothetical prote	352	104.5	5.7	666	2	B70803	hypothetical prote
280	108	5.9	341	1	TVM5JD	transforming prote	353	104.5	5.7	946	2	JC7810	inositol 1,4,5-tri
281	108	5.9	644	1	FGHUA	fibrogenen alpha c	354	104.5	5.7	963	2	T19140	hypothetical prote
282	108	5.9	866	2	D44234	fibrogenen alpha c	355	104.5	5.7	1006	2	T42731	atrophin-1 related
283	108	5.9	1494	2	T14355	protein-tyrosine-p	356	104.5	5.7	1242	2	J50670	insulin receptor s
284	108	5.9	2187	2	S30826	nascent polypeptid	357	104.5	5.7	1794	2	T38459	hypothetical diver
285	107.5	5.9	252	2	S53631	major prion protei	358	104.5	5.7	3938	2	T42761	Bassoon protein -
286	107.5	5.9	302	2	T32711	hypothetical prote	359	104	5.7	251	1	PIHUPF	salivary proline-r
287	107.5	5.9	384	2	AG3013	conserved hypothet	360	104	5.7	295	2	B48013	proline-rich prote
288	107.5	5.9	384	2	H98270	hypothetical prote	361	104	5.7	309	1	S09257	homeotic protein H
289	107.5	5.9	388	2	JC5437	spliceosome-associ	362	104	5.7	576	2	T36729	probable serine/ch
290	107.5	5.9	407	2	T08166	hypothetical prote	363	104	5.7	784	2	A26601	elastin precursor
291	107.5	5.9	497	2	S22708	homeotic protein e	364	103.5	5.7	185	2	T08768	hypothetical prote
292	107.5	5.9	539	2	T28770	hypothetical prote	365	103.5	5.7	375	2	T08134	oleosin-like prote
293	107.5	5.9	884	2	D96730	unknown protein F5	366	103.5	5.7	413	2	T12533	hypothetical prote
294	107.5	5.9	1329	2	T29074	hypothetical prote	367	103.5	5.7	473	2	I50829	collagen - chicken
295	107.5	5.9	2132	1	A55182	aggreacan precursor	368	103.5	5.7	509	2	T09572	cdc2-like protein
296	107	5.9	250	2	A35820	galectin 3 - human	369	103.5	5.7	533	2	B56110	tyrosine phosphor
297	107	5.9	341	2	JC4051	jun-D protein - ra	370	103.5	5.7	578	2	T22888	hypothetical prote
298	107	5.9	815	2	B30843	glutenin high mole	371	103.5	5.7	592	2	T22885	hypothetical prote
299	107	5.9	902	2	B40494	androgen receptor	372	103.5	5.7	629	2	T22890	hypothetical prote
300	107	5.9	925	2	T19361	hypothetical prote	373	103.5	5.7	635	2	F96660	protein F2K11.10 (
301	107	5.9	1051	1	JW0051	serine/threonine-s	374	103.5	5.7	733	2	A45301	microtubule-associ
302	106.5	5.8	252	2	T161848	major prion protei	375	103.5	5.7	830	2	S15720	glutenin high mole
303	106.5	5.8	350	2	T36611	probable integral	376	103.5	5.7	902	2	T26775	hypothetical prote
304	106.5	5.8	425	2	H70793	hypothetical prote	377	103.5	5.7	1181	2	C86349	F8K7.4 protein - A
305	106.5	5.8	462	1	LUD07	annexin VII - slim	378	103.5	5.7	1560	2	T02885	peroxisome prolif
306	106.5	5.8	505	2	T50815	cdc2-like protein	379	103.5	5.7	1734	2	A54602	microtubule-associ
307	106.5	5.8	549	2	T20720	hypothetical prote	380	103	5.6	172	2	D41132	collagen-related p
308	106.5	5.8	684	2	A56154	Abl substrate ena	381	103	5.6	382	2	S20375	collagen alpha 3(V
309	106.5	5.8	920	2	A45748	collagen alpha 1(V	382	103	5.6	551	2	S57447	HPBRII-7 protein -
310	106.5	5.8	1207	2	T00378	KIAA0641 protein -	383	103	5.6	553	2	A49364	59 protein, brain
311	106.5	5.8	1223	2	T15316	hypothetical prote	384	103	5.6	770	2	G02228	DOC-2 - human
312	106.5	5.8	1763	2	S16366	collagen alpha 2(I	385	103	5.6	782	2	T48722	hypothetical prote
313	106	5.8	145	2	T08435	la costa protein -	386	103	5.6	806	2	T13690	hypothetical prote
314	106	5.8	283	2	T19731	hypothetical prote	387	103	5.6	900	2	B70694	probable infB - My
315	106	5.8	305	2	T20906	hypothetical prote	388	103	5.6	990	2	T14756	hypothetical prote
316	106	5.8	404	2	B84745	probable RNA-bindi	389	103	5.6	1541	2	T02831	AAA protein I4171
317	106	5.8	415	2	T00614	hypothetical prote	390	102.5	5.6	339	2	T22607	hypothetical prote
318	106	5.8	715	2	G86239	protein F20B24.6 l	391	102.5	5.6	416	2	T32458	hypothetical prote
319	106	5.8	1051	2	A35763	collagen alpha 2 c	392	102.5	5.6	624	2	A55576	collagen alpha 2(X
320	106	5.8	1487	1	EDBEE1	immediate-early pr	393	102.5	5.6	731	2	T04455	hypothetical prote
321	106	5.8	1585	2	T31611	hypothetical prote	394	102.5	5.6	1032	2	D83637	serine/threonine p

395	102.5	5.6	1283	2	T49804	hypothetical prote	468	99	5.4	767	2	S41479	DNA-binding protei
396	102.5	5.6	1367	2	T13703	tamA protein - fru	469	99	5.4	1538	2	H70846	hypothetical glyci
397	102	5.6	257	2	T10586	small nuclear ribo	470	98.5	5.4	274	1	A14161	fibronectin-bindin
398	102	5.6	294	2	T34537	hypothetical prote	471	98.5	5.4	286	2	JE0417	aminoglycoside-N-a
399	102	5.6	308	2	T37286	collagen 40 - Caen	472	98.5	5.4	300	2	S19560	proline-rich prote
400	102	5.6	380	2	T28888	cuticle collagen d	473	98.5	5.4	302	2	T15936	hypothetical prote
401	102	5.6	423	2	A41207	collagen 13, nonfi	474	98.5	5.4	399	2	I49754	homeobox protein -
402	102	5.6	430	2	S52700	NUP42 protein - ye	475	98.5	5.4	420	2	I59234	octamer binding tr
403	102	5.6	502	2	A55197	wiskott-Aldrich sy	476	98.5	5.4	444	2	B36389	transcription fact
404	102	5.6	503	1	LURB11	annexin XI - rabbi	477	98.5	5.4	472	2	T03169	probable glycoprot
405	102	5.6	515	2	F70904	hypothetical prote	478	98.5	5.4	495	1	S31223	transcription fact
406	102	5.6	517	2	T10327	3C3.18c protein -	479	98.5	5.4	674	2	T05284	probable serine/th
407	102	5.6	550	2	G70597	probable proteinas	480	98.5	5.4	1036	1	A34755	nitrogen regulator
408	102	5.6	673	2	T48012	hypothetical prote	481	98.5	5.4	1054	2	T14189	hypothetical prote
409	102	5.6	1019	1	A32856	collagen alpha 1(V	482	98.5	5.4	1586	2	S39580	HBHM protein - hum
410	102	5.6	1224	2	T40765	web1 protein homol	483	98.5	5.4	1733	2	S27939	tensin - chicken
411	102	5.6	1327	2	B34911	band 3-related pro	484	98.5	5.4	1744	2	A54970	tensin, cardiac mu
412	102	5.6	1335	2	T18289	racGAP protein - s	485	98.5	5.4	1748	2	S42136	cnjB protein - Tec
413	102	5.6	1706	2	I84499	zinc finger protei	486	98.5	5.4	1761	2	T13990	collagen type IV a
414	102	5.6	1775	2	A31893	collagen alpha 1(I	487	98.5	5.4	1792	2	A57075	tensin - chicken (
415	101.5	5.6	220	2	T50624	hypothetical prote	488	98.5	5.4	2124	2	A28452	proteoglycan core
416	101.5	5.6	325	2	S02170	collagen alpha 1(I	489	98	5.4	240	2	D70894	hypothetical prote
417	101.5	5.6	349	2	T49791	hypothetical prote	490	98	5.4	303	2	T19289	hypothetical prote
418	101.5	5.6	484	2	T17756	probable chitinase	491	98	5.4	316	2	T20497	hypothetical prote
419	101.5	5.6	600	2	T14613	hypothetical prote	492	98	5.4	377	2	A48018	mucin 7 precursor,
420	101.5	5.6	627	2	T35608	polyketide hydroxy	493	98	5.4	379	2	S31719	proline-rich prote
421	101.5	5.6	678	2	A75580	hypothetical prote	494	98	5.4	633	2	S62057	proline-rich prote
422	101.5	5.6	794	2	T10519	pre-pro-legumin -	495	98	5.4	723	2	B38749	3-phosphatidylinos
423	101.5	5.6	898	2	T14764	hypothetical prote	496	98	5.4	815	2	JN0689	glutenin, high-mol
424	101.5	5.6	1026	2	T20369	hypothetical prote	497	98	5.4	993	2	A38437	probable homeotic
425	101.5	5.6	1290	2	T00018	period protein hom	498	98	5.4	998	2	T30930	hypothetical prote
426	101.5	5.6	2440	2	S39162	transcription coac	499	98	5.4	1340	2	A39808	proteoglycan core
427	101.5	5.6	2441	2	S39161	CREB-binding prote	500	98	5.4	1664	2	T18262	S-layer protein -
428	101	5.5	298	2	JC1448	collagen col-34 -	501	97.5	5.3	161	2	F86364	hypothetical prote
429	101	5.5	329	2	T32783	hypothetical prote	502	97.5	5.3	232	2	S71041	major prion protei
430	101	5.5	465	2	S33680	ribonucleoprotein	503	97.5	5.3	257	2	C84533	hypothetical prote
431	101	5.5	512	2	E59437	R02569_2 protein (504	97.5	5.3	305	2	T30165	hypothetical prote
432	101	5.5	769	2	I56546	Shaw type potassi	505	97.5	5.3	377	2	E87022	probable conserved
433	101	5.5	1023	2	T48997	epsin-like protein	506	97.5	5.3	413	1	A34888	transcription fact
434	101	5.5	1152	2	JC6316	probable protein k	507	97.5	5.3	450	2	JH0190	alpha-2-adrenergic
435	101	5.5	1592	2	T48814	hypothetical prote	508	97.5	5.3	684	2	T36771	probable integral
436	101	5.5	3149	1	Q08E8	BPLF1 protein - hu	509	97.5	5.3	698	2	T17261	hypothetical prote
437	100.5	5.5	239	2	S53633	major prion protei	510	97.5	5.3	915	2	T12526	hypothetical prote
438	100.5	5.5	335	2	A43900	spicule matrix pro	511	97.5	5.3	1050	2	T18300	serine/threonine-s
439	100.5	5.5	361	2	A40023	paired box homolog	512	97.5	5.3	1241	2	T18311	hypothetical prote
440	100.5	5.5	373	2	S32537	erythroid transcri	513	97.5	5.3	1268	2	S52781	neurocan - mouse
441	100.5	5.5	450	2	B40392	alpha-2-adrenergic	514	97.5	5.3	1495	2	S60255	transcription co-r
442	100.5	5.5	508	2	T09046	proline-rich prote	515	97.5	5.3	3942	2	T42730	Bassoon protein -
443	100.5	5.5	897	1	A39255	cytokine receptor	516	97	5.3	281	2	S26052	hypothetical prote
444	100.5	5.5	907	2	E96636	hypothetical prote	517	97	5.3	296	2	T24827	hypothetical prote
445	100.5	5.5	1048	2	T23764	hypothetical prote	518	97	5.3	316	2	S08169	collagen col-12 pr
446	100.5	5.5	2055	2	T00093	hypothetical prote	519	97	5.3	316	2	S08170	collagen col-13 pr
447	100.5	5.5	3421	1	WZBE86	367K tegument prot	520	97	5.3	360	2	T37285	collagen dpy-2 - C
448	100	5.5	289	2	T34241	hypothetical prote	521	97	5.3	380	2	A48295	collagen 1 - marin
449	100	5.5	407	2	T21956	hypothetical prote	522	97	5.3	440	2	JC7807	Wiskott-Aldrich sy
450	100	5.5	569	2	T19128	hypothetical prote	523	97	5.3	503	1	LUBO11	annexin XI form A
451	100	5.5	633	2	F84564	probable protein k	524	97	5.3	543	1	JC4070	protein kinase (EC
452	100	5.5	649	2	T46500	hypothetical prote	525	97	5.3	655	1	A55726	RNA-binding protei
453	100	5.5	677	2	S23296	collagen alpha 2(I	526	97	5.3	896	2	S36326	clathrin assembly
454	100	5.5	888	2	A55318	serine/threonine p	527	97	5.3	915	2	S36327	clathrin assembly
455	100	5.5	901	2	A44825	phosphoprotein, sy	528	97	5.3	1234	2	T30160	hypothetical prote
456	100	5.5	1061	2	A57620	steroid receptor c	529	96.5	5.3	186	2	C41132	collagen-related p
457	100	5.5	1188	2	S49915	extensin-like prot	530	96.5	5.3	220	2	A36298	proline-rich prote
458	100	5.5	1400	2	T31555	hypothetical prote	531	96.5	5.3	294	2	D70525	probable beta-1 -
459	99.5	5.5	346	1	S35500	heterogeneous ribo	532	96.5	5.3	301	2	B12119	collagen 2 - Caeno
460	99.5	5.5	450	2	T49481	alpha-2 adrenergic	533	96.5	5.3	304	2	T22602	hypothetical prote
461	99.5	5.5	679	2	A42073	potassium channel	534	96.5	5.3	304	2	T26185	hypothetical prote
462	99.5	5.5	759	2	T00875	hypothetical prote	535	96.5	5.3	304	2	T26184	hypothetical prote
463	99.5	5.5	856	2	A53503	B-lymphocyte-induc	536	96.5	5.3	333	2	T20436	hypothetical prote
464	99	5.4	368	2	G84769	hypothetical prote	537	96.5	5.3	371	2	E88633	protein F56B3.1 li
465	99	5.4	429	2	JC4965	elk1 protein - mou	538	96.5	5.3	379	2	T19069	hypothetical prote
466	99	5.4	443	2	B39794	transcription fact	539	96.5	5.3	413	2	AH2743	conserved hypothet
467	99	5.4	486	1	TVHUEG	transforming prote	540	96.5	5.3	416	2	G97524	hypothetical prote

541 96.5 5.3 420 2 A49642 transcription fact
542 96.5 5.3 428 1 TVHUEK transforming prote
543 96.5 5.3 458 2 A75386 conserved hypotet
544 96.5 5.3 544 1 FQHUMP macrophage colony-
545 96.5 5.3 649 1 B37953 transcripion regu
546 96.5 5.3 896 1 A35782 cytokine receptor
547 96.5 5.3 918 2 S23377 collagen alpha 2(V
548 96.5 5.3 925 2 JC2033 G protein-coupled
549 96.5 5.3 969 2 T15446 hypotetrical prote
550 96.5 5.3 1022 2 S04111 collagen alpha 2(V
551 96.5 5.3 1028 1 CGH726 collagen alpha 1(V
552 96.5 5.3 1198 2 T49726 hypotetrical prote
553 96.5 5.3 1344 2 T14316 rig-1 protein - mo
554 96.5 5.3 1460 1 EDBE1F immediate-early pr
555 96.5 5.3 2910 2 T42212 otogelin - mouse
556 96 5.3 174 2 T36082 proline-rich prote
557 96 5.3 186 2 T30918 hypotetrical prote
558 96 5.3 314 2 G83643 methionyl-tRNA for
559 96 5.3 670 2 S22293 zinc finger protei
560 96 5.3 846 2 H70599 hypotetrical prote
561 96 5.3 1159 2 I38465 probable potassium
562 96 5.3 1213 2 S16356 ovo protein - frui
563 96 5.3 1592 2 T16055 hypotetrical prote
564 95.5 5.2 245 2 S3627 major prion protei
565 95.5 5.2 245 2 S71045 major prion protei
566 95.5 5.2 253 2 T17312 hypotetrical prote
567 95.5 5.2 301 2 E29149 proline-rich prote
568 95.5 5.2 362 2 T45072 erythroid Kruppel-
569 95.5 5.2 388 2 T32994 hypotetrical prote
570 95.5 5.2 421 2 T51055 hypotetrical prote
571 95.5 5.2 477 2 A47236 zinc-finger protei
572 95.5 5.2 564 2 I53106 gene gli protein -
573 95.5 5.2 672 2 I40333 tracheal colonizat
574 95.5 5.2 778 2 I38487 taenin - human
575 95.5 5.2 815 2 T49744 probable ubiquitin
576 95.5 5.2 906 2 T00039 hypotetrical prote
577 95 5.2 228 2 A4982 collagen UC0L1 - p
578 95 5.2 282 2 JS0168 collagen col-8 - C
579 95 5.2 282 2 T16036 cuticle collagen C
580 95 5.2 316 2 T19288 hypotetrical prote
581 95 5.2 383 2 S32975 gene BCRF2 protei
582 95 5.2 384 2 T17229 hypotetrical prote
583 95 5.2 456 2 A40492 early growth respo
584 95 5.2 471 2 S33679 ribonucleoprotein
585 95 5.2 512 1 WMBEY4 UL54 protein - hum
586 95 5.2 589 2 F95599 protein F14JL6.6 l
587 95 5.2 660 2 D87331 TonB-dependent rec
588 95 5.2 753 2 JC2099 glutenin, high mol
589 95 5.2 789 2 A30843 glutenin high mole
590 95 5.2 791 2 UN0690 glutenin, high-mol
591 95 5.2 878 1 A40091 interleukin-3 rece
592 95 5.2 890 2 T35237 probable secreted
593 95 5.2 1100 2 JC8033 leukocyte formin p
594 95 5.2 1298 1 EDBE75 immediate-early pr
595 95 5.2 2327 2 T42630 aggrecan - bovine
596 95 5.2 2957 2 T33152 hypotetrical prote
597 94.5 5.2 331 2 T26807 hypotetrical prote
598 94.5 5.2 387 2 H86445 probable G-Box bin
599 94.5 5.2 458 2 T31631 hypotetrical prote
600 94.5 5.2 460 2 G70803 hypotetrical prote
601 94.5 5.2 646 2 T45677 ATP-dependent RNA
602 94.5 5.2 707 2 S52390 D-hordein precurs
603 94.5 5.2 808 1 QPXEX glucose dehydrogen
604 94.5 5.2 848 2 S02262 glucenin high mole
605 94.5 5.2 970 2 D59435 Gem-interacting pr
606 94.5 5.2 1025 2 S34839 collagen alpha 1(V
607 94.5 5.2 1063 2 A40253 acidic nuclear pro
608 94.5 5.2 1231 2 S30185 insulin receptor s
609 94.5 5.2 1232 2 I38496 anion exchanger 3
610 94.5 5.2 1804 2 H96597 hypotetrical prote
611 94.5 5.2 1820 2 A55494 latent transformin
612 94.5 5.2 5105 2 T32650 hypotetrical prote
613 94 5.2 287 2 A60643 antigen 5401 - Eim

614 94 5.2 327 2 T29031
615 94 5.2 355 2 T29932
616 94 5.2 487 2 T49424
617 94 5.2 519 2 B87233
618 94 5.2 592 1 IKBICA colicin A - Citrob
619 94 5.2 657 2 A39526 probable protein k
620 94 5.2 938 2 S55051 Bicaudal-C - fruit
621 94 5.2 1097 2 T13033 cyclin I - fruit f
622 94 5.2 1392 2 T51947 gene mastermind pr
623 94 5.2 1655 2 T13998 DNA-binding protei
624 94 5.2 2282 2 T42717 extensin-like prot
625 93.5 5.1 306 2 T09067 hypotetrical prote
626 93.5 5.1 307 2 T18846 zinc-finger protei
627 93.5 5.1 331 2 B47236 hypotetrical prote
628 93.5 5.1 343 2 T29547 gene NKx6.1 protei
629 93.5 5.1 364 2 I48188 homeotic protein 1
630 93.5 5.1 406 1 I50375 collagen alpha 1(X
631 93.5 5.1 482 2 B31795 insulinoma-associ
632 93.5 5.1 510 2 A42750 hypotetrical prote
633 93.5 5.1 530 2 T48627 hydroxyproline-ric
634 93.5 5.1 620 2 S06733 hypotetrical prote
635 93.5 5.1 929 2 C96623 hypotetrical prote
636 93.5 5.1 1235 1 S16948 insulin receptor s
637 93.5 5.1 1572 2 S45251 SNF2alpha protei
638 93.5 5.1 2688 2 alpha-A-crystallin
639 93.5 5.1 2796 2 JC4743 fatty-acid synthas
640 93 5.1 134 2 T36365 proline-rich prote
641 93 5.1 304 2 T22482 hypotetrical prote
642 93 5.1 316 2 T19291 histidinol-phospha
643 93 5.1 335 2 C75619 hypotetrical prote
644 93 5.1 428 2 T24769 hypotetrical prote
645 93 5.1 438 2 S53787 collagen alpha cha
646 93 5.1 441 2 T23461 hypotetrical prote
647 93 5.1 448 1 A56018 transcription fact
648 93 5.1 455 2 A55050 enigma - human
649 93 5.1 524 2 F96572 protein F12ML6.10
650 93 5.1 670 2 T00083 hypotetrical prote
651 93 5.1 847 1 A53800 mixed-lineage prot
652 93 5.1 900 2 B87957 protein Y106G6D.7
653 93 5.1 915 2 T09575 smoothenin - human
654 93 5.1 918 2 JC4361 scavenger receptor
655 93 5.1 946 2 S27921 nuclear antigen EB
656 93 5.1 948 2 T26417 hypotetrical prote
657 93 5.1 1012 2 I53172 RAE-28 - mouse
658 92.5 5.1 188 2 D29149 proline-rich prote
659 92.5 5.1 240 2 A24264 proline-rich prote
660 92.5 5.1 240 2 B24264 proline-rich prote
661 92.5 5.1 262 2 A54889 Ige-binding protei
662 92.5 5.1 278 2 B39066 proline-rich prote
663 92.5 5.1 296 2 A31219 collagen 1 - Caeno
664 92.5 5.1 301 2 T21314 hypotetrical prote
665 92.5 5.1 307 2 S30432 hypotetrical prote
666 92.5 5.1 396 2 T29773 hypotetrical prote
667 92.5 5.1 460 2 JE0367 zinc finger protei
668 92.5 5.1 477 2 T46304 hypotetrical prote
669 92.5 5.1 552 2 D70604 probable PPE prote
670 92.5 5.1 618 2 A70989 hypotetrical glyci
671 92.5 5.1 632 2 T02827 hypotetrical prote
672 92.5 5.1 696 2 S71889 immune factor 1, t
673 92.5 5.1 811 2 T36581 probable transmem
674 92.5 5.1 907 1 QQB321 membrane antigen g
675 92.5 5.1 1721 1 I38902 retinoblastoma bin
676 92.5 5.1 1970 1 S21054 DNA-directed RNA p
677 92.5 5.1 1970 2 I38186 RNA polymerase II
678 92 5.0 139 2 T33968 hypotetrical prote
679 92 5.0 334 2 G02409 protein kinase C-b
680 92 5.0 412 2 A84455 hypotetrical prote
681 92 5.0 453 2 S18804 collagen alpha 4(I
682 92 5.0 520 2 I84718 RXR-beta1 isoform
683 92 5.0 583 2 I50518 DNA binding protei
684 92 5.0 638 2 B35816 transcription regu
685 92 5.0 649 2 A35816 transcription regu
686 92 5.0 682 2 A42121 transcription fact

hypotetrical prote
hypotetrical prote
hypotetrical prote
probable secreted
colicin A - Citrob
probable protein k
Bicaudal-C - fruit
cyclin I - fruit f
gene mastermind pr
DNA-binding protei
extensin-like prot
hypotetrical prote
zinc-finger protei
hypotetrical prote
gene NKx6.1 protei
homeotic protein 1
collagen alpha 1(X
insulinoma-associ
hypotetrical prote
hydroxyproline-ric
hypotetrical prote
hypotetrical prote
SNF2alpha protei
alpha-A-crystallin
fatty-acid synthas
proline-rich prote
hypotetrical prote
hypotetrical prote
histidinol-phospha
hypotetrical prote
collagen alpha cha
hypotetrical prote
transcription fact
enigma - human
protein F12ML6.10
hypotetrical prote
mixed-lineage prot
protein Y106G6D.7
smoothenin - human
scavenger receptor
nuclear antigen EB
hypotetrical prote
RAE-28 - mouse
proline-rich prote
proline-rich prote
Ige-binding protei
proline-rich prote
collagen 1 - Caeno
hypotetrical prote
hypotetrical prote
hypotetrical prote
zinc finger protei
hypotetrical prote
probable PPE prote
hypotetrical glyci
hypotetrical prote
immune factor 1, t
probable transmem
membrane antigen g
retinoblastoma bin
DNA-directed RNA p
RNA polymerase II
hypotetrical prote
protein kinase C-b
hypotetrical prote
collagen alpha 4(I
RXR-beta1 isoform
DNA binding protei
transcription regu
transcription regu
transcription fact

687	92	5.0	814	2	S65083	5-methyltetrahydro	760	90	4.9	376	2	C95878	probable dehydrogrog
688	92	5.0	860	1	EAMS	elastin precursor	761	90	4.9	377	2	A47380	RING finger-contai
689	92	5.0	888	2	JCS399	dual leucine zippe	762	90	4.9	448	2	T15188	hypothetical prote
690	92	5.0	891	2	H75007	hypothetical prote	763	90	4.9	496	2	S26402	homeotic protein B
691	92	5.0	1106	2	JQ0405	hypothetical 119.5	764	90	4.9	505	1	S23447	annexin XI form H
692	92	5.0	1268	2	T31420	C-terminal domain-	765	90	4.9	526	2	T13687	hypothetical prote
693	92	5.0	1296	2	E81840	transcription-repa	766	90	4.9	598	2	A75531	hypothetical prote
694	92	5.0	1520	2	T00273	hypothetical prote	767	90	4.9	638	2	JC7753	ring finger B-box
695	92	5.0	1649	2	C86822	hypothetical prote	768	90	4.9	708	2	D96711	hypothetical prote
696	92	5.0	1840	2	T30250	GT1 protein - mous	769	90	4.9	708	2	T22377	hypothetical prote
697	92	5.0	2183	2	T37218	hypothetical prote	770	90	4.9	736	2	H85016	hypothetical prote
698	92	5.0	2288	2	S41080	calcium channel al	771	90	4.9	770	2	B56895	transducin-like en
699	91.5	5.0	220	2	B72715	hypothetical prote	772	90	4.9	811	1	FOLJSP	gag polyprotein -
700	91.5	5.0	240	2	S09377	small nuclear ribo	773	90	4.9	838	2	T04449	hypothetical prote
701	91.5	5.0	252	2	T03160	capsid protein - a	774	90	4.9	871	2	T43427	pob1 protein - fis
702	91.5	5.0	318	2	S27978	cuticle collagen d	775	90	4.9	965	2	G96586	hypothetical prote
703	91.5	5.0	324	2	T19798	hypothetical prote	776	90	4.9	1028	2	T01714	hypothetical prote
704	91.5	5.0	342	2	S14432	heterogeneous ribo	777	90	4.9	1033	2	I38533	AF17 protein - hum
705	91.5	5.0	356	2	T22827	hypothetical prote	778	90	4.9	1174	2	T43051	protein kinase C (
706	91.5	5.0	394	2	C84905	probable extensin	779	90	4.9	1282	2	JE0120	glycoprotein A - m
707	91.5	5.0	578	2	I56215	interleukin-10 rec	780	90	4.9	1332	2	T15670	hypothetical prote
708	91.5	5.0	627	2	A41112	spidroin 2, dtagli	781	90	4.9	1379	2	A81102	transcription-repa
709	91.5	5.0	732	2	T08420	1-phosphatidylinos	782	90	4.9	1596	2	T31338	cellulose synthase
710	91.5	5.0	1017	2	T31354	probable potassium	783	90	4.9	3534	2	T42567	tegument protein 2
711	91.5	5.0	1053	2	T09987	probable PGE prote	784	89.5	4.9	245	1	W4ULB5	E4 protein - human
712	91.5	5.0	1571	2	T00062	hypothetical prote	785	89.5	4.9	259	2	S01704	merozoite surface
713	91.5	5.0	2761	2	T09285	hypothetical prote	786	89.5	4.9	283	2	T29980	hypothetical prote
714	91	5.0	245	2	T20831	hypothetical prote	787	89.5	4.9	300	2	T24482	hypothetical prote
715	91	5.0	278	2	T48426	hypothetical prote	788	89.5	4.9	324	2	S13497	CAMP-binding prote
716	91	5.0	290	2	A32249	collagen - sea urc	789	89.5	4.9	333	2	S11484	CAMP1 protein - sl
717	91	5.0	294	2	A49688	lactose-binding le	790	89.5	4.9	369	1	TVFVAF	transferrin prote
718	91	5.0	318	2	T35213	probable secreted	791	89.5	4.9	384	2	A46403	transcription fact
719	91	5.0	342	2	S07652	transcription fact	792	89.5	4.9	406	2	G71404	probable ribonucle
720	91	5.0	349	2	T05957	hypothetical prote	793	89.5	4.9	471	2	A39024	collagen alpha 3(I
721	91	5.0	358	2	T26281	hypothetical prote	794	89.5	4.9	509	2	T37017	probable xylosidas
722	91	5.0	373	2	A96701	gene NF-E2 protein	795	89.5	4.9	511	1	A48560	U54 protein - hum
723	91	5.0	552	1	S35703	colony-stimulating	796	89.5	4.9	536	2	H71563	hypothetical prote
724	91	5.0	552	1	A31401	macrophage colony-	797	89.5	4.9	571	2	G84426	hypothetical prote
725	91	5.0	588	2	A53563	synaptotagmin III	798	89.5	4.9	584	2	G70804	hypothetical glyci
726	91	5.0	676	2	T01381	env protein - muri	799	89.5	4.9	598	2	A84616	hypothetical prote
727	91	5.0	688	2	T48796	probable ATP-depen	800	89.5	4.9	614	2	T33149	hypothetical prote
728	91	5.0	710	2	D96728	hypothetical prote	801	89.5	4.9	627	1	JC6534	protein kinase 1 (
729	91	5.0	748	2	T04011	hypothetical prote	802	89.5	4.9	686	2	B75267	prolyl endopeptida
730	91	5.0	753	2	A27041	tyrosine kinase-re	803	89.5	4.9	691	2	A40024	regulatory protein
731	91	5.0	1099	2	A56155	tumor suppressor p	804	89.5	4.9	704	2	B84530	probable RING zinc
732	91	5.0	3570	2	T45025	mucin MUC5B, trach	805	89.5	4.9	772	2	D56695	transducin-like en
733	90.5	5.0	103	2	C34770	ORF3 protein - sal	806	89.5	4.9	864	1	EART	elastin precursor
734	90.5	5.0	202	2	AB2378	hypothetical prote	807	89.5	4.9	1071	2	T18307	suppressor protein
735	90.5	5.0	233	2	JC7618	FRAT2 protein - hu	808	89.5	4.9	1096	2	H86237	protein R14N23.29
736	90.5	5.0	252	2	A55047	collagen alpha 1(V	809	89.5	4.9	1560	2	T00080	hypothetical prote
737	90.5	5.0	333	2	T26808	hypothetical prote	810	89.5	4.9	2090	2	S26058	probable transform
738	90.5	5.0	402	1	QR80T2	microtubule-associ	811	89.5	4.9	2133	2	T30637	hypothetical prote
739	90.5	5.0	419	2	T29266	hypothetical prote	812	89.5	4.9	2234	2	T09053	low voltage-activa
740	90.5	5.0	436	2	A37953	transcription regu	813	89.5	4.9	3033	1	JQ1303	genome polyprotein
741	90.5	5.0	556	2	T16143	hypothetical prote	814	89.5	4.9	13288	2	T03099	mucin, submaxillar
742	90.5	5.0	597	2	S72468	probable transcrip	815	89	4.9	148	2	I38881	caudal-type homeot
743	90.5	5.0	642	1	S34416	transcription fact	816	89	4.9	221	2	T34554	hypothetical prote
744	90.5	5.0	666	2	I52648	class A helix-loop	817	89	4.9	279	2	T05421	hypothetical prote
745	90.5	5.0	667	2	A41311	transcription fact	818	89	4.9	298	2	T27644	hypothetical prote
746	90.5	5.0	682	2	F83228	hypothetical prote	819	89	4.9	313	2	T22828	hypothetical prote
747	90.5	5.0	825	2	JC4163	DNA-binding protei	820	89	4.9	334	2	JC6082	proximal sequence
748	90.5	5.0	878	2	T17245	hypothetical prote	821	89	4.9	342	2	A46396	ets-related protei
749	90.5	5.0	1274	2	T16251	hypothetical prote	822	89	4.9	358	2	H36891	transfer complex p
750	90.5	5.0	1285	2	T14171	ataxin-2 - mouse	823	89	4.9	366	2	S11449	collagen short cha
751	90.5	5.0	1473	2	T13855	suppressor of sabl	824	89	4.9	551	2	E84549	probable ubiquitin
752	90.5	5.0	1560	2	T42727	proliferation pote	825	89	4.9	585	2	C70930	hypothetical prote
753	90.5	5.0	1829	2	T26135	hypothetical prote	826	89	4.9	688	2	A53330	collagen alpha 2(I
754	90	4.9	180	2	JC7876	prion protein homo	827	89	4.9	715	2	T12534	hypothetical prote
755	90	4.9	266	2	T30919	hypothetical prote	828	89	4.9	736	2	I51691	dishevelled homolo
756	90	4.9	297	1	WJMS29	homeotic protein H	829	89	4.9	777	2	S30271	pyocin AP41 large
757	90	4.9	307	2	T37287	collagen 36 - Caen	830	89	4.9	834	2	T42702	hypothetical prote
758	90	4.9	348	2	T29288	hypothetical prote	831	89	4.9	847	2	F96531	hypothetical prote
759	90	4.9	373	2	A54692	transcription fact	832	89	4.9	867	2	S57795	probable deoxyribo

833	89	4.9	1006	2	F87363	medium-chain-fatty	906	88	4.8	2722	2	T20532	hypothetical prote
834	89	4.9	1029	1	S21369	collagen alpha 2(V	907	88	4.8	2738	2	E88320	protein P07All.6 {
835	89	4.9	1060	2	S63252	hypothetical prote	908	88	4.8	4199	2	S76412	hypothetical prote
836	89	4.9	1070	2	S75712	cellulase (EC 3.2.	909	87.5	4.8	132	2	S14977	glycine-rich prote
837	89	4.9	1074	2	T24877	hypothetical prote	910	87.5	4.8	156	2	T29730	hypothetical prote
838	89	4.9	1076	2	T24887	hypothetical prote	911	87.5	4.8	171	2	AB3489	hypothetical membr
839	89	4.9	1151	2	T18535	high molecular mas	912	87.5	4.8	264	2	A28651	galactose-specific
840	89	4.9	1172	2	T00065	hypothetical prote	913	87.5	4.8	264	2	A45983	lactose-binding le
841	89	4.9	1189	2	JC6118	SH2-containing ino	914	87.5	4.8	303	1	TVHJUD	transforming fact
842	89	4.9	1489	2	D70807	hypothetical glyci	915	87.5	4.8	304	2	A32993	transcription fact
843	89	4.9	1901	2	F70806	hypothetical glyci	916	87.5	4.8	318	2	A40944	1-phosphofructokin
844	89	4.9	1958	2	B40505	hypothetical prote	917	87.5	4.8	325	2	T18594	hypothetical prote
845	88.5	4.9	114	2	E81034	hypothetical prote	918	87.5	4.8	333	2	B84195	hypothetical prote
846	88.5	4.9	169	2	T34520	hypothetical prote	919	87.5	4.8	419	2	G70602	hypothetical prote
847	88.5	4.9	306	2	T21938	hypothetical prote	920	87.5	4.8	462	2	E70955	hypothetical prote
848	88	4.9	311	2	T08781	hypothetical prote	921	87.5	4.8	462	4	S33798	FUS/CHOP mutant fu
849	88.5	4.9	327	2	T34203	hypothetical prote	922	87.5	4.8	525	2	JN0059	hypothetical 57.4K
850	88.5	4.9	371	2	I45878	conglutinin - bovi	923	87.5	4.8	526	1	S33799	RNA-binding protei
851	88.5	4.9	375	2	D87427	conserved hypothet	924	87.5	4.8	533	2	S49525	glycoprotein G - s
852	88.5	4.9	385	2	D41732	heterogeneous nucl	925	87.5	4.8	666	2	D87243	conserved integral
853	88.5	4.9	400	2	S35528	surface antigen -	926	87.5	4.8	676	2	I50643	gammaFBP-C - chick
854	88.5	4.9	420	2	T46910	hypothetical prote	927	87.5	4.8	682	2	C45020	basic-helix-loop-h
855	88.5	4.9	459	2	S52250	paired box transcr	928	87.5	4.8	686	2	A38235	microtubule-associ
856	88.5	4.9	464	2	S59513	collagen II Al pro	929	87.5	4.8	715	2	S76492	lipoprotein nlpd -
857	88.5	4.9	472	1	B49340	membrane-bound alc	930	87.5	4.8	723	2	T14765	hypothetical prote
858	88.5	4.9	547	2	D87259	phosphoglucutase	931	87.5	4.8	747	1	EABO	elastin precursor,
859	88.5	4.9	545	2	A36046	collagen alpha cha	932	87.5	4.8	796	2	E96654	hypothetical prote
860	88.5	4.9	576	2	A26628	homeotic protein I	933	87.5	4.8	867	2	T41308	hypothetical zinc-
861	88.5	4.9	586	2	H86914	conserved hypothet	934	87.5	4.8	910	2	S68983	auxilin - bovine
862	88.5	4.9	592	2	T42078	serine/threonine p	935	87.5	4.8	1064	2	T13963	formin related pro
863	88.5	4.9	761	2	JC5759	brain-specific ser	936	87.5	4.8	1076	1	A35622	nuclear pore prote
864	88.5	4.9	775	2	A61228	collagen alpha 2(I	937	87.5	4.8	1170	2	S30010	probable finger pr
865	88.5	4.9	784	2	T20074	hypothetical prote	938	87.5	4.8	1221	2	T23472	hypothetical prote
866	88.5	4.9	838	1	EEWTH	glutenin, high mol	939	87.5	4.8	1322	2	T24140	hypothetical prote
867	88.5	4.9	882	2	A53253	microtubule-associ	940	87.5	4.8	1772	2	T36105	probable large gly
868	88.5	4.9	1037	2	B87254	translation initia	941	87	4.8	189	2	T46088	proline-rich prote
869	88.5	4.9	1087	2	T31100	probable potassium	942	87	4.8	235	2	T33380	hypothetical prote
870	88.5	4.9	1366	2	T35985	probable large Pro	943	87	4.8	297	2	T35700	hypothetical prote
871	88.5	4.9	1616	2	I37183	gene APXL protein	944	87	4.8	300	2	T19929	hypothetical prote
872	88.5	4.9	1696	2	T00057	hypothetical prote	945	87	4.8	303	2	T28999	hypothetical prote
873	88.5	4.9	3869	2	A48205	All-1 protein +GTE	946	87	4.8	363	2	T16831	hypothetical prote
874	88	4.8	144	2	S77128	hypothetical prote	947	87	4.8	394	2	T33641	hypothetical prote
875	88	4.8	259	1	A46286	RNA-binding protei	948	87	4.8	419	2	T04886	DAG protein homolo
876	88	4.8	269	2	S74919	hypothetical prote	949	87	4.8	430	2	T28143	tapasin 1 homolog,
877	88	4.8	274	2	T25404	hypothetical prote	950	87	4.8	443	2	C70780	probable pPE prote
878	88	4.8	284	2	T28887	collagen dpy-10 -	951	87	4.8	451	1	A40168	transcription fact
879	88	4.8	284	2	B41224	homeotic protein p	952	87	4.8	463	2	T13425	regulatory protein
880	88	4.8	299	2	T29956	hypothetical prote	953	87	4.8	481	2	B70908	hypothetical prote
881	88	4.8	314	2	T34269	hypothetical prote	954	87	4.8	529	2	S44649	f42h10.7 protein -
882	88	4.8	353	2	B34504	heterogeneous nucl	955	87	4.8	570	1	Q0BE2R	BVRF1 (EC-RF2) pro
883	88	4.8	373	2	A47234	homeobox protein H	956	87	4.8	633	2	B40983	collagen alpha 1(X
884	88	4.8	376	2	T10455	heat shock related	957	87	4.8	686	2	S66693	hypothetical prote
885	88	4.8	403	2	T39846	probable nuclear p	958	87	4.8	711	2	S05381	VGf8a protein prec
886	88	4.8	434	2	T43197	nucleoporin homolo	959	87	4.8	841	2	A43254	protein-tyrosine-p
887	88	4.8	494	2	A42170	zinc finger protei	960	87	4.8	862	2	S51493	major nitrogen reg
888	88	4.8	497	2	JC5076	myc-associated zin	961	87	4.8	869	2	A55384	transcription fact
889	88	4.8	502	2	T08776	hypothetical prote	962	87	4.8	908	2	A33280	sarcalumenin presu
890	88	4.8	543	2	D83262	hypothetical prote	963	87	4.8	954	1	S68178	mixed-lineage prot
891	88	4.8	564	2	H70804	hypothetical prote	964	87	4.8	975	2	S33121	homeotic protein C
892	88	4.8	619	2	A97887	surface protein ps	965	87	4.8	1023	2	B59430	KIAA0189 protein f
893	88	4.8	619	2	A41971	surface protein ps	966	87	4.8	1176	2	T49482	hypothetical prote
894	88	4.8	623	1	S33167	gene pointed prote	967	87	4.8	1291	2	T00019	period protein hom
895	88	4.8	696	2	H83024	hypothetical prote	968	87	4.8	1589	2	T42233	submaxillary mucin
896	88	4.8	718	1	S33168	gene pointed prote	969	87	4.8	1732	2	T43026	probable DNA-direc
897	88	4.8	739	1	JQ1893	80.7K alpha trans-	970	87	4.8	2183	2	T42764	coagulation factor
898	88	4.8	753	2	JQ0532	Op protein - Kenne	971	86.5	4.7	177	2	S65780	glycine/proline-ri
899	88	4.8	759	2	A49398	cycloartenol synth	972	86.5	4.7	177	2	S70794	vsd4 protein - Myc
900	88	4.8	771	2	S35681	ESG protein - mous	973	86.5	4.7	229	1	W4WL8	B4 protein - human
901	88	4.8	1203	2	I55466	N-methyl-D-asparta	974	86.5	4.7	245	2	A54909	carbohydrate-bindi
902	88	4.8	1344	1	A35175	mucin 1 precursor,	975	86.5	4.7	270	2	A36034	fibrinogen alpha c
903	88	4.8	2038	2	A43742	female sterile hom	976	86.5	4.7	285	2	G01958	homeobox protein -
904	88	4.8	2526	2	T20531	hypothetical prote	977	86.5	4.7	290	2	B88638	protein F58F6.2 [i
905	88	4.8	2555	2	A40043	notch protein homo	978	86.5	4.7	293	2	G70896	hypothetical prote

979	86.5	4.7	300	2	JQ2220	hydroxyproline-ric	1052	85.5	4.7	1433	1	A36734	bacillopeptidase F
980	86.5	4.7	303	2	T52305	En/Spm-like transp	1053	85.5	4.7	1602	2	T31671	Rab3 GDP/GTP excha
981	86.5	4.7	314	2	T32985	hypothetical prote	1054	85.5	4.7	2274	2	T30258	adenomatous polyop
982	86.5	4.7	371	1	JN0450	conglutinin precu	1055	85	4.7	212	2	A44994	eggshell protein 1
983	86.5	4.7	378	1	OZ0QAB	circumsporozoite p	1056	85	4.7	244	2	F70834	hypothetical prote
984	86.5	4.7	449	1	S30205	transcription fact	1057	85	4.7	268	2	H84684	En/Spm-like transp
985	86.5	4.7	506	2	AG1864	hypothetical prote	1058	85	4.7	285	2	T29982	hypothetical prote
986	86.5	4.7	583	2	T02045	kinase associated	1059	85	4.7	304	2	T18345	MGC2 protein precu
987	86.5	4.7	589	2	C70767	probable pknJ - My	1060	85	4.7	308	2	S77938	EBNA-LP protein -
988	86.5	4.7	656	2	A41870	dnaA protein - Str	1061	85	4.7	317	2	T29960	hypothetical prote
989	86.5	4.7	665	1	VCMVVR	env polyprotein pr	1062	85	4.7	319	2	T32250	hypothetical prote
990	86.5	4.7	671	2	A35912	homeotic protein o	1063	85	4.7	326	2	A41732	heterogeneous ribo
991	86.5	4.7	678	2	A70762	probable PPE prote	1064	85	4.7	339	2	S20880	homeotic protein H
992	86.5	4.7	742	1	TNBBE1	80.7K alpha trans-	1065	85	4.7	349	2	A41349	histone-specific t
993	86.5	4.7	779	2	A35006	cell surface glyco	1066	85	4.7	349	2	S77570	transcription fact
994	86.5	4.7	790	2	T12203	transcription fact	1067	85	4.7	356	2	S16907	collagen alpha 1(I
995	86.5	4.7	907	2	A45560	sporozoite surface	1068	85	4.7	384	2	T13469	large surface anti
996	86.5	4.7	940	2	T00056	hypothetical prote	1069	85	4.7	386	1	S22315	sRNP-associated p
997	86.5	4.7	1132	2	A35098	MHC class III hist	1070	85	4.7	401	2	H75554	NifS-related prote
998	86.5	4.7	1575	2	S68448	synaptojanin, 170K	1071	85	4.7	407	2	T30585	transferase homolo
999	86.5	4.7	1839	1	RRWPEM	genome polyprotein	1072	85	4.7	464	2	S22697	extensin - Volvox
1000	86.5	4.7	2140	2	T18543	probable cell-adhe	1073	85	4.7	481	1	B43674	protein kinase (EC
1001	86.5	4.7	2825	2	T14271	Doc4 protein, stre	1074	85	4.7	488	2	S13423	stromelysin 3 (EC
1002	86	4.7	2840	2	A35448	small nuclear ribo	1075	85	4.7	488	2	A25156	cellulase (EC 3.2.
1003	86	4.7	255	2	JQ0320	hypothetical 24.7K	1076	85	4.7	495	2	T17478	hypothetical prote
1004	86	4.7	289	2	T20177	hypothetical prote	1077	85	4.7	505	2	T07023	hypothetical prote
1005	86	4.7	295	2	A44984	collagen - nematod	1078	85	4.7	532	2	T07903	tubulin delta chai
1006	86	4.7	374	2	F87596	hypothetical prote	1079	85	4.7	546	2	T20209	DNA-binding protei
1007	86	4.7	397	2	T32513	hypothetical prote	1080	85	4.7	555	1	S24061	transcription fact
1008	86	4.7	398	2	A82366	conserved hypotet	1081	85	4.7	589	2	G87485	hypothetical prote
1009	86	4.7	402	2	A44766	hypothetical prote	1082	85	4.7	597	2	T35746	hypothetical prote
1010	86	4.7	414	2	C86301	arginine/serine-ri	1083	85	4.7	705	2	T01730	hypothetical prote
1011	86	4.7	416	1	SKXLAG	dermal gland prote	1084	85	4.7	714	2	D85014	hypothetical prote
1012	86	4.7	466	2	A47561	transcription fact	1085	85	4.7	718	1	A26615	calpain inhibitor
1013	86	4.7	483	2	S52374	regulatory protein	1086	85	4.7	744	2	F95013	pneumococcal surfa
1014	86	4.7	549	2	B86264	hypothetical prote	1087	85	4.7	756	2	JC5590	cycloartenol synth
1015	86	4.7	613	2	T42671	hypothetical prote	1088	85	4.7	771	2	B38252	granulocyte colony
1016	86	4.7	641	2	T03095	homeoprotein Sail	1089	85	4.7	793	1	S60735	splicing factor SF
1017	86	4.7	670	2	A83255	excinuclease ABC s	1090	85	4.7	815	2	B56708	extracellular sign
1018	86	4.7	715	1	TNBE77	77K alpha trans-in	1091	85	4.7	845	2	T17291	hypothetical prote
1019	86	4.7	800	2	I51853	dsRNA-binding proc	1092	85	4.7	931	2	T49710	related to glucan
1020	86	4.7	812	2	T48016	probable zinc-fing	1093	85	4.7	1018	2	T43168	hypothetical prote
1021	86	4.7	1113	2	T14260	period protein Per	1094	85	4.7	1022	2	T24663	hypothetical prote
1022	86	4.7	1227	2	A33638	erythrocyte anion	1095	85	4.7	1115	2	T13955	period protein Per
1023	86	4.7	1269	2	S35366	furin (EC 3.4.21.7	1096	85	4.7	1244	2	S25327	cytoskeleton assem
1024	86	4.7	1300	2	T03166	probable immediate	1097	85	4.7	1246	2	S56752	helicase SKI2W - h
1025	86	4.7	1557	2	T13160	protein CNK - frui	1098	85	4.7	1259	2	T16038	hypothetical prote
1026	86	4.7	1634	2	T26517	hypothetical prote	1099	85	4.7	1346	2	T17412	polyketide synthas
1027	86	4.7	2471	2	A49128	cell-fate determin	1100	85	4.7	1350	2	T30341	zinc finger protei
1028	85.5	4.7	232	2	E75547	hypothetical prote	1101	85	4.7	1355	2	S40022	spalt protein - fr
1029	85.5	4.7	281	2	C88638	protein F58F6.1 [i	1102	85	4.7	1386	2	T49316	profilaggrin relat
1030	85.5	4.7	323	2	T24582	hypothetical prote	1103	85	4.7	1436	2	A46496	antigen Wc1.1 prec
1031	85.5	4.7	338	2	H96765	hypothetical prote	1104	85	4.7	1647	2	T49412	hypothetical prote
1032	85.5	4.7	400	1	SAVILA	large surface anti	1105	85	4.7	1733	1	B45344	probable nuclear a
1033	85.5	4.7	424	2	T05785	hypothetical prote	1106	85	4.7	1974	2	T16703	hypothetical prote
1034	85.5	4.7	424	2	T33663	hypothetical prote	1107	85	4.7	2043	2	T18524	scavenger receptor
1035	85.5	4.7	445	2	S43492	surface antigen -	1108	84.5	4.6	245	1	W4WL5	immun1 precursor,
1036	85.5	4.7	509	2	T34871	probable membrane	1109	84.5	4.6	268	2	A49303	E4 protein - human
1037	85.5	4.7	542	2	A44358	zyxin - chicken	1110	84.5	4.6	278	2	S75883	homeotic protein C
1038	85.5	4.7	558	2	E70756	hypothetical glyci	1111	84.5	4.6	307	2	T16842	hypothetical prote
1039	85.5	4.7	566	2	T34842	probable transfera	1112	84.5	4.6	310	2	H70792	hypothetical prote
1040	85.5	4.7	572	2	G02845	zyxin - human	1113	84.5	4.6	315	2	D48560	immediate-early pr
1041	85.5	4.7	580	2	T34481	probable mucin DKF	1114	84.5	4.6	347	2	S10571	transcription init
1042	85.5	4.7	647	2	A84265	hypothetical prote	1115	84.5	4.6	353	1	A35615	transcription init
1043	85.5	4.7	671	2	T30337	probable export as	1116	84.5	4.6	420	2	JC4716	zinc finger DNA-bi
1044	85.5	4.7	792	1	EAHU	elastin precursor,	1117	84.5	4.6	441	1	QRHUT1	microtubule-associ
1045	85.5	4.7	796	2	S57844	lethal(3)malignant	1118	84.5	4.6	470	2	A30136	developmental cont
1046	85.5	4.7	837	2	A57542	p96 protein - mous	1119	84.5	4.6	482	2	S76376	hypothetical prote
1047	85.5	4.7	839	2	F75518	hypothetical prote	1120	84.5	4.6	512	1	FOMVGS	gag polyprotein -
1048	85.5	4.7	856	2	T13159	E1B-55kDa-associat	1121	84.5	4.6	513	2	T41011	hypothetical prote
1049	85.5	4.7	968	2	T00353	hypothetical prote	1122	84.5	4.6	514	2	B83644	chromosomal replic
1050	85.5	4.7	1091	2	T13170	diaphanous protein	1123	84.5	4.6	528	2	G02127	fus-like protein -
1051	85.5	4.7	1257	2	S28764	neurocan precursor	1124	84.5	4.6	534	2	S71800	transcription fact

1125	84.5	4.6	551	2	T39092	hypothetical ser-p	1198	83.5	4.6	541	2	T48811	hypothetical prote
1126	84.5	4.6	575	1	WFEOM	mullerian inhibiti	1199	83.5	4.6	552	2	F75311	ABC transporter, A
1127	84.5	4.6	582	2	A70841	probable oxalyl-Co	1200	83.5	4.6	557	2	T21596	extracellular prot
1128	84.5	4.6	593	2	T01575	beta-fructofuranos	1201	83.5	4.6	600	2	T06292	hypothetical prote
1129	84.5	4.6	601	1	QRMSN1	probable hormone r	1202	83.5	4.6	625	2	T50992	hypothetical prote
1130	84.5	4.6	629	2	T34726	probable dehydroge	1203	83.5	4.6	632	2	T15954	hypothetical prote
1131	84.5	4.6	646	2	T02643	hypothetical prote	1204	83.5	4.6	644	2	A53184	myc far upstream e
1132	84.5	4.6	647	2	A45244	exo-alpha-sialidas	1205	83.5	4.6	662	2	T23757	hypothetical prote
1133	84.5	4.6	678	2	JC4245	transcription fact	1206	83.5	4.6	693	2	H95255	choline binding pr
1134	84.5	4.6	697	2	JC2365	fused proteinase-c	1207	83.5	4.6	707	2	A46691	E-box-binding prot
1135	84.5	4.6	704	2	T34034	hypothetical prote	1208	83.5	4.6	744	2	S70619	finger protein bow
1136	84.5	4.6	770	2	S59623	tropoelastin - she	1209	83.5	4.6	823	2	A36378	probable transcrip
1137	84.5	4.6	911	2	A47675	68K outer membrane	1210	83.5	4.6	883	2	A96662	hypothetical prote
1138	84.5	4.6	924	2	T50996	probable AMP deami	1211	83.5	4.6	892	2	T27005	hypothetical prote
1139	84.5	4.6	964	2	T41547	hypothetical prote	1212	83.5	4.6	897	2	E65127	Probable bifunctio
1140	84.5	4.6	1086	2	JC6079	chitin synthase (E	1213	83.5	4.6	963	2	T04002	hypothetical prote
1141	84.5	4.6	1100	2	T30967	transcription acti	1214	83.5	4.6	992	1	GNWVR3	structural polypro
1142	84.5	4.6	1174	2	A40853	potassium channel	1215	83.5	4.6	1133	2	A54164	sterol regulatory
1143	84.5	4.6	1198	2	T28678	polyketide synthas	1216	83.5	4.6	1197	2	H82696	hypothetical prote
1144	84.5	4.6	1263	2	T13805	spalt-related prot	1217	83.5	4.6	1330	2	H89567	protein T08A9.1 [i
1145	84.5	4.6	1381	2	E170806	hypothetical glyci	1218	83.5	4.6	1791	2	T02345	hypothetical prote
1146	84.5	4.6	1603	2	S17983	gene posterior sex	1219	83.5	4.6	1932	1	A28490	DNA-directed RNA p
1147	84.5	4.6	2336	2	A45386	omega-conotoxin-se	1220	83.5	4.6	2468	2	A83412	hypothetical prote
1148	84.5	4.6	3507	2	T34513	hypothetical prote	1221	83.5	4.6	3436	2	S55659	tegument protein 6
1149	84	4.6	161	2	B42627	cement precursor p	1222	83	4.6	289	2	A43562	homeotic protein H
1150	84	4.6	164	2	F87296	hypothetical prote	1223	83	4.6	296	2	T15550	hypothetical prote
1151	84	4.6	165	2	T24470	hypothetical prote	1224	83	4.6	297	2	I54320	homeobox protein -
1152	84	4.6	170	2	F83325	hypothetical prote	1225	83	4.6	297	2	A40560	homeotic protein H
1153	84	4.6	184	1	CGRT2S	collagen alpha 2(I	1226	83	4.6	299	2	AF3421	peptidoglycan bind
1154	84	4.6	296	2	T23380	hypothetical prote	1227	83	4.6	301	2	B84533	hypothetical prote
1155	84	4.6	311	2	T15268	hypothetical prote	1228	83	4.6	302	2	T45937	hypothetical prote
1156	84	4.6	324	2	T18763	hypothetical prote	1229	83	4.6	319	2	T05584	hypothetical prote
1157	84	4.6	325	2	D70728	hypothetical prote	1230	83	4.6	328	2	S35336	transcription fact
1158	84	4.6	330	2	T26004	hypothetical prote	1231	83	4.6	329	2	JS0167	collagen col-6 - C
1159	84	4.6	346	2	T46916	hypothetical prote	1232	83	4.6	330	2	C75429	probable shikimate
1160	84	4.6	348	2	A34705	collagen - Caenorh	1233	83	4.6	371	2	F70555	hypothetical prote
1161	84	4.6	409	2	T02776	y4dM protein - Rhi	1234	83	4.6	372	2	AG2827	HFLK protein [mpo
1162	84	4.6	411	2	D86995	probable D-alanyl-	1235	83	4.6	373	2	E97605	proteinase chain h
1163	84	4.6	412	2	AF2320	hypothetical prote	1236	83	4.6	387	2	T34507	cutical collagen 6
1164	84	4.6	461	2	S34472	MFH-1 protein - mo	1237	83	4.6	389	2	F86212	hypothetical prote
1165	84	4.6	483	2	T25992	hypothetical prote	1238	83	4.6	411	2	S34164	homeotic protein H
1166	84	4.6	497	2	S69545	apoptosis inhibito	1239	83	4.6	417	2	S47539	homeotic protein H
1167	84	4.6	519	2	G84598	probable bZIP tran	1240	83	4.6	426	2	JQ1696	pistil extensin-li
1168	84	4.6	635	2	S01164	homeotic protein L	1241	83	4.6	440	2	S51614	Algal-CAM - Volvox
1169	84	4.6	646	2	T34532	hypothetical prote	1242	83	4.6	461	2	T36599	probable beta-lact
1170	84	4.6	666	1	VCWVHL	env polyprotein pr	1243	83	4.6	483	2	A55033	keratin 12 - mouse
1171	84	4.6	676	2	S41022	hypothetical prote	1244	83	4.6	556	2	D70940	probable PPE prote
1172	84	4.6	767	2	T19690	hypothetical prote	1245	83	4.6	563	2	T47520	hypothetical prote
1173	84	4.6	817	2	S51342	verprolin - yeast	1246	83	4.6	568	2	I58106	gene DMR-N9 protei
1174	84	4.6	836	2	T30312	pilin biosynthetic	1247	83	4.6	573	2	A33533	cell surface glyco
1175	84	4.6	1320	2	JC5630	TCOF1 protein - mo	1248	83	4.6	620	2	T30150	yeast ndr1-like pr
1176	84	4.6	1323	2	T00037	hypothetical prote	1249	83	4.6	635	2	F75477	hypothetical prote
1177	84	4.6	1538	2	F70874	probable ppsB prot	1250	83	4.6	654	2	S69673	SAC7 protein - yea
1178	84	4.6	1805	2	A34736	nestin - rat	1251	83	4.6	660	2	T03038	probable inhibitor
1179	84	4.6	1985	2	S19151	hypothetical prote	1252	83	4.6	704	2	A48097	rabphilin-3A - bov
1180	84	4.6	3412	1	GNWVTB	genome polyprotein	1253	83	4.6	728	2	H59435	phosphoinositide-3
1181	83.5	4.6	228	2	S53504	extensin-like prot	1254	83	4.6	730	2	T49736	hypothetical prote
1182	83.5	4.6	262	1	TLBPM1	tail fiber protein	1255	83	4.6	730	2	F96559	hypothetical prote
1183	83.5	4.6	302	2	T21257	hypothetical prote	1256	83	4.6	797	2	S53590	hypothetical prote
1184	83.5	4.6	319	2	F75420	hypothetical prote	1257	83	4.6	839	2	E84824	hypothetical prote
1185	83.5	4.6	324	2	A31920	collagen sgt-1 pre	1258	83	4.6	852	2	T46091	hypothetical prote
1186	83.5	4.6	347	2	A43815	transforming prote	1259	83	4.6	864	2	T23231	hypothetical prote
1187	83.5	4.6	365	2	A39481	serum response fac	1260	83	4.6	903	2	T00074	hypothetical prote
1188	83.5	4.6	428	2	S32228	glutamate-ammonia	1261	83	4.6	988	2	S37078	chloride channel p
1189	83.5	4.6	434	2	S73331	hypothetical prote	1262	83	4.6	1161	2	T45294	hypothetical prote
1190	83.5	4.6	447	2	T35824	probable oxidoredu	1263	83	4.6	1215	2	I52882	autoantigen - huma
1191	83.5	4.6	453	2	A53735	exoenzyme S - Pseu	1264	83	4.6	1258	2	JC5765	inositol polyphosp
1192	83.5	4.6	474	2	G84372	dihydrolipoamide d	1265	83	4.6	1259	2	T47182	hypothetical prote
1193	83.5	4.6	495	2	T26300	hypothetical prote	1266	83	4.6	1402	2	S42748	finger protein - f
1194	83.5	4.6	504	2	T50983	probable pleiotrop	1267	83	4.6	1520	1	TVFFA	protein-tyrosine k
1195	83.5	4.6	517	2	T49937	hypothetical prote	1268	83	4.6	2232	2	T34434	hypothetical prote
1196	83.5	4.6	524	2	A82580	polyvinylalcohol d	1269	83	4.6	2415	1	A39086	aggreccan precursor
1197	83.5	4.6	538	2	S35474	gag polyprotein -	1270	83	4.6	2472	2	E83594	still frameshift p

1271	83	4.6	2517	2	S58380	1344	82	4.5	1119	2	T50995	related to cytoske
1272	83	4.6	2843	1	RBHUAP	1345	82	4.5	1181	2	T30578	myosin IC - slime
1273	82.5	4.5	167	2	T2579	1346	82	4.5	1353	2	T00347	hypothetical prote
1274	82.5	4.5	171	2	A34493	1347	82	4.5	1506	2	T51900	related to PAN2 pr
1275	82.5	4.5	179	2	A85217	1348	82	4.5	1829	2	T14280	RW1 protein - mous
1276	82.5	4.5	210	2	B44984	1349	82	4.5	3414	1	GNWVNE	genome polypotein
1277	82.5	4.5	257	2	T50550	1350	81.5	4.5	176	2	A86441	hypothetical prote
1278	82.5	4.5	277	2	T38857	1351	81.5	4.5	215	2	S34163	homeotic protein H
1279	82.5	4.5	297	2	T27525	1352	81.5	4.5	221	2	T22260	hypothetical prote
1280	82.5	4.5	324	2	G86222	1353	81.5	4.5	237	2	H70554	hypothetical prote
1281	82.5	4.5	334	2	T51602	1354	81.5	4.5	259	2	A86408	FH protein interac
1282	82.5	4.5	348	2	I49262	1355	81.5	4.5	273	2	C70551	hypothetical prote
1283	82.5	4.5	351	2	E82643	1356	81.5	4.5	285	2	T19220	hypothetical prote
1284	82.5	4.5	364	2	C87455	1357	81.5	4.5	306	2	G96014	hypothetical prote
1285	82.5	4.5	461	2	T10741	1358	81.5	4.5	312	2	A61183	hypothetical prote
1286	82.5	4.5	476	2	S64953	1359	81.5	4.5	316	1	QRHUT2	microtubule-associ
1287	82.5	4.5	480	2	T36822	1360	81.5	4.5	336	2	E72591	hypothetical prote
1288	82.5	4.5	486	2	A41537	1361	81.5	4.5	341	2	H86476	protein F1504.35 (
1289	82.5	4.5	513	1	EUTQ1	1362	81.5	4.5	347	2	T14313	hypothetical prote
1290	82.5	4.5	513	2	S45380	1363	81.5	4.5	347	2	T15375	hypothetical prote
1291	82.5	4.5	513	2	S11439	1364	81.5	4.5	363	2	T16755	hypothetical prote
1292	82.5	4.5	520	1	FOLJGL	1365	81.5	4.5	381	2	S60561	I kappa B-like pro
1293	82.5	4.5	531	2	C83153	1366	81.5	4.5	429	2	T06296	extensin-like prot
1294	82.5	4.5	532	2	JC6170	1367	81.5	4.5	446	2	D70597	probable signal pe
1295	82.5	4.5	618	2	T42864	1368	81.5	4.5	450	2	T29060	hypothetical prote
1296	82.5	4.5	650	2	T04487	1369	81.5	4.5	454	2	S11511	transforming prote
1297	82.5	4.5	732	2	A43315	1370	81.5	4.5	509	1	WMVZMX	M9-R protein - myx
1298	82.5	4.5	788	2	S05661	1371	81.5	4.5	533	2	J50304	developmental cont
1299	82.5	4.5	799	2	T48889	1372	81.5	4.5	546	1	S13757	RNA helicase DBP2
1300	82.5	4.5	839	2	H90577	1373	81.5	4.5	589	2	JG0196	protein kinase DYR
1301	82.5	4.5	888	2	F87500	1374	81.5	4.5	596	2	A45195	adenylcyclase ty
1302	82.5	4.5	896	2	B43817	1375	81.5	4.5	622	2	I37984	keratin 9, type I,
1303	82.5	4.5	948	2	A57640	1376	81.5	4.5	636	2	H75635	hypothetical prote
1304	82.5	4.5	963	2	T40290	1377	81.5	4.5	637	2	A56263	beta-galactosidase
1305	82.5	4.5	1275	2	JU0092	1378	81.5	4.5	646	2	T26427	hypothetical prote
1306	82.5	4.5	1278	2	T27925	1379	81.5	4.5	669	2	T08827	hypothetical prote
1307	82.5	4.5	1290	2	T67853	1380	81.5	4.5	681	2	JX0338	rabphilin-3A - mou
1308	82.5	4.5	1415	1	EDBE3A	1381	81.5	4.5	691	2	C84300	cell division cycl
1309	82.5	4.5	1456	2	T01397	1382	81.5	4.5	706	2	S19958	basic helix-loop-h
1310	82.5	4.5	1514	2	T34869	1383	81.5	4.5	778	2	T17679	proline-rich prote
1311	82.5	4.5	2240	2	T37057	1384	81.5	4.5	801	2	T29018	hypothetical prote
1312	82	4.5	193	2	B75493	1385	81.5	4.5	825	2	T47164	hypothetical prote
1313	82	4.5	198	2	I49558	1386	81.5	4.5	834	2	S66258	glucosidase I - hu
1314	82	4.5	208	2	C34503	1387	81.5	4.5	905	2	S55059	fertilin alpha-I -
1315	82	4.5	240	2	A33270	1388	81.5	4.5	906	2	A43817	transforming prote
1316	82	4.5	240	2	S20068	1389	81.5	4.5	989	2	T47503	hypothetical prote
1317	82	4.5	240	2	A34503	1390	81.5	4.5	1001	2	T17365	serine/threonine p
1318	82	4.5	277	2	T04441	1391	81.5	4.5	1055	2	A96682	protein FIE2.12 (
1319	82	4.5	372	2	T45410	1392	81.5	4.5	1108	2	AD3032	conserved hypothet
1320	82	4.5	420	2	JW0076	1393	81.5	4.5	1140	2	H98253	hypothetical prote
1321	82	4.5	447	2	G84687	1394	81.5	4.5	1184	2	A42904	adenylcyclase ty
1322	82	4.5	448	2	T15542	1395	81.5	4.5	1305	2	T31096	cyclin G-associate
1323	82	4.5	450	2	T17234	1396	81.5	4.5	2403	2	A59386	sanko - human
1324	82	4.5	479	1	A31753	1397	81.5	4.5	3635	2	T10053	laminin alpha 5 ch
1325	82	4.5	534	2	AB0392	1398	81	4.4	122	2	T30126	hypothetical prote
1326	82	4.5	550	1	FGRTA	1399	81	4.4	184	2	T16044	hypothetical prote
1327	82	4.5	612	2	T23420	1400	81	4.4	200	2	G72471	hypothetical prote
1328	82	4.5	621	2	D96554	1401	81	4.4	222	2	A88102	protein W09G10.1 (
1329	82	4.5	623	2	S55652	1402	81	4.4	241	2	S53522	crystallin beta B1
1330	82	4.5	640	2	A41726	1403	81	4.4	293	2	A30769	regulatory protein
1331	82	4.5	642	2	S27806	1404	81	4.4	303	2	B75485	fructokinase - Dei
1332	82	4.5	657	2	S10001	1405	81	4.4	310	2	A41776	syndecan 1 precurs
1333	82	4.5	658	1	S23391	1406	81	4.4	324	2	T14636	hypothetical prote
1334	82	4.5	667	2	S74354	1407	81	4.4	344	2	S41707	PopAI protein - Ps
1335	82	4.5	710	1	QCB822	1408	81	4.4	358	2	S40776	ribonucleoprotein
1336	82	4.5	714	2	S77385	1409	81	4.4	405	2	A70845	probable penicilli
1337	82	4.5	728	2	S43768	1410	81	4.4	433	2	S51773	transcription fact
1338	82	4.5	764	2	T45793	1411	81	4.4	437	2	B53193	hedgehog homolog v
1339	82	4.5	856	2	T16543	1412	81	4.4	473	2	A47284	myocyte enhancer-b
1340	82	4.5	870	2	S74291	1413	81	4.4	483	2	S12741	transcription fact
1341	82	4.5	892	2	A41697	1414	81	4.4	486	2	H87311	hypothetical prote
1342	82	4.5	958	2	C87504	1415	81	4.4	513	2	H69735	endo-1,4-beta-xyla
1343	82	4.5	1097	2	T49187	1416	81	4.4	517	2	T37225	hypothetical prote

1417 81 521 2 A37806
1418 81 521 2 A37806
1419 81 521 2 A37806
1420 81 521 2 A37806
1421 81 521 2 A37806
1422 81 521 2 A37806
1423 81 521 2 A37806
1424 81 521 2 A37806
1425 81 521 2 A37806
1426 81 521 2 A37806
1427 81 521 2 A37806
1428 81 521 2 A37806
1429 81 521 2 A37806
1430 81 521 2 A37806
1431 81 521 2 A37806
1432 81 521 2 A37806
1433 81 521 2 A37806
1434 81 521 2 A37806
1435 81 521 2 A37806
1436 81 521 2 A37806
1437 81 521 2 A37806
1438 81 521 2 A37806
1439 81 521 2 A37806
1440 81 521 2 A37806
1441 81 521 2 A37806
1442 81 521 2 A37806
1443 81 521 2 A37806
1444 81 521 2 A37806
1445 81 521 2 A37806
1446 81 521 2 A37806
1447 81 521 2 A37806
1448 81 521 2 A37806
1449 81 521 2 A37806
1450 81 521 2 A37806
1451 81 521 2 A37806
1452 81 521 2 A37806
1453 81 521 2 A37806
1454 81 521 2 A37806
1455 81 521 2 A37806
1456 81 521 2 A37806
1457 81 521 2 A37806
1458 81 521 2 A37806
1459 81 521 2 A37806
1460 81 521 2 A37806
1461 81 521 2 A37806
1462 81 521 2 A37806
1463 81 521 2 A37806
1464 81 521 2 A37806
1465 81 521 2 A37806
1466 81 521 2 A37806
1467 81 521 2 A37806
1468 81 521 2 A37806
1469 81 521 2 A37806
1470 81 521 2 A37806
1471 81 521 2 A37806
1472 81 521 2 A37806
1473 81 521 2 A37806
1474 81 521 2 A37806
1475 81 521 2 A37806
1476 81 521 2 A37806
1477 81 521 2 A37806
1478 81 521 2 A37806
1479 81 521 2 A37806
1480 81 521 2 A37806
1481 81 521 2 A37806
1482 81 521 2 A37806
1483 81 521 2 A37806
1484 81 521 2 A37806
1485 81 521 2 A37806
1486 81 521 2 A37806
1487 81 521 2 A37806
1488 81 521 2 A37806
1489 81 521 2 A37806

amidase (EC 3.5.1.1)
gag polyprotein -
probable dihydrolyl
B-cell antigen CD1
gamma-glutamyltran
probable pPE type
keratin, 67K type
protein-tyrosine k
related to spliceo
probable exodeoxyr
hypothetical prote
cycloartenol synth
ovarian tumor prot
hypothetical prote
transmembrane olig
sialidase - Actino
probable large ATP
hypothetical prote
1-phosphatidylinos
ADP-ribosylation f
hypothetical prote
hypothetical prote
KIAA1204 protein [br
probable polyketid
hypothetical prote
hypothetical prote
eggshell protein 2
infected cell prot
tristetrapoline p
hypothetical prote
homeotic protein H
probable spliceos
erythroid Kruppel -
large surface anti
conserved hypothet
hypothetical BCR/A
hypothetical prote
transcription fact
transcription fact
acute myeloid leuk
xylulokinase (EC 2
transcription fact
nerve growth facto
UL54 protein - hum
transcription fact
hypothetical glyci
probable zinc fing
catalase (EC 1.11.
glutamic acid-rich
modulator recognit
proline-serine ric
episialin - mouse
gene F protein - r
phosphoenolpyruvat
bcr (breakpoint cl
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hRNA-binding prot
probable phosphate
hypothetical prote
chitin synthase (E
autotransporter (E
T49492
progesterone recep
hypothetical prote
faciogenital dyspl
hypothetical prote
frequency clock pr

1490 80.5 4.4 1063 1 GNVW77
1491 80.5 4.4 1146 2 B35962
1492 80.5 4.4 1182 2 A35962
1493 80.5 4.4 1271 1 TVHUBR
1494 80.5 4.4 1294 2 T48349
1495 80.5 4.4 1307 2 T25563
1496 80.5 4.4 1718 2 T14803
1497 80.5 4.4 2211 1 KFB05
1498 80.5 4.4 2259 2 S29236
1499 80.5 4.4 3375 2 T19821
1500 80 4.4 264 2 T33897
structural polypro
protein-tyrosine k
protein-tyrosine k
bcr (breakpoint cl
EIN2 protein - Ara
hypothetical prote
hypothetical prote
coagulation factor
calcium channel pr
hypothetical prote
hypothetical prote
ALIGNMENTS
RESULT 1
T13049
eyelid - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13049
R;Treisman, J.E.; Luk, A.; Rubin, G.M.; Heberlein, U.
Submitted to the EMBL Data Library, March 1998
A;Reference number: Z17592
A;Accession: T13049
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2715 <TRE>
A;Cross-references: UNIPROT:Q8IN94; UNIPARC:UPI000007D87E; EMBL:AF053091; NID:g2981220;
C;Genetics:
A;Gene: eld
A;Cross-references: FlyBase:FBgn0003013
C;Function:
A;Description: could act as a transcription factor antagonistic to the Wg pathway
C;Keywords: DNA binding
Query Match 9.1%; Score 165.5; DB 2; Length 2715;
Best Local Similarity 23.9%; Pred. No. 0.0063;
Matches 90; Conservative 23; Mismatches 132; Indels 131; Gaps 20;
QY 45 POLGQPSSTGPS-NSEHPQALDPRNSNDLRLVPLKLSVPPSDGPPAGGSVAVQWPPSWG 103
Db 406 PNRPMFGSSPSGSGHPLPPASPH-----HVPPLQQQPPPPPHVSAG-----PPSS 454
QY 104 LPANDSWPEDPMQMAAAEDRLGEALPELSVLSAAALAPGSGPLG-----ES 155
Db 455 SPGHAFSPSPQSPQASPSHQELIGQNSDS---SSGGAHSGMSGP-PGTPNQVWNP 510
QY 156 SPDATG-----LSPEASLLHQDSERRLPRNSLSGAGGKILSORPPWSLIHRV----- 203
Db 511 TSPSTSSGSRMSPSVAQNHPISR-----PASNOSSGGPM--QQPP-----VGAGGPP 558
QY 204 -LPDHPWMTLNP-----SVSWGGGGP-----SVSWGGGGP-----G 224
Db 559 PMPPHGMGPPQQQQSQASNSASSNSPQTPPPAPPNQGNNMATPPPPQG 618
QY 225 TNGTGRPM-PHPGIGINNQPPTSGW-----NINRYPGSGWGNINRYPGGSW----- 272
Db 619 AAGGGYMPMPMHG--GYKMGFGGSPGAGQYPPQPPQYPPGNYPPRPQYPPGAYATGP 676
QY 273 -----GNINRYPGSGWGNHLYPGINNPP-----FPPGVLRPPGSSWNIPAGFP-- 315
Db 677 PPPPTSQAGAGGANSMPGSAQAG--GYPRGMPNHTQYPPYQVWPPSPQOTVPGGAPGG 734
QY 316 -----NPPSP 320
Db 735 AMVGNHVQKGKTPPP 750
RESULT 2
S45252
SNF2beta protein - human

C;Species: Homo sapiens (man)
C;Date: 10-Dec-1994 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C;Accession: S45252
R;Chiba, H.; Muramatsu, M.; Nomoto, A.; Kato, H.
Nucleic Acids Res. 22, 1815-1820, 1994
A;Title: Two human homologues of *Saccharomyces cerevisiae* SWI2/SNF2 and *Drosophila* brahma
A;Reference number: S45251; MUID:94268902; PMID:8208605
A;Accession: S45252
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1647 <CHI>
A;Cross-references: UNIPROT:P51532; UNIPARC:UPI00001135AB; GB:D26156; NID:g505087; PIDN:
C;Superfamily: human SNF2alpha protein; bromodomain homology
F;1485-1540/Domain: bromodomain homology <BRO>

Query Match 8.9%; Score 163; DB 2; Length 1647;
Best Local Similarity 25.3%; Pred. No. 0.0054;
Matches 94; Conservative 22; Mismatches 125; Indels 130; Gaps 20;

QY 45 POLGQPSSTGPNSEHPQALDPRSNDLARVPLKLSVPPSDGFPFAGGSAVQRW-----P 99
DB 6 PPLGGTPRPGSPGPGSPG-----AMLGSPSG--PSPGSAHSMGSPSPG 49
QY 100 PSWGLPAMDSWP---PEDPWQMAAAAEADRLGEALPEELSY-----LSSAAALAPGSGPL 151
DB 50 PSAGHPIPTQPGPGYQPDNNHQMHPKPMESMHEKMSDDPRYNQMKMGMRSGGHAGMGPP 109
QY 152 PCSESSPDATGL-SPEASLLHQDSERRLPRSN-----SLGAGGKILSORPPWSL--- 199
DB 110 PSFMDHSGYPSPLGGSEHASP-----VPASGSPSGQMSPPGGAPLDGADPQALQQQN 166
QY 200 -----IHRV-----LPDH-----PWGTLN-----PSVS 217
DB 167 RGPTPEFNQHLQRAQIMAYKMLARGQLPDHLQMAVQKRPMPGQQQQMPTLPPPSVS 226
QY 218 WGGGGPGTGWGTRMP-----HPEGIWINQPPGTGW---GNINRYPGGSGWGNINR 266
DB 227 ATGPGPGPGPGPGPGAPPNYSRPHGMGPNMPPGPGPGVPPGPGPGPG----- 279
QY 267 YPGSGGNINRYPGGSGWNI-----HLYP-----GINNPPPGVLRPPGGSWNIP--- 311
DB 280 -PPKRW-----PEGMANAAAPTSTPQKLIPQPTGRPSAPPAPV--PPAASPVMPPT 330
QY 312 --AGFPNPPSP 320
DB 331 QSPGQPAQAP 341

RESULT 3
A43291
collagen alpha 2(I) chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A43291; A54328
R;Phillips, C.L.; Morgan, A.L.; Lever, L.W.; Wenstrup, R.J.
Genomics 13, 1345-1346, 1992
A;Title: Sequence analysis of a full-length cDNA for the murine pro alpha 2(I) collagen
A;Reference number: A43291; MUID:92372043; PMID:1505972
A;Accession: A43291
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1373 <PHI>
A;Cross-references: UNIPROT:Q01149; UNIPARC:UPI0000044DC6; GB:X58251; NID:g50488; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIP:112027)
R;Phillips, C.L.; Lever, L.W.; Pinnell, S.R.; Quarles, L.D.; Wenstrup, R.J.
J. Invest. Dermatol. 97, 980-984, 1991
A;Title: Construction of a full-length murine Proalpha2(I) collagen cDNA by the polymerase
A;Reference number: A54328; MUID:92084969; PMID:1748823
A;Accession: A54328
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-110 <PH2>
A;Cross-references: UNIPARC:UPI0000173BA1

C;Genetics:
A;Gene: COL1A2
C;Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology
C;Keywords: Coiled coil; extracellular matrix; glycoprotein; trimer; triple helix
F;1145-1373/Domain: fibrillar collagen carboxyl-terminal homology <FCC>

Query Match 8.6%; Score 157; DB 1; Length 1373;
Best Local Similarity 27.0%; Pred. No. 0.011;
Matches 83; Conservative 29; Mismatches 133; Indels 62; Gaps 18;

QY 46 QLGQPSSTGPNSEHPQALDPRSNDLARVPLKLSVPPSDGFPFAGGSAVQRW----- 99
DB 230 RVGAPGAPAGSDGSGVGPVPAG-----PIGAGPP--GFGAPGPKGLGVPVGNPGP 281
QY 100 --PSW-----GLPAMDS--WPPEDPWQMAAAAEADRLGEALPEELSYLSSAAALAPGSGP 150
DB 282 AGPAGPRGEVGLPGLSPVCPGPNPGTNGLTGAKGATG-----LPGVAGAPGL-PGPRG 334
QY 151 LPGESSPDATGLSPEASLLHQDSERRLPRSNLGGAGKILSORPPWSLIHRVLPDHPWG 210
DB 335 IPGPAG--AAGATGARGLVGEPGPAGSKGSGNKGEPSVGAQGPFG-----PSGBEG 385
QY 211 TLNPSVSWGGGGPGTGWTRPMHPHPEGIWINNQ-----PQGT--SWGNIN-RYPGGSWG 262
DB 386 KRGSPEAGSAGPAGPPLRGSPGSLPLGADGRAGVMGPPGNRGSTGPAGIRGPNGDAG 445
QY 263 NINRYPG-----GSGWGNINRYPGGSGWNIHLYPGIN--NPFPVGLRPPGSSWNIPAG 313
DB 446 RPGE-PQLMGPRGLPSPGNVG--PSGKEGPVGL-FOIDGRPGIGPAGPGEAGNI--G 499
QY 314 FPNPPSP 320
DB 500 FPGPKGP 506

RESULT 4
S39059
protein BRG1 - human
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C;Accession: S39059
R;Khavari, P.A.; Peterson, C.L.; Tamkun, J.W.; Mendel, D.B.; Crabtree, G.R.
Nature 366, 170-174, 1993
A;Title: BRG1 contains a conserved domain of the SWI2/SNF2 family necessary for normal
A;Reference number: S39059; MUID:94050144; PMID:8232556
A;Accession: S39059
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1613 <KHA>
A;Cross-references: UNIPROT:Q9HBD3; UNIPARC:UPI0000175F66
C;Superfamily: human SNF2alpha protein; bromodomain homology
F;1451-1506/Domain: bromodomain homology <BRO>

Query Match 8.6%; Score 156.5; DB 2; Length 1613;
Best Local Similarity 25.1%; Pred. No. 0.014;
Matches 89; Conservative 26; Mismatches 96; Indels 143; Gaps 22;

QY 52 STGPNSEHPQAL-----DPRSNDLARVPLK----- 78
DB 45 SPGPPSAGHPIPTQPGPGYQPDNNHQMHPKPMESMHEKMSDDPRYNQMKMGMRSGGHAG 104
QY 79 LSVPP-----SDGFP-PAGGSAVQRPPSWGLPAMDSWPPEDPWQMAAAAEADRLGEAL 131
DB 105 MGPPPPMDQYSQYPSPLGGSEHASP-----VPA--SGPSSGP-QMSS----- 146
QY 132 PEELSYLSSAAALAPGSGPLFGESSPDATGLSPEASLLHQDSERRLPRSNLGGAGKIL 191
DB 147 -----GPGAPLDG-ADPQALQGNRGPPTFNQNLHQL-RAQIMAY--KML 189
QY 192 SQRPWSLIHRVLPDH-----PWGTLN-----PSVSWGGGGPGTGWGTRMP- 233
DB 190 ARGQP-----LPDLQMAVQKRPMPGQQQQMPTLPPPSVSATGPGPGPGPGPG 242

QY 234 -----HPEGWGINNPPGTSM-----GNINRYPGSGWGNINYPGSGWGNINRYPGSGW 283
 Db 243 PAPNTVSRHGMGPNPFGSGVPGMPGQPPGG-----PKPW-----PEGPM 288
 QY 284 GNI-----HLYP-----GINNPPFGVLRPPGSSWNIP-----AGFNPPPSP 320
 Db 289 ANAAATSTPQKLIPQPTGRSPAPPAV--PPAASVMPPTQSPGQAPAPAP 340

RESULT 5
 CGHU2S
 N;Alternate names: procollagen alpha 2(I) chain
 C;Species: Homo sapiens (man)
 C;Date: 30-Jun-1989 #sequence revision 25-Aug-1995 #text change 31-Dec-2004
 A;Accession: A28500; S00824; S09176; I55311; A58111; A28472; A42165; A34405; A90567; I55305; A02865
 R;de Wet, W.; Bernard, M.; Benson-Chanda, V.; Chu, M.L.; Dickson, L.; Weil, D.; Ramirez, J. Biol. Chem. 262, 16032-16036, 1987
 A;Title: Organization of the human pro-alpha-2(I) collagen gene.
 A;Reference number: A28500; MUID:88058962; PMID:2824475
 A;Accession: A28500
 A;Molecule type: DNA; mRNA
 A;Residues: 1-248, N', 250-1366 <DEW>
 A;Cross-references: UNIPARC:UPI000173B96; UNIPROT:Q14038; UNIPROT:Q9UMM83; UNIPROT:Q9UMM6; UNIPROT:Q9UMM7
 R;Kuivaniemi, H.; Tromp, G.; Chu, M.L.; Prockop, D.J.
 Biochem. J. 252, 633-640, 1988
 A;Title: Structure of a full-length cDNA clone for the prepro-alpha-2(I) chain of human procollagen type I.
 A;Reference number: S00824; MUID:88339824; PMID:3421913
 A;Accession: S00824
 A;Molecule type: mRNA
 A;Residues: 1-275, 'A', 277-332, 'V', 334-337, 'A', 339-482, 'A', 484-548, 'D', 550-765 <KU11>
 A;Cross-references: UNIPARC:UPI00016A6FC; EMBL:Y00724; NID:G30022; PIDN:CAA68709.1; PIDN:CAA68709.2
 R;Dickson, L.A.; de Wet, W.; di Liberto, M.; Weil, D.; Ramirez, F.
 Nucleic Acids Res. 13, 3427-3438, 1985
 A;Title: Analysis of the promoter region and the N-propeptide domain of the human procollagen type I.
 A;Reference number: S09176; MUID:85242047; PMID:4011429
 A;Accession: S09176
 A;Molecule type: DNA
 A;Residues: 1-23, 33-58, 'P', 60-93 <DIC>
 A;Cross-references: UNIPARC:UPI0000173B96; UNIPARC:UPI0000173B97; EMBL:X02488; NID:G3009
 R;Weil, D.; D'Alessio, M.; Ramirez, F.; Eyre, D.R.
 J. Biol. Chem. 265, 16007-16011, 1990
 A;Title: Structural and functional characterization of a splicing mutation in the pro-alpha-2(I) chain of human procollagen type I.
 A;Reference number: I55311; MUID:90368825; PMID:2394758
 A;Accession: I55311
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 76-93 <WE11>
 A;Cross-references: UNIPARC:UPI00006F17F; GB:M35391; NID:G189684; PIDN:AAA60041.1; PIDN:AAA60041.2
 A;Accession: A58111
 A;Molecule type: protein
 A;Residues: 23-75, 94-96 <WEI2>
 A;Cross-references: UNIPARC:UPI0000173B98
 A;Note: mutant sequence from a patient with Ehlers-Danlos syndrome type VII
 R;Wirtz, M.K.; Glanville, R.W.; Steinmann, B.; Rao, V.H.; Hollister, D.W.
 J. Biol. Chem. 262, 16376-16385, 1987
 A;Title: Ehlers-Danlos syndrome type VII. Deletion of 18 amino acids comprising the N-terminal propeptide region.
 A;Reference number: A28472; MUID:88059013; PMID:3680255
 A;Accession: A28472
 A;Molecule type: protein
 A;Residues: 32-75, 94-111 <WIR>
 A;Cross-references: UNIPARC:UPI0000173B99
 A;Note: mutant sequence of patient with Ehlers-Danlos syndrome type VII
 R;Chiodo, A.A.; Hockey, A.; Cole, W.G.
 J. Biol. Chem. 267, 6361-6369, 1992
 A;Title: A base substitution at the splice acceptor site of intron 5 of the COL1A2 gene.
 A;Reference number: A42165; MUID:92210617; PMID:1556139
 A;Accession: A42165
 A;Molecule type: mRNA
 A;Residues: 50-126 <CHI>
 A;Cross-references: UNIPARC:UPI0000173B9A

A;Note: parts of this sequence were determined by protein sequencing; a mutant sequence from a patient with Ehlers-Danlos syndrome type VII
 R;Weil, D.; D'Alessio, M.; Ramirez, F.; Steinmann, B.; Wirtz, M.K.; Glanville, R.W.; Hollister, D.W.
 J. Biol. Chem. 264, 16804-16809, 1989
 A;Title: Temperature-dependent expression of a collagen splicing defect in the fibroblasts of a patient with Ehlers-Danlos syndrome type VII
 A;Reference number: A34405; MUID:89380311; PMID:2777808
 A;Accession: A34405
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 58-108 <WEI3>
 A;Cross-references: UNIPARC:UPI0000173B9B; GB:J05049
 A;Note: the accession cited by the authors is not found in GenBank
 A;Note: parts of this sequence were determined by protein sequencing; a mutant having 93 amino acids
 R;Click, E.M.; Bornstein, P.
 Biochemistry 9, 4699-4706, 1970
 A;Title: Isolation and characterization of the cyanogen bromide peptides from the alpha 1(I) chain of human procollagen type I
 A;Reference number: A90567; MUID:71038625; PMID:5529814
 A;Accession: A90567
 A;Molecule type: protein
 A;Residues: 'Z', '81', 'B', '83-96; 417-447 <CLI>
 A;Cross-references: UNIPARC:UPI0000173B9C; UNIPARC:UPI0000173B9D
 A;Note: the compositions of peptides CNB1, CNB2, and CNB3 were determined; evidence from mass spectrometry
 R;Kuivaniemi, H.; Sabol, C.; Tromp, G.; Sippola-Thiele, M.; Prockop, D.J.
 J. Biol. Chem. 263, 11407-11413, 1988
 A;Title: A 19-base pair deletion in the pro-alpha 2(I) gene of type I procollagen that causes efficient cleavage of the propeptide
 A;Reference number: I55264; MUID:88298792; PMID:3403536
 A;Accession: I55264
 A;Status: translation not shown; translated from GB/EMBL/DBJ
 A;Molecule type: DNA; mRNA
 A;Residues: 145-197 <KU12>
 A;Cross-references: UNIPARC:UPI000016AE4F; GB:M21671; NID:G189521; PIDN:AAA59994.1; PIDN:AAA59994.2
 A;Note: single base mutation in intron leads to abnormal splicing of mRNA
 R;Chipman, S.D.; Shapiro, J.R.; McKinstry, M.B.; Stover, M.L.; Branson, P.; Rowe, D.W.
 J. Bone Miner. Res. 7, 793-805, 1992
 A;Title: Expression of mutant alpha 1(I)-procollagen in osteoblast and fibroblast cultures
 A;Reference number: I55485; MUID:92351816; PMID:1642148
 A;Accession: I55485
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 163-181, 200-213 <CH2>
 A;Cross-references: UNIPARC:UPI0000071E28; GB:S41099; NID:G252702; PIDN:AAB22761.1; PIDN:AAB22761.2
 A;Note: mutant sequence from a patient with osteogenesis imperfecta type IV
 R;Morgan, P.H.; Jacobs, H.G.; Segrest, J.P.; Cunningham, L.W.
 J. Biol. Chem. 245, 5042-5048, 1970
 A;Title: Comparative study of glycopeptides derived from selected vertebrate collagens. A study of the role of the propeptide region
 A;Reference number: A92069; MUID:71001508; PMID:4319110
 A;Accession: A92069
 A;Molecule type: protein
 A;Residues: 175-180 <MOR>
 A;Cross-references: UNIPARC:UPI000014DF12
 A;Experimental source: skin
 A;Note: attachment of 2-O-alpha-D-glucosyl-O-beta-D-galactose to 5-hydroxylysine
 R;Fietzek, P.P.; Furthmayr, H.; Kuehn, K.
 Eur. J. Biochem. 47, 257-261, 1974
 A;Title: Comparative sequence studies on alpha2-CB2 from calf, human, rabbit and pig-skin
 A;Reference number: A91224; MUID:75008198; PMID:4412529
 A;Accession: A91224
 A;Molecule type: protein
 A;Residues: 418-447 <FIE>
 A;Cross-references: UNIPARC:UPI0000173B9E
 R;Tromp, G.; Prockop, D.J.
 Proc. Natl. Acad. Sci. U.S.A. 85, 5254-5258, 1988
 A;Title: Single base mutation in the pro alpha 2(I) collagen gene that causes efficient cleavage of the propeptide
 A;Reference number: I59125; MUID:88276936; PMID:2839839
 A;Accession: I59125
 A;Status: translation not shown; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 520-573 <TRO>
 A;Cross-references: UNIPARC:UPI0000073009; GB:M21353; NID:G180881; PIDN:AAA52053.1; PIDN:AAA52053.2
 A;Note: single base mutation in intron leads to splicing out of exon 28
 R;Bernard, M.P.; Myers, J.C.; Chu, M.L.; Ramirez, F.; Eikenberry, E.F.; Prockop, D.J.
 Biochemistry 22, 1139-1145, 1983
 A;Title: Structure of a cDNA for the proalpha-2 chain of human type I procollagen. Comparison with the structure of the alpha 1(I) chain


```
RESULT 7
AF1857
hypothetical protein al10407 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AF1857
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AF1857
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-255 <KUR>
A:Cross-references: UNIPROT:Q8YZ00; UNIPARC:UPI00000CDD35; GB:BA000019; PIDN:BA72365.1;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: al10407

Query Match      8.3%; Score 150.5; DB 2; Length 255;
Best Local Similarity 25.7%; Pred. No. 0.0047;
Matches 83; Conservative 30; Mismatches 103; Indels 107; Gaps 18;

QY 10 APGLLVCLHPLGLFARSIGVVEKVSQFNTLNPOLGQPGSTGPSNHEHPQALDPRS 69
DB 23 SPFGAL---LNTP-----GVEETIIQAFG-----RAVGGSGNN-----53
QY 70 NDLARVPLKLSVPPSDGFPAGGSQVORWPPSWGLPAMDSPW---PEDPQWMAAA--AE 124
DB 54 -----PFGSGAFTGGGAPAGGNPFS-----NFGNENAPASPLTGGVWFWTAINQGNNSD 103
QY 125 DRIGELALPELSYLSAALACPGSLPGESSPDATGLSPASLLHQDSERRLPRSNLS 184
DB 104 PLTGGGNP----FAGGSNPFAGSDPLTGGSNPFAGSNPFAG-----GSNPF 147
QY 185 GAGGKILSORPWSLLHRLVDPHPW-GTLNPSVSWGGGPGTGWTRPMPHPGGINN 243
DB 148 AGGG-----ENPFAGGSNPLT--GGGNPFAG--GSNPF-----176
QY 244 QPPGTSGNINRYPGGS---WGNINRYPGGS---WGNINRYPGGS---WGNILHYPGINN 294
DB 177 -----AGGENPFAGSNPFAGSNPFAGSNPFAGSNPFAGSNPFAGSNPFAGSN 231
QY 295 PFPFGVLRPPGSSWNIPAGFPNP 317
DB 232 PFAGG-SNPFAGGNPFAGGSNP 253

RESULT 8
S09824
hypothetical protein UL61 - human cytomegalovirus (strain AD169)
C:Species: human cytomegalovirus, human herpesvirus 5
A:Note: host Homo sapiens (man)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S09824
R:Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.;
M.; Barrel, B.G.
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
A:Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus
A:Reference number: S09749; MUID:90369039; PMID:2161319
A:Accession: S09824
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-431 <CHE>
A:Cross-references: UNIPROT:P16818; UNIPARC:UPI0000137BD6; EMBL:X17403; NID:g59591; PIDN
A:Note: this sequence was submitted to the EMBL Data Library, December 1989
A:Note: this reading frame extends between two stop codons and does not begin with a sta

Query Match      8.3%; Score 150.5; DB 2; Length 431;
Best Local Similarity 27.8%; Pred. No. 0.0082;

Matches 87; Conservative 25; Mismatches 126; Indels 75; Gaps 17;

QY 48 GOPSSTGPSNSEHP---QPAL---DPRSNDLARVPLKLSVPPSDG-----FPPAGGSV 95
DB 79 GEGSVTQANAQKADREPAARPRPRS-----RLAAGPSRGGGAQPEPPGRSRE 130
QY 96 QWPP-SWGLPAMDSPWPPDPQWMAAAEDRLGEALPELSYLSAALAPGSGPLPGE 154
DB 131 TRKPSSTPLPELLTGP-----APNLPGPIAVEPGRRPSPPP 168
QY 155 SS-PDATGLSPASLLHQDSERLPRSNLSGAGGKILSORPWSLLHRL-----VLDP 206
DB 169 STRPTVRRRRPTAATSRKKKARGPKASKAGRELGSGSP---VAHRTSLTGTGVRDP 225
QY 207 HPWG-----TLNPSVSWGGGPGT-----GWGTRPMPHPGGINNQPP--GTSGNI 253
DB 226 AFRGGGRARTPGP-VHSAAGGPGSRRSRSPGAARDPCPEPEERGGGKPLGSPRATDG 284
QY 254 NRYPG-GSWGNINRYPGSGWGNINRYPGSGWGNIHLYPGINNPPPGVLRPPGSSWNIPA 312
DB 285 NRDPGAGVPARPGRRMGSGSGRGGTGPR--GPRAAPGARPTAPDGA---PG-RWDGPA 338
QY 313 GPNPSPRLWG 325
DB 339 DGPAPGLGRGGW 351

RESULT 9
CGHULD
collagen alpha 1(X) chain precursor - human
N:Alternate names: procollagen alpha 1(X) chain
C:Species: Homo sapiens (man)
C>Date: 23-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S26396; S30086; S18249; A43901; I51870; S21856
R:Reichenberger, E.; Beier, F.; Luvalle, P.; Olsen, B.R.; von der Mark, K.; Bertling, W.
FEBS Lett. 311, 305-310, 1992
A:Title: Genomic organization and full-length cDNA sequence of human collagen X.
A:Reference number: S26396; MUID:93012005; PMID:1397333
A:Accession: S26396
A:Molecule type: DNA
A:Residues: 1-680 <REI>
A:Cross-references: UNIPROT:Q03692; UNIPARC:UPI0000126D28; EMBL:X68952; EMBL:X72578; EMBL
R:Apte, S.S.
submitted to the EMBL Data Library, March 1992
A:Reference number: S30085
A:Accession: S30086
A:Molecule type: DNA
A:Residues: 'TIPFGWCVWCLL', 52-680 <APT>
A:Cross-references: UNIPARC:UPI0000173C3C; EMBL:X65120; NID:g23129
A:Note: the initial difference is probably due to translation of an intronic sequence
R:Apte, S.; Mattei, M.G.; Olsen, B.R.
FEBS Lett. 282, 393-396, 1991
A:Title: Cloning of human alpha-1(X) collagen DNA and localization of the COL10A1 gene to
A:Reference number: S15826; MUID:91243838; PMID:2037056
A:Accession: S15826
A:Molecule type: DNA
A:Residues: 561-647, 'G', 649-666 <AP2>
A:Cross-references: UNIPARC:UPI000018A6F4; EMBL:X58879; NID:g30013; PIDN:CAA41686.1; PID
R:Thomas, J.T.; Cresswell, C.J.; Rash, B.; Nicolai, H.; Jones, T.; Solomon, E.; Grant, M.
Biochem. J. 280, 617-623, 1991
A:Title: The human collagen X gene. Complete primary translated sequence and chromosomal
A:Reference number: S18249; MUID:92109659; PMID:1764025
A:Accession: S18249
A:Molecule type: DNA
A:Residues: 1-26, 'T', 28-680 <THO>
A:Cross-references: UNIPARC:UPI0000173C3D; EMBL:X60382; NID:g30094; PIDN:CAA42933.1; PID
R:Reichenberger, E.; Agner, T.; von der Mark, K.; Stoss, H.; Bertling, W.
Dev. Biol. 148, 562-572, 1991
A:Title: In situ hybridization studies on the expression of type X collagen in fetal hum
A:Reference number: A43901; MUID:92077285; PMID:1743401
A:Accession: A43901
A:Molecule type: mRNA
```


J. Biol. Chem. 269, 4042-4046, 1994

A;Title: The human alpha1(XV) collagen chain contains a large amino-terminal non-triple
A;Reference number: A53146; MUID:94140817; PMID:8307960

A;Accession: A53146

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-9, S'11-48, V'50-94, A'96-149, A'151-203, V'205-408, A'410-569 <MUR>

A;Cross-references: UNIPARC:UPI000016A3AB; GB:D21230; NID:G415605; PIDN:BAA04762.1; PID:
R;Myers, J.C.; Kivirikko, S.; Gordon, M.K.; Dion, A.S.; Pihlajaniemi, T.
Proc. Natl. Acad. Sci. U.S.A. 89, 10144-10148, 1992

A;Title: Identification of a previously unknown human collagen chain, alpha1(XV), charac
A;Reference number: S28778; MUID:93066196; PMID:1279671

A;Accession: S28778

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 544-640, P'642-811, P'813-1252 <MYE>

A;Cross-references: UNIPARC:UPI000017A164

C;Genetics:

A;Gene: GDB:COL15A1

A;Cross-references: GDB:1132578; OMIM:120325

A;Map position: 9q21-9q22

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-1388/Product: collagen alpha 1(XV) chain #status predicted <MAT>

F;1216-1388/Region: multiplexin collagen carboxyl-terminal homologous

Query Match 8.0%; Score 145.5; DB 2; Length 1388;
Best Local Similarity 24.1%; Pred. No. 0.062;
Matches 83; Conservative 25; Mismatches 118; Indels 119; Gaps 15;

Qy	47	LGQPSSTGSPNSEHPQPALDPRNDLARVPLKLSV-----PPSDGFFPAGGSVQVR 98
Db	445	LGEATEVGPSE-----DSLTTAAATSVLSFTFEDEASGVPTDGLAPLATWAPER 497
Qy	99	PPSNGLPAMDSPWPPDPQWMAAAADRLGEALPEELSYLSAAALAPGCGPLPGSSSPD 158
Db	498	AVTSG-----PGDEEDLAATTEPLTAGGEE-----SGSPPPDGPPLPL 538
Qy	159	ATGLSP-----ASLLHQDSESRRLPRNSLGGAGKILSORPPWSLIHRVLPDHPNGTLN 213
Db	539	PT-VAPERWITTPAQREHVGMKGQAGPKGKGAGEELPG-----PPEPSGPVG 585
Qy	214	PSVSMGGGGPGTGWGT-----RPMHPGEGIWGINNOP--PGTWSGNINR 255
Db	586	PTAGAEAGSGLGWSDVSGSGDLVGEQLLRGPPGPPGPGPLGIPGPGT---DVFM 642
Qy	256	YPGSGWGNIN-----RYPPGSGWGNINRYPGSGWG 284
Db	643	GPPGSPCEDGPAGEGPPGPEGGVGDGATGLPGMKCKGARGPNSGVGE----KGDGP 697
Qy	285	NIHLYPG-----INNPPPGVLRPPGSSWNTPAGFPNPPSPRLONG 325
Db	698	NRGL-PGPPGKKGQAGPGVMGPPG-----PPGPPGPPGPGCTMG 736

RESULT 12

G01763

atrophin-1 - homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004

C;Accession: G01763

R;Margolis, R.L.

submitted to the EMBL Data Library, March 1995

A;Reference number: G08343

A;Accession: G01763

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1184 <WAR>

A;Cross-references: UNIPROT:P54259; UNIPARC:UPI0000167F59; EMBL:U23851; NID:G915325; PID:
C;Genetics:

A;Gene: GDB:DRPLA; B37

A;Cross-references: GDB:270336; OMIM:125370

A;Map position: 12p-12p

Db	462	GPR----	GPPG-----	PPGPPGVGLPGEPGRFRFGINGSYAPGAGLPGVPGKE-GPPGF	510	
Qy	233	PHPEGIWGNQPPGTSWGNINRYPGGSGWGNINRYPG-----	GSWGNINRYPG-----	GS	282	
Db	511	PGPPG-----	PPG-----	PPGKEGP-----	PGVAGQKGSVDVG-IPGPKGSKGD	549
Qy	283	WGNHLYPGINN-PPPPGVLRPPGSSWNIPAGFPNPPSP	320			
Db	550	LGPIGM-PGKSLAGSPGVGPEG-----	PPGPPGPPGP	582		

Search completed: July 30, 2007, 16:41:38
Job time : 65 secs

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 30, 2007, 16:38:09 ; Search time 63 Seconds
(without alignments)
728.635 Million cell updates/sec

Title: US-10-063-569-64

Perfect score: 1824

Sequence: 1 MGRVAGSCAPLGILLVCLH.....SSWNIPAGFPNPPSPRLQWG 325

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 975083 seqs, 141243105 residues

Total number of hits satisfying chosen parameters: 975083

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1500 summaries

Database :

Issued Patents_AA:*

1: /EMC Celerra_SIDS3/ptodata/1/iaa/5_COMB.pbp:*

2: /EMC Celerra_SIDS3/ptodata/1/iaa/6_COMB.pbp:*

3: /EMC Celerra_SIDS3/ptodata/1/iaa/7_COMB.pbp:*

4: /EMC Celerra_SIDS3/ptodata/1/iaa/H_COMB.pbp:*

5: /EMC Celerra_SIDS3/ptodata/1/iaa/PCTRUS_COMB.pbp:*

6: /EMC Celerra_SIDS3/ptodata/1/iaa/RE_COMB.pbp:*

7: /EMC Celerra_SIDS3/ptodata/1/iaa/backfiles1.pbp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1824	100.0	325	3	US-10-063-639A-64 Sequence 64, Appl
2	1824	100.0	325	3	US-10-183-001-238 Sequence 238, Appl
3	1824	100.0	325	3	US-10-180-998-238 Sequence 238, Appl
4	1824	100.0	325	3	US-10-201-769-238 Sequence 238, Appl
5	1824	100.0	325	3	US-10-063-638A-64 Sequence 64, Appl
6	1824	100.0	325	3	US-10-063-510-64 Sequence 64, Appl
7	1824	100.0	325	3	US-10-063-741-64 Sequence 64, Appl
8	1824	100.0	325	3	US-10-063-584-64 Sequence 64, Appl
9	1824	100.0	325	3	US-10-174-576-238 Sequence 238, Appl
10	1824	100.0	325	3	US-10-174-581-238 Sequence 238, Appl
11	1824	100.0	325	3	US-10-006-867-64 Sequence 64, Appl
12	1824	100.0	325	3	US-10-063-659-64 Sequence 64, Appl
13	1824	100.0	325	3	US-10-063-742-64 Sequence 64, Appl
14	1824	100.0	325	3	US-10-063-703-64 Sequence 64, Appl
15	1824	100.0	325	3	US-10-063-709-64 Sequence 64, Appl
16	1824	100.0	325	3	US-10-063-581-64 Sequence 64, Appl
17	1824	100.0	325	3	US-10-063-583-64 Sequence 64, Appl
18	1824	100.0	325	3	US-10-063-593-64 Sequence 64, Appl
19	1824	100.0	325	3	US-10-063-599-64 Sequence 64, Appl
20	1824	100.0	325	3	US-10-063-646-64 Sequence 64, Appl
21	1824	100.0	325	3	US-10-063-660-64 Sequence 64, Appl
22	1824	100.0	325	3	US-10-207-916-238 Sequence 238, Appl
23	1824	100.0	325	3	US-10-063-647-64 Sequence 64, Appl
24	1824	100.0	325	3	US-10-063-661-64 Sequence 64, Appl
25	1824	100.0	325	3	US-10-063-651-64 Sequence 64, Appl
26	1824	100.0	325	3	US-10-063-530-64 Sequence 64, Appl
27	1824	100.0	325	3	US-10-063-540-64 Sequence 64, Appl
28	1824	100.0	325	3	US-10-063-648-64 Sequence 64, Appl
29	1824	100.0	325	3	US-10-063-657-64 Sequence 64, Appl
30	1824	100.0	325	3	US-10-063-702-64 Sequence 64, Appl
31	1824	100.0	325	3	US-10-063-529-64 Sequence 64, Appl
32	1824	100.0	325	3	US-10-063-644-64 Sequence 64, Appl
33	1824	100.0	325	3	US-10-063-585-64 Sequence 64, Appl
34	1824	100.0	325	3	US-10-063-591A-64 Sequence 64, Appl
35	1824	100.0	325	3	US-10-063-532-64 Sequence 64, Appl
36	1824	100.0	325	3	US-10-063-536-64 Sequence 64, Appl
37	1824	100.0	325	3	US-10-063-654-64 Sequence 64, Appl
38	1824	100.0	325	3	US-10-063-582-64 Sequence 64, Appl
39	1824	100.0	325	3	US-10-063-524-64 Sequence 64, Appl
40	1824	100.0	325	3	US-10-063-523-64 Sequence 64, Appl
41	1824	100.0	325	3	US-10-174-583-238 Sequence 238, Appl
42	1824	100.0	325	3	US-10-063-551-64 Sequence 64, Appl
43	1824	100.0	325	3	US-10-063-650-64 Sequence 64, Appl
44	1824	100.0	325	3	US-10-063-523-64 Sequence 64, Appl
45	1824	100.0	325	3	US-10-063-592A-64 Sequence 64, Appl
46	1824	100.0	325	3	US-10-063-705-64 Sequence 64, Appl
47	1824	100.0	325	3	US-10-063-598-64 Sequence 64, Appl
48	1824	100.0	325	3	US-10-063-554-64 Sequence 64, Appl
49	1824	100.0	325	3	US-10-063-597-64 Sequence 64, Appl
50	1824	100.0	325	3	US-10-063-600-64 Sequence 64, Appl
51	1824	100.0	325	3	US-10-063-652A-64 Sequence 64, Appl
52	1824	100.0	325	3	US-10-063-602-64 Sequence 64, Appl
53	1824	100.0	325	3	US-10-063-560-64 Sequence 64, Appl
54	1824	100.0	325	3	US-10-063-517-64 Sequence 64, Appl
55	1824	100.0	325	3	US-10-063-548-64 Sequence 64, Appl
56	1824	100.0	325	3	US-10-063-553-64 Sequence 64, Appl
57	1824	100.0	325	3	US-10-063-653A-64 Sequence 64, Appl
58	1810	99.2	325	2	US-09-994-365-6 Sequence 6, Appl
59	163	8.9	543	2	US-09-535-008-63 Sequence 63, Appl
60	163	8.9	577	2	US-09-535-008-61 Sequence 61, Appl
61	163	8.9	1646	2	US-09-535-008-67 Sequence 67, Appl
62	163	8.9	1647	2	US-09-535-008-2 Sequence 2, Appl
63	163	8.9	1647	2	US-09-824-574-4 Sequence 4, Appl
64	163	8.9	1647	2	US-09-538-092-1172 Sequence 1172, Ap
65	163	8.9	1649	2	US-09-535-008-75 Sequence 75, Appl
66	163	8.9	1650	2	US-09-535-008-71 Sequence 71, Appl
67	163	8.9	1659	2	US-09-535-008-71 Sequence 71, Appl
68	163	8.9	1678	2	US-09-535-008-65 Sequence 65, Appl
69	163	8.9	1679	2	US-09-535-008-65 Sequence 65, Appl
70	163	8.9	1681	2	US-09-535-008-73 Sequence 73, Appl
71	163	8.9	1682	2	US-09-535-008-73 Sequence 73, Appl
72	161.5	8.9	420	2	US-09-302-540-13993 Sequence 13993, A
73	154.5	8.5	324	2	US-09-949-016-7664 Sequence 7664, Ap
74	151	8.3	1024	2	US-08-931-820-2 Sequence 2, Appl
75	151	8.3	1366	2	US-08-963-825-19 Sequence 19, Appl
76	151	8.3	1366	2	US-09-500-811-19 Sequence 19, Appl
77	151	8.3	1366	2	US-09-570-573-19 Sequence 19, Appl
78	151	8.3	1366	2	US-09-548-608-19 Sequence 19, Appl
79	150	8.2	680	2	US-09-949-001-15 Sequence 15, Appl
80	150	8.2	680	2	US-09-949-001-20 Sequence 20, Appl
81	147	8.1	812	3	US-10-108-260A-3673 Sequence 3673, Ap
82	146	8.0	1040	2	US-10-153-469A-30 Sequence 30, Appl
83	146	8.0	1040	2	US-10-153-469A-32 Sequence 32, Appl
84	146	8.0	1040	2	US-10-104-889-30 Sequence 30, Appl
85	146	8.0	1040	2	US-10-104-889-32 Sequence 32, Appl
86	146	8.0	1366	2	US-09-585-887-10 Sequence 10, Appl
87	146	8.0	1366	2	US-09-289-578-10 Sequence 10, Appl
88	146	8.0	1366	2	US-09-949-016-5882 Sequence 5882, Ap
89	146	8.0	1366	3	US-10-171-311-38 Sequence 38, Appl
90	145	7.9	276	3	US-10-703-032-136520 Sequence 20, Appl
91	145	7.9	1717	3	US-09-958-359-20 Sequence 20, Appl
92	144.5	7.9	540	3	US-10-617-217A-170 Sequence 170, App
93	144	7.9	1184	2	US-09-266-225D-18 Sequence 18, Appl
94	142	7.8	1185	2	US-09-041-886-23 Sequence 23, Appl
95	142	7.8	1185	2	US-09-538-092-1209 Sequence 1209, Ap
96	142	7.8	1190	3	US-09-619-049-456 Sequence 456, App
97	141	7.7	437	3	US-10-703-032-125651 Sequence 125651, Sequence 2, Appl
98	141	7.7	539	1	US-08-735-041A-2 Sequence 2, Appl
99	141	7.7	539	2	US-09-190-476B-2 Sequence 2, Appl

100	141	7.7	539	2	US-09-190-889A-2	Sequence 2, Appli	173	126	6.9	1464	3	US-10-171-311-36	Sequence 36, Appli
101	141	7.7	539	2	US-09-190-938B-2	Sequence 2, Appli	174	126	6.9	1464	3	US-10-149-352-2	Sequence 2, Appli
102	141	7.7	539	5	US-09-190-938B-2	Sequence 2, Appli	175	125.5	6.9	744	2	US-09-949-016-9607	Sequence 9607, Ap
103	140.5	7.7	448	3	US-08-749-391-2	Sequence 14, Appl	176	125.5	6.9	752	2	US-08-975-762-61	Sequence 61, Appl
104	140.5	7.7	448	1	US-08-749-391-2	Sequence 2, Appli	177	125.5	6.9	752	2	US-09-295-028-61	Sequence 61, Appl
105	140.5	7.7	485	2	US-09-390-200-2	Sequence 2, Appli	178	125.5	6.9	752	2	US-08-106-582-61	Sequence 61, Appl
106	140.5	7.7	960	2	US-09-219-849-5	Sequence 5, Appli	179	125.5	6.9	752	2	US-09-159-469-61	Sequence 61, Appl
107	139.5	7.6	623	2	US-09-949-016-6530	Sequence 530, Ap	180	125.5	6.9	752	2	US-09-693-542-61	Sequence 61, Appl
108	139	7.6	1728	2	US-09-949-002-532	Sequence 532, Ap	181	125.5	6.9	752	2	US-09-693-542-61	Sequence 61, Appl
109	138.5	7.6	1179	2	US-09-949-016-7088	Sequence 7088, Ap	182	125	6.9	276	2	US-09-538-092-889	Sequence 889, App
110	134.5	7.4	1115	3	US-09-915-543-17	Sequence 17, Appl	183	125	6.9	545	1	US-08-494-168-10	Sequence 10, Appl
111	134	7.3	262	2	US-10-133-234A-5	Sequence 5, Appli	184	125	6.9	895	3	US-10-476-724A-2	Sequence 2, Appli
112	134	7.3	1806	2	US-09-919-497-56	Sequence 56, Appl	185	125	6.9	895	3	US-10-476-724A-4	Sequence 4, Appli
113	133	7.3	332	2	US-09-252-991A-17541	Sequence 17541, A	186	125	6.9	1268	2	US-09-949-016-7487	Sequence 7487, Ap
114	133	7.3	404	2	US-10-094-749-3089	Sequence 3089, Ap	187	124.5	6.8	1014	3	US-10-194-441A-1	Sequence 1, Appli
115	133	7.3	1690	2	US-09-949-016-5894	Sequence 5894, Ap	188	124.5	6.8	1060	2	US-08-931-820-3	Sequence 3, Appli
116	132	7.2	652	2	US-10-104-047-3364	Sequence 3364, Ap	189	124.5	6.8	1418	2	US-08-963-825-20	Sequence 20, Appl
117	131	7.2	742	2	US-09-949-016-7729	Sequence 7729, Ap	190	124.5	6.8	1418	2	US-08-010-939-1	Sequence 1, Appli
118	131	7.2	918	2	US-09-041-886-11	Sequence 11, Appl	191	124.5	6.8	1418	2	US-09-500-811-20	Sequence 20, Appl
119	131	7.2	918	3	US-10-791-017C-8	Sequence 8, Appli	192	124.5	6.8	1418	2	US-09-570-573-20	Sequence 20, Appl
120	131	7.2	957	2	US-09-252-991A-20408	Sequence 20408, A	193	124.5	6.8	1418	2	US-09-548-608-20	Sequence 20, Appl
121	130.5	7.2	919	2	US-09-538-092-895	Sequence 895, App	194	124	6.8	299	2	US-09-252-991A-17615	Sequence 17615, A
122	130.5	7.2	919	3	US-10-849-545A-4	Sequence 4, Appli	195	124	6.8	955	2	US-09-949-016-9369	Sequence 8369, Ap
123	130.5	7.2	923	2	US-09-497-822C-19	Sequence 19, Appl	196	124	6.8	1126	3	US-10-108-260A-3665	Sequence 3665, Ap
124	130.5	7.2	923	3	US-10-886-384-19	Sequence 19, Appl	197	124	6.8	1315	2	US-08-899-595-3	Sequence 3, Appli
125	130.5	7.2	938	2	US-09-949-016-9992	Sequence 9992, Ap	198	124	6.8	1516	2	US-09-949-016-8209	Sequence 8209, Ap
126	130.5	7.2	1218	2	US-09-949-016-7065	Sequence 7065, Ap	199	124	6.8	1739	2	US-09-795-061-2	Sequence 2, Appli
127	130	7.1	592	3	US-10-745-393-3	Sequence 3, Appli	200	123.5	6.8	401	2	US-09-219-849-34	Sequence 34, Appl
128	130	7.1	1745	2	US-09-795-061-4	Sequence 4, Appli	201	123.5	6.8	599	2	US-09-602-459-22	Sequence 22, Appl
129	130	7.1	1745	2	US-09-949-002-405	Sequence 405, App	202	123.5	6.8	599	2	US-09-602-459-23	Sequence 23, Appl
130	130	7.1	1771	2	US-09-949-002-492	Sequence 492, App	203	123.5	6.8	599	3	US-10-672-040-22	Sequence 22, Appl
131	129.5	7.1	259	2	US-09-431-887-33	Sequence 33, Appl	204	123.5	6.8	599	3	US-10-672-040-23	Sequence 23, Appl
132	128.5	7.0	320	2	US-09-949-016-8196	Sequence 8196, Ap	205	123.5	6.8	663	3	US-10-029-345A-40	Sequence 40, Appl
133	128.5	7.0	1003	2	US-10-094-749-2528	Sequence 2528, Ap	206	123.5	6.8	1516	3	US-10-230-824-8	Sequence 8, Appli
134	128	7.0	247	2	US-09-252-991A-24320	Sequence 24320, A	207	123	6.7	416	2	US-09-949-016-7756	Sequence 7756, Ap
135	128	7.0	591	2	US-09-949-016-10914	Sequence 10914, A	208	123	6.7	744	3	US-10-171-311-40	Sequence 40, Appl
136	128	7.0	591	2	US-09-949-016-10915	Sequence 10915, A	209	123	6.7	1316	3	US-10-379-981-9	Sequence 9, Appli
137	128	7.0	707	2	US-09-919-039-278	Sequence 278, App	210	123	6.7	2142	2	US-09-538-092-1142	Sequence 1142, Ap
138	128	7.0	707	2	US-09-538-092-993	Sequence 993, App	211	123	6.7	2142	2	US-09-949-002-371	Sequence 371, App
139	128	7.0	977	3	US-09-252-991A-16655	Sequence 16655, A	212	122.5	6.7	272	2	US-09-774-639-167	Sequence 167, App
140	127.5	7.0	445	3	US-09-619-049-795	Sequence 795, App	213	122.5	6.7	527	2	US-09-370-838-216	Sequence 216, App
141	127.5	7.0	735	2	US-09-949-016-10120	Sequence 10120, A	214	122.5	6.7	527	2	US-09-854-133-216	Sequence 216, App
142	127.5	7.0	1670	2	US-09-949-016-5883	Sequence 5883, Ap	215	122.5	6.7	589	2	US-09-252-991A-28836	Sequence 28836, A
143	127	7.0	793	2	US-09-270-767-42801	Sequence 42801, A	216	122.5	6.7	1057	2	US-08-931-820-4	Sequence 4, Appli
144	127	7.0	1106	2	US-09-538-092-874	Sequence 874, App	217	122.5	6.7	1078	2	US-08-963-825-21	Sequence 21, Appl
145	126.5	6.9	442	2	US-09-252-991A-30607	Sequence 30607, A	218	122.5	6.7	1078	2	US-09-500-811-21	Sequence 21, Appl
146	126.5	6.9	693	2	US-09-949-016-7806	Sequence 7806, Ap	219	122.5	6.7	1078	2	US-09-570-573-21	Sequence 21, Appl
147	126.5	6.9	714	3	US-10-233-885-44	Sequence 44, Appl	220	122.5	6.7	1078	2	US-09-548-608-21	Sequence 21, Appl
148	126.5	6.9	1017	2	US-08-468-996-10	Sequence 10, Appl	221	122.5	6.7	1413	3	US-10-288-798-24	Sequence 24, Appl
149	126	6.9	416	2	US-09-710-239-25	Sequence 25, Appl	222	122	6.7	264	2	US-09-431-887-24	Sequence 24, Appl
150	126	6.9	500	2	US-09-710-239-22	Sequence 22, Appl	223	122	6.7	574	3	US-10-168-097A-76	Sequence 76, Appl
151	126	6.9	510	2	US-09-710-239-26	Sequence 26, Appl	224	122	6.7	631	2	US-09-270-767-44123	Sequence 44123, A
152	126	6.9	862	2	US-09-710-239-33	Sequence 33, Appl	225	122	6.7	762	1	US-08-642-255-120	Sequence 120, App
153	126	6.9	1057	2	US-08-931-820-1	Sequence 1, Appli	226	122	6.7	762	1	US-08-397-633A-31	Sequence 31, Appl
154	126	6.9	1057	2	US-10-153-469A-16	Sequence 16, Appl	227	121.5	6.7	254	2	US-09-431-887-20	Sequence 20, Appl
155	126	6.9	1057	2	US-10-153-469A-20	Sequence 20, Appl	228	121.5	6.7	254	2	US-09-431-887-21	Sequence 21, Appl
156	126	6.9	1057	2	US-10-104-889-16	Sequence 16, Appl	229	121.5	6.7	254	2	US-09-431-887-22	Sequence 22, Appl
157	126	6.9	1057	2	US-10-104-889-20	Sequence 20, Appl	230	121.5	6.7	331	2	US-09-538-092-845	Sequence 845, App
158	126	6.9	1107	2	US-10-153-469A-11	Sequence 11, Appl	231	121	6.6	279	3	US-10-703-032-108000	Sequence 108000,
159	126	6.9	1107	2	US-10-104-889-11	Sequence 11, Appl	232	121	6.6	839	3	US-10-245-913-54	Sequence 54, Appl
160	126	6.9	1169	2	US-10-153-469A-6	Sequence 6, Appli	233	121	6.6	839	3	US-10-245-913-54	Sequence 54, Appl
161	126	6.9	1169	2	US-10-104-889-6	Sequence 6, Appli	234	121	6.6	839	3	US-10-242-095-54	Sequence 54, Appl
162	126	6.9	1171	2	US-10-153-469A-8	Sequence 8, Appli	235	121	6.6	839	3	US-10-242-652-54	Sequence 54, Appl
163	126	6.9	1171	2	US-10-104-889-8	Sequence 8, Appli	236	121	6.6	1255	1	US-09-080-897-4	Sequence 4, Appli
164	126	6.9	1341	2	US-08-963-825-18	Sequence 18, Appl	237	121	6.6	1255	2	US-08-899-595-1	Sequence 1, Appli
165	126	6.9	1341	2	US-09-500-811-18	Sequence 18, Appl	238	121	6.6	1255	2	US-09-323-735-4	Sequence 4, Appli
166	126	6.9	1341	2	US-09-570-573-18	Sequence 18, Appl	239	121	6.6	2280	3	US-09-619-049-624	Sequence 624, App
167	126	6.9	1341	2	US-09-548-608-18	Sequence 18, Appl	240	120.5	6.6	1712	2	US-09-961-403-9	Sequence 9, Appli
168	126	6.9	1388	2	US-10-153-469A-10	Sequence 10, Appl	241	120	6.6	380	2	US-09-270-767-37269	Sequence 37269, A
169	126	6.9	1388	2	US-10-104-889-10	Sequence 10, Appl	242	120	6.6	404	2	US-09-270-767-52486	Sequence 52486, A
170	126	6.9	1461	2	US-09-585-887-9	Sequence 9, Appli	243	120	6.6	380	2	US-09-550-115-11	Sequence 11, Appl
171	126	6.9	1461	2	US-09-289-578-9	Sequence 9, Appli	244	120	6.6	492	2	US-08-468-996-11	Sequence 11, Appl
172	126	6.9	1464	2	US-09-331-347C-21	Sequence 21, Appl	245	120	6.6	617	3	US-10-658-989A-2	Sequence 2, Appli

246	120	6.6	821	3	US-10-658-989A-3	Sequence 3, Appli	319	116	6.4	762	1	US-08-397-633A-26	Sequence 26, Appli
247	120	6.6	1014	3	US-10-194-441A-48	Sequence 48, Appli	320	116	6.4	822	2	US-09-219-849-49	Sequence 49, Appli
248	119.5	6.6	264	2	US-09-431-887-27	Sequence 27, Appli	321	116	6.4	907	1	US-09-010-928B-4	Sequence 4, Appli
249	119.5	6.6	333	2	US-09-710-239-27	Sequence 27, Appli	322	116	6.4	1135	2	US-09-294-298A-21	Sequence 21, Appli
250	119.5	6.6	337	2	US-09-252-991A-31851	Sequence 31851, A	323	116	6.4	1325	2	US-09-294-298A-6	Sequence 6, Appli
251	119.5	6.6	638	2	US-10-001-887-108	Sequence 108, App	324	116	6.4	1376	2	US-09-294-298A-4	Sequence 4, Appli
252	119.5	6.6	1258	2	US-09-538-092-886	Sequence 886, App	325	116	6.4	1423	2	US-09-294-298A-2	Sequence 2, Appli
253	119.5	6.6	1291	2	US-09-252-991A-19504	Sequence 19504, A	326	115.5	6.3	195	3	US-10-703-032-177731	Sequence 177731, A
254	119.5	6.6	1603	2	US-09-949-016-6136	Sequence 6136, Ap	327	115.5	6.3	254	1	US-08-242-188-1	Sequence 1, Appli
255	119.5	6.6	1609	2	US-09-949-016-10910	Sequence 10910, A	328	115.5	6.3	254	1	US-08-509-261A-1	Sequence 1, Appli
256	119	6.5	492	2	US-08-468-996-12	Sequence 12, Appli	329	115.5	6.3	254	1	US-08-660-626-7	Sequence 7, Appli
257	119	6.5	1099	2	US-09-881-654-4	Sequence 4, Appli	330	115.5	6.3	254	1	US-08-692-892-1	Sequence 1, Appli
258	119	6.5	1099	2	US-10-637-323-4	Sequence 4, Appli	331	115.5	6.3	254	1	US-08-713-939A-1	Sequence 1, Appli
259	119	6.5	1099	3	US-10-658-782-6	Sequence 6, Appli	332	115.5	6.3	254	1	US-08-868-162A-21	Sequence 21, Appli
260	119	6.5	1442	3	US-08-316-650-12	Sequence 12, Appli	333	115.5	6.3	254	2	US-09-031-168-7	Sequence 7, Appli
261	119	6.5	1442	5	PCT-US95-02251-12	Sequence 12, Appli	334	115.5	6.3	254	2	US-09-128-450-19	Sequence 19, Appli
262	118.5	6.5	498	1	US-08-660-963-12	Sequence 12, Appli	335	115.5	6.3	254	2	US-09-128-450-28	Sequence 28, Appli
263	118.5	6.5	511	2	US-09-252-991A-26078	Sequence 26078, A	336	115.5	6.3	254	2	US-09-036-579-1	Sequence 1, Appli
264	118.5	6.5	550	2	US-09-252-991A-21295	Sequence 21295, A	337	115.5	6.3	254	2	US-09-823-494-19	Sequence 19, Appli
265	118.5	6.5	699	2	US-10-237-551-143	Sequence 143, App	338	115.5	6.3	254	2	US-09-823-494-28	Sequence 28, Appli
266	118.5	6.5	699	2	US-10-237-551-254	Sequence 254, App	339	115.5	6.3	254	2	US-09-550-374-1	Sequence 1, Appli
267	118.5	6.5	1064	1	US-08-642-255-62	Sequence 62, Appli	340	115.5	6.3	254	2	US-09-627-218B-10	Sequence 10, Appli
268	118	6.5	219	2	US-09-380-015B-2	Sequence 2, Appli	341	115.5	6.3	254	2	US-09-943-906-1	Sequence 1, Appli
269	118	6.5	255	1	US-08-242-188-4	Sequence 4, Appli	342	115.5	6.3	254	2	US-09-669-516C-7	Sequence 7, Appli
270	118	6.5	255	1	US-08-509-261A-4	Sequence 4, Appli	343	115.5	6.3	254	2	US-10-435-602-1	Sequence 1, Appli
271	118	6.5	255	1	US-08-660-626-10	Sequence 10, Appli	344	115.5	6.3	254	3	US-09-155-794-7	Sequence 7, Appli
272	118	6.5	255	1	US-08-692-892-4	Sequence 4, Appli	345	115.5	6.3	254	3	US-09-602-775C-29	Sequence 29, Appli
273	118	6.5	255	1	US-08-713-939A-4	Sequence 4, Appli	346	115.5	6.3	254	3	US-11-027-139-1	Sequence 1, Appli
274	118	6.5	255	1	US-08-868-162A-24	Sequence 24, Appli	347	115.5	6.3	254	3	US-10-355-780-10	Sequence 10, Appli
275	118	6.5	255	2	US-09-031-168-10	Sequence 10, Appli	348	115.5	6.3	254	3	US-10-949-880-7	Sequence 7, Appli
276	118	6.5	255	2	US-09-036-579-4	Sequence 4, Appli	349	115.5	6.3	329	3	US-10-108-260A-2847	Sequence 2847, Ap
277	118	6.5	255	2	US-09-550-374-4	Sequence 4, Appli	350	115.5	6.3	355	2	US-08-483-533-41	Sequence 41, Appli
278	118	6.5	255	2	US-09-943-906-4	Sequence 4, Appli	351	115.5	6.3	355	2	US-09-283-471A-41	Sequence 41, Appli
279	118	6.5	255	2	US-09-669-516C-10	Sequence 10, Appli	352	115.5	6.3	355	5	PCT-US91-06532-3	Sequence 3, Appli
280	118	6.5	255	2	US-10-435-602-4	Sequence 4, Appli	353	115.5	6.3	369	3	US-10-108-260A-3622	Sequence 3622, Ap
281	118	6.5	255	3	US-11-027-139-4	Sequence 4, Appli	354	115.5	6.3	625	2	US-09-252-991A-19871	Sequence 19871, A
282	118	6.5	256	2	US-08-128-450-22	Sequence 22, Appli	355	115.5	6.3	656	2	US-09-949-016-8336	Sequence 8336, Ap
283	118	6.5	256	2	US-09-823-494-22	Sequence 22, Appli	356	115.5	6.3	1323	1	US-08-026-138E-4	Sequence 4, Appli
284	118	6.5	256	2	US-09-155-794-1	Sequence 1, Appli	357	115	6.3	257	2	US-09-431-887-30	Sequence 30, Appli
285	118	6.5	256	3	US-09-602-775C-28	Sequence 28, Appli	358	115	6.3	318	3	US-10-703-032-114664	Sequence 114664, A
286	118	6.5	256	3	US-10-949-880-1	Sequence 1, Appli	359	115	6.3	337	2	US-10-360-101-212	Sequence 21, App
287	118	6.5	264	2	US-09-128-450-21	Sequence 21, Appli	360	115	6.3	457	2	US-09-416-213-2	Sequence 2, Appli
288	118	6.5	264	2	US-09-823-494-21	Sequence 21, Appli	361	115	6.3	457	2	US-09-416-214-2	Sequence 2, Appli
289	118	6.5	264	2	US-09-155-794-2	Sequence 2, Appli	362	115	6.3	457	2	US-09-035-676-2	Sequence 2, Appli
290	118	6.5	264	3	US-09-602-775C-26	Sequence 26, Appli	363	115	6.3	457	2	US-09-394-142B-22	Sequence 22, Appli
291	118	6.5	264	3	US-10-949-880-2	Sequence 2, Appli	364	115	6.3	457	2	US-10-161-346-2	Sequence 2, Appli
292	118	6.5	416	2	US-09-252-991A-24575	Sequence 24575, A	365	115	6.3	463	2	US-09-252-991A-29731	Sequence 29731, A
293	118	6.5	726	2	US-09-949-016-10050	Sequence 10050, A	366	115	6.3	466	2	US-08-526-136-13	Sequence 13, Appli
294	118	6.5	1065	1	US-08-642-255-72	Sequence 72, Appli	367	115	6.3	467	2	US-09-949-016-7070	Sequence 7070, Ap
295	118	6.5	1248	1	US-09-080-897-2	Sequence 2, Appli	368	115	6.3	467	2	US-09-949-016-7071	Sequence 7071, Ap
296	118	6.5	1248	2	US-09-323-735-2	Sequence 2, Appli	369	115	6.3	639	2	US-09-252-991A-28453	Sequence 28453, A
297	117.5	6.4	755	2	US-09-319-497-57	Sequence 57, Appli	370	115	6.3	705	2	US-09-538-092-945	Sequence 945, App
298	117.5	6.4	1318	2	US-10-237-551-197	Sequence 197, App	371	115	6.3	707	3	US-10-195-144-31	Sequence 31, App
299	117	6.4	394	2	US-09-252-991A-19344	Sequence 19344, A	372	115	6.3	1587	2	US-09-949-016-11062	Sequence 11062, A
300	117	6.4	633	1	US-08-642-255-73	Sequence 73, Appli	373	115	6.3	1742	3	US-09-958-359-23	Sequence 23, Appli
301	117	6.4	682	1	US-08-642-255-126	Sequence 126, App	374	115	6.3	2442	2	US-09-514-247A-10	Sequence 10, Appli
302	117	6.4	682	1	US-08-397-633A-36	Sequence 36, Appli	375	115	6.3	2442	2	US-09-538-092-1370	Sequence 1370, Ap
303	117	6.4	710	2	US-10-104-047-3402	Sequence 3402, Ap	376	115	6.3	2442	3	US-10-109-886-10	Sequence 10, Appli
304	116.5	6.4	424	2	US-09-538-092-1338	Sequence 1338, Ap	377	114.5	6.3	489	2	US-09-949-016-7068	Sequence 7068, Ap
305	116.5	6.4	660	2	US-09-252-991A-22842	Sequence 22842, A	378	114.5	6.3	489	2	US-09-949-016-7069	Sequence 7069, Ap
306	116.5	6.4	696	2	US-08-906-865-4	Sequence 4, Appli	379	114.5	6.3	623	2	US-09-029-348-3	Sequence 3, Appli
307	116.5	6.4	696	2	US-09-129-668-4	Sequence 4, Appli	380	114.5	6.3	626	2	US-09-029-348-2	Sequence 2, Appli
308	116.5	6.4	1036	2	US-09-771-161A-255	Sequence 255, App	381	114.5	6.3	717	2	US-10-200-012-10	Sequence 10, Appli
309	116.5	6.4	1036	2	US-09-771-161A-256	Sequence 256, App	382	114.5	6.3	720	2	US-09-252-991A-2312	Sequence 2312, A
310	116.5	6.4	1733	3	US-09-958-359-21	Sequence 21, Appli	383	114.5	6.3	1208	2	US-09-463-702A-2	Sequence 2, Appli
311	116	6.4	315	2	US-09-252-991A-18926	Sequence 18926, A	384	114.5	6.3	1208	2	US-09-699-135-2	Sequence 2, Appli
312	116	6.4	501	2	US-09-710-239-17	Sequence 17, Appli	385	114.5	6.3	1208	3	US-09-889-325-4	Sequence 4, Appli
313	116	6.4	533	1	US-09-949-016-6629	Sequence 6629, Ap	386	114	6.2	263	1	US-08-242-188-3	Sequence 3, Appli
314	116	6.4	543	1	US-08-469-412A-7	Sequence 7, Appli	387	114	6.2	263	1	US-08-509-261A-3	Sequence 3, Appli
315	116	6.4	543	2	US-09-021-715-7	Sequence 7, Appli	388	114	6.2	263	1	US-08-660-626-9	Sequence 9, Appli
316	116	6.4	602	2	US-09-949-016-10221	Sequence 10221, A	389	114	6.2	263	1	US-08-692-892-3	Sequence 3, Appli
317	116	6.4	761	1	US-08-707-237A-84	Sequence 84, Appli	390	114	6.2	263	1	US-08-713-939A-3	Sequence 3, Appli
318	116	6.4	762	1	US-08-642-255-114	Sequence 114, App	391	114	6.2	263	1	US-08-868-162A-23	Sequence 23, Appli

392	114	6.2	263	2	US-09-031-168-9	Sequence 9, Appli	465	112	6.1	226	3	US-10-949-880-8	Sequence 8, Appli
393	114	6.2	263	2	US-09-036-579-3	Sequence 3, Appli	466	112	6.1	257	2	US-09-431-887-29	Sequence 29, Appl
394	114	6.2	263	2	US-09-550-374-3	Sequence 3, Appli	467	112	6.1	574	2	US-09-270-767-45812	Sequence 45812, A
395	114	6.2	263	2	US-09-943-906-3	Sequence 3, Appli	468	112	6.1	629	2	US-09-949-016-11700	Sequence 11700, A
396	114	6.2	263	2	US-09-669-516C-9	Sequence 9, Appli	469	112	6.1	823	3	US-10-857-673-11	Sequence 11, Appl
397	114	6.2	263	2	US-10-435-602-3	Sequence 3, Appli	470	112	6.1	830	2	US-09-252-991A-22004	Sequence 22004, A
398	114	6.2	263	3	US-11-027-139-3	Sequence 3, Appli	471	112	6.1	950	2	US-09-252-991A-25927	Sequence 25927, A
399	114	6.2	264	2	US-09-627-218B-11	Sequence 11, Appl	472	112	6.1	1078	2	US-09-949-016-11185	Sequence 11185, A
400	114	6.2	264	3	US-10-355-780-11	Sequence 11, Appl	473	112	6.1	1143	2	US-09-949-016-6137	Sequence 6137, Ap
401	114	6.2	503	2	US-09-599-287A-2	Sequence 2, Appli	474	112	6.1	1694	1	US-08-494-168-2	Sequence 2, Appli
402	114	6.2	503	2	US-10-078-547-2	Sequence 2, Appli	475	111.5	6.1	219	2	US-10-153-469A-44	Sequence 44, Appl
403	114	6.2	548	1	US-08-469-412A-2	Sequence 2, Appli	476	111.5	6.1	219	2	US-10-153-469A-46	Sequence 46, Appl
404	114	6.2	548	2	US-09-021-715-2	Sequence 2, Appli	477	111.5	6.1	219	2	US-10-104-889-44	Sequence 44, Appl
405	114	6.2	572	2	US-09-489-039A-11826	Sequence 11826, A	478	111.5	6.1	219	2	US-10-104-889-46	Sequence 46, Appl
406	114	6.2	713	2	US-09-949-016-9700	Sequence 9700, Ap	479	111.5	6.1	613	3	US-10-260-937-14	Sequence 14, Appl
407	114	6.2	829	2	US-09-881-239-5	Sequence 5, Appli	480	111.5	6.1	684	2	US-09-961-403-5	Sequence 5, Appli
408	114	6.2	829	3	US-10-658-782-4	Sequence 4, Appli	481	111.5	6.1	845	3	US-09-983-531A-6	Sequence 6, Appli
409	114	6.2	902	1	US-08-396-479B-6	Sequence 6, Appli	482	111.5	6.1	870	1	US-09-010-928B-2	Sequence 2, Appli
410	114	6.2	902	1	US-08-818-823-6	Sequence 6, Appli	483	111.5	6.1	1345	2	US-09-949-016-11209	Sequence 11209, A
411	114	6.2	962	2	US-09-442-100-6	Sequence 6, Appli	484	111	6.1	208	3	US-10-745-393-1	Sequence 1, Appli
412	114	6.2	962	2	US-08-939-106-6	Sequence 6, Appli	485	111	6.1	253	1	US-08-242-188-2	Sequence 2, Appli
413	114	6.2	962	2	US-09-442-102-6	Sequence 6, Appli	486	111	6.1	253	1	US-08-509-261A-2	Sequence 2, Appli
414	113.5	6.2	256	2	US-09-431-887-31	Sequence 31, Appl	487	111	6.1	253	1	US-08-660-626-8	Sequence 8, Appli
415	113.5	6.2	257	2	US-09-153-794-3	Sequence 3, Appli	488	111	6.1	253	1	US-08-692-892-2	Sequence 2, Appli
416	113.5	6.2	257	3	US-10-949-880-3	Sequence 3, Appli	489	111	6.1	253	1	US-08-713-939A-2	Sequence 2, Appli
417	113.5	6.2	430	2	US-09-252-991A-16681	Sequence 16681, A	490	111	6.1	253	1	US-08-868-162A-22	Sequence 22, Appl
418	113.5	6.2	443	2	US-09-538-092-1002	Sequence 1002, Ap	491	111	6.1	253	1	US-09-031-168-8	Sequence 8, Appli
419	113.5	6.2	465	3	US-10-703-032-106094	Sequence 106094,	492	111	6.1	253	2	US-09-128-450-20	Sequence 20, Appl
420	113.5	6.2	482	2	US-09-949-016-9106	Sequence 9106, Ap	493	111	6.1	253	2	US-09-036-579-2	Sequence 2, Appli
421	113.5	6.2	493	2	US-09-949-016-7855	Sequence 7855, Ap	494	111	6.1	253	2	US-09-823-494-20	Sequence 20, Appl
422	113.5	6.2	507	2	US-10-598-287A-24	Sequence 24, Appl	495	111	6.1	253	2	US-09-550-374-2	Sequence 2, Appli
423	113.5	6.2	507	2	US-10-078-547-24	Sequence 24, Appl	496	111	6.1	253	2	US-09-431-887-1	Sequence 1, Appli
424	113.5	6.2	960	2	US-09-219-849-6	Sequence 6, Appli	497	111	6.1	253	2	US-09-431-887-2	Sequence 2, Appli
425	113.5	6.2	1358	3	US-10-778-804-11	Sequence 11, Appl	498	111	6.1	253	2	US-09-431-887-3	Sequence 3, Appli
426	113.5	6.2	1720	3	US-10-433-794-9	Sequence 9, Appli	499	111	6.1	253	2	US-09-431-887-4	Sequence 4, Appli
427	113.5	6.2	2414	1	US-08-227-536-2	Sequence 2, Appli	500	111	6.1	253	2	US-09-431-887-8	Sequence 8, Appli
428	113.5	6.2	2414	2	US-09-538-092-1289	Sequence 1289, Ap	501	111	6.1	253	2	US-09-431-887-16	Sequence 16, Appl
429	113.5	6.2	2414	5	PCT-US95-04682-2	Sequence 2, Appli	502	111	6.1	253	2	US-09-431-887-18	Sequence 18, Appl
430	113	6.2	247	2	US-09-538-092-890	Sequence 890, App	503	111	6.1	253	2	US-09-431-887-19	Sequence 19, Appl
431	113	6.2	252	2	US-09-431-887-32	Sequence 32, Appl	504	111	6.1	253	2	US-09-943-906-2	Sequence 2, Appli
432	113	6.2	254	2	US-09-128-450-26	Sequence 26, Appl	505	111	6.1	253	2	US-09-669-516C-8	Sequence 8, Appli
433	113	6.2	254	2	US-09-823-494-26	Sequence 26, Appl	506	111	6.1	253	2	US-09-919-172-57	Sequence 57, Appl
434	113	6.2	254	2	US-09-431-887-23	Sequence 23, Appl	507	111	6.1	253	2	US-09-976-594-72	Sequence 72, Appl
435	113	6.2	254	2	US-09-155-794-6	Sequence 6, Appli	508	111	6.1	253	2	US-09-904-987-3	Sequence 3, Appli
436	113	6.2	254	3	US-09-602-775C-30	Sequence 30, Appl	509	111	6.1	253	2	US-10-435-602-2	Sequence 2, Appli
437	113	6.2	254	3	US-10-949-880-6	Sequence 6, Appli	510	111	6.1	253	2	US-09-155-794-4	Sequence 4, Appli
438	113	6.2	258	2	US-09-949-016-9409	Sequence 9409, Ap	511	111	6.1	253	2	US-09-155-794-5	Sequence 5, Appli
439	113	6.2	357	1	US-07-609-716-66	Sequence 66, Appl	512	111	6.1	253	3	US-09-602-775C-27	Sequence 27, Appl
440	113	6.2	357	1	US-08-642-255-33	Sequence 33, Appl	513	111	6.1	253	3	US-11-027-139-2	Sequence 2, Appli
441	113	6.2	357	2	US-08-475-411A-66	Sequence 66, Appl	514	111	6.1	253	3	US-10-949-880-4	Sequence 4, Appli
442	113	6.2	357	2	US-08-478-029A-66	Sequence 66, Appl	515	111	6.1	253	3	US-10-949-880-5	Sequence 5, Appli
443	113	6.2	477	2	US-09-252-991A-19831	Sequence 19831, A	516	111	6.1	373	2	US-09-252-991A-28919	Sequence 28919, A
444	113	6.2	527	2	US-09-712-363-156	Sequence 156, App	517	111	6.1	595	2	US-09-219-849-48	Sequence 48, Appl
445	113	6.2	529	2	US-09-381-656-1	Sequence 1, Appli	518	111	6.1	595	2	US-09-219-849-50	Sequence 50, Appl
446	113	6.2	553	2	US-09-083-351-2	Sequence 2, Appli	519	111	6.1	689	2	US-09-949-016-11276	Sequence 11276, A
447	113	6.2	553	2	US-09-083-352-2	Sequence 2, Appli	520	111	6.1	763	2	US-09-949-016-10382	Sequence 10382, A
448	113	6.2	553	2	US-09-612-809B-2	Sequence 2, Appli	521	111	6.1	825	2	US-10-210-428-1	Sequence 1, Appli
449	113	6.2	684	1	US-08-555-669-12	Sequence 12, Appl	522	111	6.1	825	2	US-10-237-551-161	Sequence 161, App
450	113	6.2	684	2	US-09-073-663-12	Sequence 12, Appl	523	111	6.1	825	3	US-10-882-074-1	Sequence 1, Appli
451	112.5	6.2	260	2	US-09-431-887-6	Sequence 6, Appli	524	111	6.1	826	2	US-09-237-551-47	Sequence 47, Appl
452	112.5	6.2	285	3	US-10-703-032-110699	Sequence 110699,	525	111	6.1	826	2	US-10-237-551-47	Sequence 47, Appl
453	112.5	6.2	310	2	US-09-219-849-47	Sequence 47, Appl	526	111	6.1	1518	3	US-09-989-890-184	Sequence 184, App
454	112.5	6.2	391	2	US-09-949-016-6646	Sequence 6646, Ap	527	110.5	6.1	1518	3	US-10-703-032-111578	Sequence 111578,
455	112.5	6.2	392	2	US-09-949-016-10150	Sequence 10150, A	528	110.5	6.1	173	3	US-10-703-032-156672	Sequence 156672,
456	112.5	6.2	406	2	US-10-104-047-3010	Sequence 3010, Ap	529	110.5	6.1	212	3	US-10-108-260A-2593	Sequence 2593, Ap
457	112.5	6.2	416	2	US-09-252-991A-16734	Sequence 16734, A	530	110.5	6.1	303	2	US-09-270-767-61338	Sequence 61338, A
458	112.5	6.2	479	2	US-09-252-991A-21297	Sequence 21297, A	531	110.5	6.1	681	3	US-10-252-991A-22519	Sequence 22519, A
459	112.5	6.2	552	2	US-09-219-849-7	Sequence 7, Appli	532	110.5	6.1	693	2	US-10-108-260A-3849	Sequence 3849, Ap
460	112.5	6.2	929	2	US-09-254-594-3	Sequence 3, Appli	533	110.5	6.1	783	2	US-09-252-991A-18035	Sequence 18035, A
461	112.5	6.2	930	2	US-10-113-794A-1	Sequence 1, Appli	534	110.5	6.1	1345	3	US-10-433-794-17	Sequence 17, Appl
462	112.5	6.2	1626	3	US-10-202-167-2	Sequence 2, Appli	535	110.5	6.1	1351	2	US-09-548-473B-1	Sequence 1, Appli
463	112	6.1	211	3	US-10-703-032-110284	Sequence 110284,	536	110.5	6.1	1610	2	US-09-488-473B-4	Sequence 4, Appli
464	112	6.1	226	2	US-09-155-794-8	Sequence 8, Appli	537	110.5	6.1	1665	2	US-09-858-664A-2	Sequence 2, Appli

538	110.5	6.1	1665	2	US-10-274-978-2	Sequence 2, Appli	611	108.5	5.9	1249	2	US-09-964-899-33	Sequence 33, Appli
539	110.5	6.1	1665	2	US-10-697-263-2	Sequence 2, Appli	612	108.5	5.9	1418	2	US-09-252-991A-32367	Sequence 32367, A
540	110.5	6.1	2596	2	US-10-548-473B-6	Sequence 6, Appli	613	108	5.9	228	2	US-09-252-991A-32898	Sequence 32898, A
541	110.5	6.1	2630	3	US-10-077-130-5	Sequence 2, Appli	614	108	5.9	242	3	US-10-133-234A-4	Sequence 4, Appli
542	110.5	6.1	7968	3	US-10-077-130-5	Sequence 5, Appli	615	108	5.9	264	3	US-10-703-032-109622	Sequence 109622,
543	110	6.0	208	2	US-09-128-450-18	Sequence 18, Appl	616	108	5.9	347	2	US-09-623-497-1	Sequence 1, Appli
544	110	6.0	208	2	US-09-823-494-18	Sequence 18, Appl	617	108	5.9	417	1	US-08-175-155-69	Sequence 69, Appl
545	110	6.0	295	2	US-09-252-991A-32692	Sequence 32692, A	618	108	5.9	417	1	US-08-477-509B-104	Sequence 104, App
546	110	6.0	330	1	US-08-642-255-32	Sequence 32, Appl	619	108	5.9	417	1	US-08-642-255-102	Sequence 102, App
547	110	6.0	408	1	US-07-609-716-65	Sequence 65, Appl	620	108	5.9	417	1	US-08-707-237A-76	Sequence 76, Appl
548	110	6.0	408	2	US-08-475-411A-65	Sequence 65, Appl	621	108	5.9	417	2	US-08-482-085B-104	Sequence 104, App
549	110	6.0	408	2	US-08-478-029A-65	Sequence 65, Appl	622	108	5.9	417	2	US-09-444-791A-104	Sequence 104, App
550	110	6.0	414	2	US-09-252-991A-27895	Sequence 27895, A	623	108	5.9	534	2	US-09-029-348-5	Sequence 5, Appli
551	110	6.0	529	2	US-10-164-230-61	Sequence 61, Appl	624	108	5.9	620	2	US-09-931-009B-1	Sequence 1, Appli
552	110	6.0	577	2	US-09-949-016-11572	Sequence 11572, A	625	108	5.9	644	2	US-09-919-039-121	Sequence 121, App
553	110	6.0	694	2	US-09-949-016-7117	Sequence 7117, Ap	626	108	5.9	802	3	US-10-465-920-1	Sequence 1, Appli
554	110	6.0	902	3	US-10-886-384-21	Sequence 21, Appl	627	108	5.9	829	1	US-08-642-255-132	Sequence 3610, Ap
555	110	6.0	996	2	US-09-497-822C-21	Sequence 21, Appl	628	108	5.9	829	1	US-08-642-255-132	Sequence 132, App
556	110	6.0	1160	2	US-08-808-599A-24	Sequence 24, Appl	629	108	5.9	829	1	US-08-397-633A-53	Sequence 53, Appl
557	110	6.0	1228	3	US-09-917-383-1	Sequence 1, Appli	630	108	5.9	831	2	US-10-360-101-236	Sequence 236, App
558	109.5	6.0	138	3	US-10-703-032-169559	Sequence 169559,	631	108	5.9	837	1	US-08-175-155-68	Sequence 68, Appl
559	109.5	6.0	256	2	US-09-431-887-25	Sequence 25, Appl	632	108	5.9	837	1	US-08-477-509B-103	Sequence 103, App
560	109.5	6.0	256	2	US-09-431-887-26	Sequence 26, Appl	633	108	5.9	837	1	US-08-642-255-101	Sequence 101, App
561	109.5	6.0	256	2	US-09-431-887-28	Sequence 28, Appl	634	108	5.9	837	1	US-08-707-237A-75	Sequence 75, Appl
562	109.5	6.0	269	1	US-08-452-531-4	Sequence 4, Appli	635	108	5.9	837	2	US-08-482-085B-103	Sequence 103, App
563	109.5	6.0	269	1	US-08-460-746A-4	Sequence 4, Appli	636	108	5.9	847	2	US-09-444-791A-103	Sequence 4, Appli
564	109.5	6.0	269	1	US-08-460-555-4	Sequence 4, Appli	637	108	5.9	866	2	US-09-373-157-4	Sequence 373, Appl
565	109.5	6.0	269	2	US-08-460-066-4	Sequence 4, Appli	638	108	5.9	866	2	US-09-949-002-302	Sequence 302, App
566	109.5	6.0	300	3	US-10-703-032-131240	Sequence 131240,	639	108	5.9	875	2	US-09-949-016-8582	Sequence 8582, Ap
567	109.5	6.0	327	3	US-10-703-032-128959	Sequence 128959,	640	108	5.9	875	2	US-09-949-002-455	Sequence 455, App
568	109.5	6.0	362	2	US-09-252-991A-24615	Sequence 24615, A	641	108	5.9	897	1	US-08-397-633A-50	Sequence 50, Appl
569	109.5	6.0	411	3	US-10-108-260A-4496	Sequence 4496, Ap	642	108	5.9	930	2	US-09-177-650-96	Sequence 96, Appl
570	109.5	6.0	534	2	US-09-252-991A-20468	Sequence 20468, A	643	108	5.9	930	3	US-10-096-578-96	Sequence 96, Appl
571	109.5	6.0	1265	2	US-09-862-027-80	Sequence 80, Appl	644	108	5.9	1050	3	US-09-428-711A-16	Sequence 16, Appl
572	109.5	6.0	1343	2	US-09-949-016-16641	Sequence 16641, A	645	108	5.9	1050	3	US-10-021-698A-129	Sequence 129, App
573	109	6.0	158	3	US-10-703-032-111601	Sequence 111601,	646	108	5.9	1130	2	US-09-233-857-3	Sequence 3, Appli
574	109	6.0	168	3	US-10-703-032-178090	Sequence 178090,	647	108	5.9	1312	2	US-09-041-886-19	Sequence 19, Appl
575	109	6.0	240	2	US-09-252-991A-21852	Sequence 21852, A	648	108	5.9	1312	2	US-09-648-281-2	Sequence 2, Appli
576	109	6.0	318	2	US-09-252-991A-22374	Sequence 22374, A	649	108	5.9	1312	2	US-09-707-919A-19	Sequence 19, Appl
577	109	6.0	506	2	US-09-252-991A-20617	Sequence 20617, A	650	108	5.9	1312	2	US-09-083-268-3	Sequence 3, Appli
578	109	6.0	506	2	US-09-949-016-11282	Sequence 11282, A	651	108	5.9	1312	2	US-08-981-998A-3	Sequence 3, Appli
579	109	6.0	544	3	US-10-658-989A-4	Sequence 4, Appli	652	107.5	5.9	209	3	US-10-658-989A-1	Sequence 1, Appli
580	109	6.0	602	2	US-10-104-047-3324	Sequence 3324, Ap	653	107.5	5.9	252	2	US-09-431-887-17	Sequence 17, Appl
581	109	6.0	625	3	US-10-029-345A-39	Sequence 39, Appl	654	107.5	5.9	331	2	US-09-270-767-45830	Sequence 45830, A
582	109	6.0	625	3	US-10-029-345A-110	Sequence 110, App	655	107.5	5.9	438	2	US-09-252-991A-32407	Sequence 32407, A
583	109	6.0	643	1	US-08-551-356-4	Sequence 4, Appli	656	107.5	5.9	600	2	US-10-029-180-120	Sequence 120, App
584	109	6.0	643	5	PCT-US933-12687-4	Sequence 4, Appli	657	107.5	5.9	600	2	US-10-094-749-2713	Sequence 2713, Ap
585	109	6.0	644	1	US-08-206-176-2	Sequence 2, Appli	658	107.5	5.9	612	2	US-08-894-454-163	Sequence 163, App
586	109	6.0	666	3	US-10-168-067C-33	Sequence 33, Appl	659	107.5	5.9	612	2	US-09-949-016-6634	Sequence 6634, Ap
587	109	6.0	1125	2	US-09-513-783A-152	Sequence 152, App	660	107	5.9	249	2	US-09-538-092-951	Sequence 951, App
588	109	6.0	1125	2	US-09-430-656-152	Sequence 152, App	661	107	5.9	250	1	US-08-562-311-2	Sequence 2, Appli
589	109	6.0	1125	2	US-10-100-957A-152	Sequence 152, App	662	107	5.9	250	2	US-08-946-914-10	Sequence 10, Appl
590	109	6.0	1190	3	US-10-168-067C-1	Sequence 1, Appli	663	107	5.9	250	2	US-09-656-450-10	Sequence 10, Appl
591	109	6.0	1610	2	US-09-513-783A-22	Sequence 22, Appl	664	107	5.9	250	2	US-09-919-039-298	Sequence 298, App
592	109	6.0	1610	2	US-09-430-656-22	Sequence 22, Appl	665	107	5.9	250	2	US-09-877-790-2	Sequence 2, Appli
593	109	6.0	1610	2	US-10-100-957A-22	Sequence 22, Appl	666	107	5.9	250	2	US-10-133-234A-1	Sequence 1, Appli
594	108.5	5.9	252	1	US-08-642-255-61	Sequence 61, Appl	667	107	5.9	250	3	US-11-104-677-1	Sequence 1, Appli
595	108.5	5.9	253	2	US-09-431-887-7	Sequence 7, Appli	668	107	5.9	256	3	US-10-703-032-137132	Sequence 137132,
596	108.5	5.9	253	2	US-09-431-887-9	Sequence 9, Appli	669	107	5.9	415	2	US-09-252-991A-20613	Sequence 20613, A
597	108.5	5.9	253	2	US-09-431-887-10	Sequence 10, Appl	670	107	5.9	545	2	US-09-902-540-15915	Sequence 15915, A
598	108.5	5.9	253	2	US-09-431-887-11	Sequence 11, Appl	671	107	5.9	557	2	US-09-949-016-7621	Sequence 7621, Ap
599	108.5	5.9	253	2	US-09-431-887-12	Sequence 12, Appl	672	107	5.9	646	2	US-09-964-899-53	Sequence 53, Appl
600	108.5	5.9	253	2	US-09-431-887-14	Sequence 14, Appl	673	107	5.9	1051	2	US-09-428-711A-14	Sequence 14, Appl
601	108.5	5.9	299	2	US-09-252-991A-17588	Sequence 17588, A	674	107	5.9	1051	3	US-10-398-920-3	Sequence 3, Appli
602	108.5	5.9	336	2	US-09-902-540-12666	Sequence 12666, A	675	107	5.9	1130	2	US-09-442-100-4	Sequence 4, Appli
603	108.5	5.9	376	2	US-09-252-991A-25525	Sequence 25525, A	676	107	5.9	1130	2	US-08-939-106-4	Sequence 4, Appli
604	108.5	5.9	480	3	US-09-540-209B-7586	Sequence 7586, Ap	677	107	5.9	1130	2	US-09-442-102-4	Sequence 4, Appli
605	108.5	5.9	621	2	US-09-252-991A-30689	Sequence 30689, A	678	107	5.9	1130	2	US-09-949-016-6536	Sequence 6536, Ap
606	108.5	5.9	656	1	US-08-343-443B-2	Sequence 2, Appli	679	106.5	5.8	200	2	US-09-710-239-28	Sequence 28, Appl
607	108.5	5.9	656	2	US-09-214-564A-4	Sequence 4, Appli	680	106.5	5.8	201	3	US-10-703-032-134968	Sequence 134968,
608	108.5	5.9	656	2	US-09-538-092-1250	Sequence 1250, Ap	681	106.5	5.8	238	2	US-08-975-762-27	Sequence 27, Appl
609	108.5	5.9	656	3	US-10-791-017C-2	Sequence 2, Appli	682	106.5	5.8	238	2	US-08-821-324-27	Sequence 27, Appl
610	108.5	5.9	1027	2	US-10-360-101-221	Sequence 221, App	683	106.5	5.8	238	2	US-09-295-028-27	Sequence 27, Appl

684	106.5	5.8	238	2	US-09-106-582-27	Sequence 27, Appl	757	104	5.7	251	2	US-09-538-092-840	Sequence 840, App
685	106.5	5.8	238	2	US-09-159-469-27	Sequence 27, Appl	758	104	5.7	374	3	US-10-107-857-15	Sequence 15, Appl
686	106.5	5.8	238	2	US-09-693-542-27	Sequence 27, Appl	759	104	5.7	416	3	US-10-108-260A-4319	Sequence 4319, Ap
687	106.5	5.8	246	3	US-09-297-040-4	Sequence 4, Appli	760	104	5.7	504	2	US-09-219-849-3	Sequence 3, Appli
688	106.5	5.8	426	3	US-09-252-991A-21503	Sequence 21503, A	761	104	5.7	510	2	US-09-252-991A-33084	Sequence 33084, A
689	106.5	5.8	532	1	US-08-494-168-9	Sequence 9, Appli	762	104	5.7	530	2	US-09-252-991A-20846	Sequence 20846, A
690	106.5	5.8	667	3	US-10-108-260A-4123	Sequence 4123, Ap	763	104	5.7	561	1	US-08-642-255-52	Sequence 52, Appl
691	106.5	5.8	684	2	US-09-823-240A-9	Sequence 9, Appli	764	104	5.7	585	2	US-09-252-991A-31529	Sequence 31529, A
692	106.5	5.8	1207	2	US-10-098-600B-16	Sequence 16, Appl	765	104	5.7	611	2	US-10-029-180-119	Sequence 119, App
693	106.5	5.8	1207	2	US-09-949-002-376	Sequence 376, App	766	104	5.7	638	3	US-10-703-032-141937	Sequence 141937,
694	106.5	5.8	1384	2	US-08-976-255-11	Sequence 11, Appl	767	104	5.7	666	2	US-10-104-047-2217	Sequence 2217, Ap
695	106	5.8	171	3	US-10-703-032-130212	Sequence 130212,	768	104	5.7	720	2	US-09-219-849-4	Sequence 4, Appli
696	106	5.8	187	3	US-10-703-032-105758	Sequence 105758,	769	104	5.7	777	1	US-08-642-255-53	Sequence 53, Appl
697	106	5.8	191	3	US-10-703-032-205932	Sequence 205932,	770	104	5.7	808	2	US-09-252-991A-33826	Sequence 33826, A
698	106	5.8	196	3	US-10-703-032-141190	Sequence 141190,	771	104	5.7	1065	2	US-09-949-016-11618	Sequence 11618, A
699	106	5.8	245	2	US-10-104-047-3323	Sequence 3323, Ap	772	104	5.7	1321	1	US-08-317-310A-64	Sequence 64, Appl
700	106	5.8	391	2	US-09-342-681C-2	Sequence 2, Appli	773	103.5	5.7	166	2	US-09-252-991A-18554	Sequence 18554, A
701	106	5.8	391	2	US-10-012-605C-6	Sequence 6, Appli	774	103.5	5.7	187	2	US-09-489-039A-9840	Sequence 9840, Ap
702	106	5.8	391	3	US-09-949-016-6074	Sequence 6074, Ap	775	103.5	5.7	250	3	US-10-703-032-167339	Sequence 167339,
703	106	5.8	391	3	US-09-813-329-8	Sequence 8, Appli	776	103.5	5.7	270	3	US-10-703-032-125879	Sequence 125879,
704	106	5.8	391	3	US-10-218-547A-42	Sequence 42, Appl	777	103.5	5.7	274	3	US-10-703-032-139748	Sequence 139748,
705	106	5.8	391	3	US-09-729-658C-2	Sequence 2, Appli	778	103.5	5.7	462	2	US-09-252-991A-20814	Sequence 20814, A
706	106	5.8	391	3	US-10-719-205-6	Sequence 6, Appli	779	103.5	5.7	463	2	US-10-029-180-80	Sequence 80, Appl
707	106	5.8	593	2	US-09-964-899-15	Sequence 15, Appl	780	103.5	5.7	533	2	US-08-216-592A-4	Sequence 4, Appli
708	106	5.8	615	2	US-09-252-991A-26695	Sequence 26695, A	781	103.5	5.7	614	3	US-10-080-334-244	Sequence 244, App
709	106	5.8	619	2	US-09-252-991A-26352	Sequence 26352, A	782	103.5	5.7	673	3	US-09-963-693B-330	Sequence 330, App
710	106	5.8	767	2	US-09-252-991A-28262	Sequence 28262, A	783	103.5	5.7	722	2	US-09-894-998A-15	Sequence 15, Appl
711	106	5.8	1287	2	US-10-094-749-2627	Sequence 2627, Ap	784	103.5	5.7	722	2	US-10-237-551-15	Sequence 15, Appl
712	106	5.8	1307	2	US-09-252-991A-20867	Sequence 20867, A	785	103.5	5.7	722	2	US-10-237-551-159	Sequence 159, App
713	106	5.8	1319	2	US-09-538-092-1291	Sequence 1291, Ap	786	103.5	5.7	722	2	US-10-237-551-235	Sequence 235, App
714	106	5.8	1548	2	US-09-252-991A-22301	Sequence 22301, A	787	103.5	5.7	722	3	US-10-623-429-10	Sequence 10, Appl
715	105.5	5.8	97	3	US-10-703-032-205833	Sequence 205833,	788	103.5	5.7	930	2	US-09-254-594-6	Sequence 6, Appli
716	105.5	5.8	232	3	US-10-703-032-123117	Sequence 123117,	789	103.5	5.7	955	2	US-09-252-991A-24254	Sequence 24254, A
717	105.5	5.8	384	2	US-09-252-991A-30256	Sequence 30256, A	790	103.5	5.7	1109	2	US-09-949-016-10771	Sequence 10771, A
718	105.5	5.8	533	1	US-07-952-800-2	Sequence 2, Appli	791	103.5	5.7	1203	2	US-09-949-016-6615	Sequence 6615, Ap
719	105.5	5.8	549	1	US-08-494-168-8	Sequence 8, Appli	792	103.5	5.7	1203	2	US-10-067-457-3	Sequence 3, Appli
720	105.5	5.8	599	2	US-09-949-016-8890	Sequence 8890, Ap	793	103.5	5.7	1243	1	US-08-557-139-2	Sequence 2, Appli
721	105.5	5.8	645	2	US-09-964-899-17	Sequence 17, Appl	794	103.5	5.7	1734	3	US-09-862-027-81	Sequence 81, Appl
722	105.5	5.8	732	1	US-08-317-522A-5	Sequence 5, Appli	795	103.5	5.7	1734	3	US-10-042-865-82	Sequence 82, Appl
723	105.5	5.8	1197	2	US-09-252-991A-30833	Sequence 30833, A	796	103	5.6	182	2	US-09-270-767-59542	Sequence 59542, A
724	105.5	5.8	1268	2	US-09-270-767-45320	Sequence 45320, A	797	103	5.6	237	2	US-09-721-908-4	Sequence 4, Appli
725	105	5.8	234	3	US-09-538-092-888	Sequence 888, App	798	103	5.6	280	3	US-10-703-032-114785	Sequence 114785,
726	105	5.8	234	3	US-10-703-032-105759	Sequence 105759,	799	103	5.6	306	3	US-09-949-016-7825	Sequence 7825, Ap
727	105	5.8	251	2	US-09-949-016-7560	Sequence 7560, Ap	800	103	5.6	326	3	US-10-703-032-208179	Sequence 208179,
728	105	5.8	317	3	US-10-703-032-134963	Sequence 134963,	801	103	5.6	337	2	US-08-991-426-4	Sequence 4, Appli
729	105	5.8	341	2	US-09-252-991A-20302	Sequence 20302, A	802	103	5.6	337	2	US-09-143-470-4	Sequence 4, Appli
730	105	5.8	1028	3	US-09-939-853A-17	Sequence 17, Appl	803	103	5.6	337	2	US-08-649-006A-4	Sequence 4, Appli
731	105	5.8	1426	3	US-09-915-543-15	Sequence 15, Appl	804	103	5.6	337	3	US-09-771-023-4	Sequence 4, Appli
732	105	5.8	2353	2	US-08-984-709A-50	Sequence 50, Appl	805	103	5.6	337	3	US-10-448-664-4	Sequence 4, Appli
733	105	5.8	3122	2	US-10-237-551-201	Sequence 201, App	806	103	5.6	337	3	US-10-397-559-4	Sequence 4, Appli
734	105	5.8	3122	2	US-10-237-551-250	Sequence 250, App	807	103	5.6	400	2	US-09-252-991A-31900	Sequence 31900, A
735	104.5	5.7	228	2	US-09-219-849-38	Sequence 38, Appl	808	103	5.6	505	3	US-10-703-032-208190	Sequence 208190,
736	104.5	5.7	252	2	US-09-431-887-13	Sequence 13, Appl	809	103	5.6	553	2	US-09-949-016-7961	Sequence 7961, Ap
737	104.5	5.7	280	3	US-10-703-032-122290	Sequence 122290,	810	103	5.6	555	2	US-09-949-016-7080	Sequence 7080, Ap
738	104.5	5.7	431	3	US-10-746-592-23	Sequence 23, Appl	811	103	5.6	743	2	US-09-771-161A-164	Sequence 164, App
739	104.5	5.7	535	2	US-09-029-348-1	Sequence 1, Appli	812	103	5.6	743	2	US-09-771-161A-254	Sequence 254, App
740	104.5	5.7	537	2	US-09-029-348-4	Sequence 4, Appli	813	103	5.6	774	3	US-09-548-933-1	Sequence 1, Appli
741	104.5	5.7	558	2	US-09-252-991A-26115	Sequence 26115, A	814	103	5.6	774	3	US-09-767-597-1	Sequence 1, Appli
742	104.5	5.7	666	2	US-09-050-739-70	Sequence 70, Appl	815	103	5.6	1274	2	US-09-095-443-2	Sequence 2, Appli
743	104.5	5.7	666	2	US-09-804-980-70	Sequence 70, Appl	816	103	5.6	1636	3	US-10-433-794-1	Sequence 1, Appli
744	104.5	5.7	841	2	US-09-252-991A-26919	Sequence 26919, A	817	102.5	5.6	183	3	US-10-703-032-129561	Sequence 129561,
745	104.5	5.7	1006	3	US-10-415-147-12	Sequence 12, Appl	818	102.5	5.6	186	3	US-10-703-032-206962	Sequence 206962,
746	104.5	5.7	1006	3	US-10-114-270-84	Sequence 84, Appl	819	102.5	5.6	358	3	US-10-617-217A-139	Sequence 137, App
747	104.5	5.7	1242	2	US-09-508-691-1	Sequence 1, Appli	820	102.5	5.6	367	2	US-09-252-991A-16628	Sequence 16628, A
748	104.5	5.7	1242	2	US-09-903-248-5	Sequence 5, Appli	821	102.5	5.6	396	3	US-10-617-217A-139	Sequence 139, App
749	104.5	5.7	1242	2	US-09-903-199-5	Sequence 5, Appli	822	102.5	5.6	464	3	US-09-252-991A-26212	Sequence 26212, A
750	104.5	5.7	1242	2	US-09-903-216-5	Sequence 5, Appli	823	102.5	5.6	551	2	US-09-605-703B-1226	Sequence 1226, Ap
751	104.5	5.7	1242	2	US-09-903-063-5	Sequence 5, Appli	824	102.5	5.6	855	2	US-09-281-766-19	Sequence 19, Appl
752	104.5	5.7	1242	3	US-09-859-604-5	Sequence 5, Appli	825	102.5	5.6	855	2	US-09-612-858-19	Sequence 19, Appl
753	104.5	5.7	1242	3	US-09-903-023-5	Sequence 5, Appli	826	102.5	5.6	865	2	US-09-957-995A-19	Sequence 19, Appl
754	104.5	5.7	1290	2	US-09-150-460B-6	Sequence 6, Appli	827	102.5	5.6	865	3	US-10-899-538-19	Sequence 19, Appl
755	104	5.7	156	3	US-10-703-032-105757	Sequence 105757,	828	102.5	5.6	2017	3	US-10-114-270-86	Sequence 86, Appl
756	104	5.7	242	3	US-10-703-032-163051	Sequence 163051,	829	102	5.6	174	2	US-10-104-047-2398	Sequence 2398, Ap

830	102	5.6	199	3	US-10-703-032-210393	Sequence 210393,	903	100.5	5.5	643	2	US-10-192-985-1	Sequence 1, Appli
831	102	5.6	261	3	US-09-710-239-16	Sequence 16, Appl	904	100.5	5.5	743	2	US-09-252-991A-28327	Sequence 28327, A
832	102	5.6	416	3	US-10-703-032-115576	Sequence 115576,	905	100.5	5.5	897	1	US-07-960-389-2	Sequence 2, Appli
833	102	5.6	421	2	US-09-920-540-14807	Sequence 14807, A	906	100.5	5.5	959	2	US-09-252-991A-21747	Sequence 21747, A
834	102	5.6	486	2	US-09-270-767-41521	Sequence 41521, A	907	100.5	5.5	1048	2	US-09-921-099A-11	Sequence 11, Appl
835	102	5.6	502	2	US-09-839-577A-14	Sequence 14, Appl	908	100.5	5.5	1048	3	US-10-619-992-11	Sequence 11, Appl
836	102	5.6	502	3	US-10-168-097A-2	Sequence 2, Appli	909	100	5.5	194	3	US-10-703-032-171299	Sequence 171299,
837	102	5.6	502	3	US-10-455-713-14	Sequence 14, Appl	910	100	5.5	244	2	US-09-461-325-463	Sequence 463, App
838	102	5.6	565	2	US-10-104-047-2296	Sequence 2296, Ap	911	100	5.5	244	2	US-10-012-542-463	Sequence 463, App
839	102	5.6	758	2	US-09-904-987-5	Sequence 5, Appli	912	100	5.5	244	2	US-10-115-123-463	Sequence 463, App
840	102	5.6	1027	2	US-09-252-991A-26216	Sequence 26216, A	913	100	5.5	316	2	US-09-252-991A-25345	Sequence 25345, A
841	102	5.6	1506	2	US-10-142-650-4	Sequence 4, Appli	914	100	5.5	324	3	US-10-703-032-128981	Sequence 128981,
842	102	5.6	1706	1	US-08-459-568-2	Sequence 2, Appli	915	100	5.5	431	3	US-09-734-329B-23	Sequence 23, Appl
843	102	5.6	1706	1	US-08-399-411-2	Sequence 2, Appli	916	100	5.5	563	2	US-09-311-021-36	Sequence 36, Appl
844	102	5.6	1706	2	US-08-516-859A-2	Sequence 2, Appli	917	100	5.5	508	2	US-09-252-991A-24250	Sequence 24250, A
845	102	5.6	1706	2	US-09-586-472-2	Sequence 2, Appli	918	100	5.5	628	2	US-09-345-473B-48	Sequence 48, Appl
846	102	5.6	1706	2	US-09-528-706-2	Sequence 2, Appli	919	100	5.5	628	2	US-09-862-027-48	Sequence 48, Appl
847	102	5.6	1706	2	US-10-024-450-2	Sequence 2, Appli	920	100	5.5	794	2	US-09-252-991A-28569	Sequence 28569, A
848	102	5.6	1706	2	US-10-142-650-3	Sequence 3, Appli	921	100	5.5	1036	2	US-08-891-640-3	Sequence 3, Appli
849	101.5	5.6	141	2	US-09-270-767-38716	Sequence 38716, A	922	100	5.5	1036	2	US-09-842-256-3	Sequence 5, Appli
850	101.5	5.6	141	2	US-09-270-767-53933	Sequence 53933, A	923	100	5.5	1036	2	US-08-701-154A-5	Sequence 5, Appli
851	101.5	5.6	172	2	US-09-800-729-138	Sequence 138, App	924	100	5.5	1476	2	US-09-252-991A-29427	Sequence 29427, A
852	101.5	5.6	237	2	US-09-270-767-45021	Sequence 45021, A	925	100	5.5	4019	2	US-09-854-133-425	Sequence 425, App
853	101.5	5.6	273	3	US-10-703-032-115162	Sequence 115162,	926	99.5	5.5	209	3	US-10-703-032-184625	Sequence 184625,
854	101.5	5.6	293	2	US-09-252-991A-29137	Sequence 29137, A	927	99.5	5.5	246	3	US-10-703-032-121148	Sequence 121148,
855	101.5	5.6	332	2	US-09-252-991A-31956	Sequence 31956, A	928	99.5	5.5	255	3	US-10-703-032-119000	Sequence 119000,
856	101.5	5.6	362	2	US-10-703-032-117744	Sequence 117744, A	929	99.5	5.5	271	2	US-09-252-991A-30514	Sequence 30514, A
857	101.5	5.6	385	3	US-10-703-032-106381	Sequence 106381,	930	99.5	5.5	297	2	US-09-252-991A-32590	Sequence 32590, A
858	101.5	5.6	390	2	US-09-252-991A-22732	Sequence 22732, A	931	99.5	5.5	374	3	US-10-305-278-172	Sequence 172, App
859	101.5	5.6	395	2	US-09-252-991A-17341	Sequence 17341, A	932	99.5	5.5	388	3	US-10-703-032-139938	Sequence 139938,
860	101.5	5.6	416	3	US-10-703-032-127765	Sequence 127765,	933	99.5	5.5	399	2	US-10-703-032-127210	Sequence 127210,
861	101.5	5.6	868	2	US-09-800-729-106	Sequence 106, App	934	99.5	5.5	401	2	US-09-252-991A-19289	Sequence 19289, A
862	101.5	5.6	921	2	US-09-800-729-199	Sequence 199, App	935	99.5	5.5	414	2	US-10-173-999-8	Sequence 8, Appli
863	101.5	5.6	1001	2	US-10-415-147-3	Sequence 3, Appli	936	99.5	5.5	440	2	US-10-012-231A-52	Sequence 52, Appl
864	101.5	5.6	1809	3	US-10-114-270-98	Sequence 98, Appl	937	99.5	5.5	440	2	US-10-015-389A-52	Sequence 52, Appl
865	101.5	5.6	2266	3	US-09-611-257A-37	Sequence 37, Appl	938	99.5	5.5	440	2	US-10-006-768A-52	Sequence 52, Appl
866	101.5	5.6	2273	2	US-09-426-998-5	Sequence 5, Appli	939	99.5	5.5	440	2	US-10-015-671A-52	Sequence 52, Appl
867	101.5	5.6	2441	1	US-08-194-468-2	Sequence 2, Appli	940	99.5	5.5	440	2	US-10-015-393A-52	Sequence 52, Appl
868	101.5	5.6	2441	2	US-08-961-739-2	Sequence 2, Appli	941	99.5	5.5	440	2	US-10-011-833A-52	Sequence 52, Appl
869	101.5	5.6	2441	2	US-09-514-247A-8	Sequence 8, Appli	942	99.5	5.5	440	2	US-10-006-041A-52	Sequence 52, Appl
870	101.5	5.6	2441	2	US-09-686-316-2	Sequence 2, Appli	943	99.5	5.5	440	2	US-10-012-064A-52	Sequence 52, Appl
871	101.5	5.6	2441	3	US-10-109-886-8	Sequence 8, Appli	944	99.5	5.5	440	2	US-10-015-392A-52	Sequence 52, Appl
872	101	5.5	187	2	US-09-680-175-4	Sequence 4, Appli	945	99.5	5.5	440	3	US-10-011-795B-52	Sequence 52, Appl
873	101	5.5	247	3	US-10-108-260A-2734	Sequence 2734, Ap	946	99.5	5.5	440	3	US-10-015-386A-52	Sequence 52, Appl
874	101	5.5	264	2	US-09-252-991A-30092	Sequence 30092, A	947	99.5	5.5	440	3	US-10-012-121A-52	Sequence 52, Appl
875	101	5.5	286	3	US-10-703-032-179920	Sequence 179920,	948	99.5	5.5	440	3	US-10-006-485A-52	Sequence 52, Appl
876	101	5.5	333	3	US-10-703-032-116148	Sequence 116148,	949	99.5	5.5	440	3	US-10-006-746A-52	Sequence 52, Appl
877	101	5.5	346	3	US-10-703-032-139660	Sequence 139660,	950	99.5	5.5	440	3	US-10-012-752A-52	Sequence 52, Appl
878	101	5.5	374	2	US-09-949-016-7191	Sequence 7191, Ap	951	99.5	5.5	440	3	US-10-017-253A-52	Sequence 52, Appl
879	101	5.5	441	2	US-09-252-991A-27502	Sequence 27502, A	952	99.5	5.5	440	3	US-10-015-519A-52	Sequence 52, Appl
880	101	5.5	444	2	US-09-949-016-10073	Sequence 10073, A	953	99.5	5.5	440	3	US-10-015-715A-52	Sequence 52, Appl
881	101	5.5	481	2	US-09-949-016-9581	Sequence 9581, Ap	954	99.5	5.5	440	3	US-10-007-236A-52	Sequence 52, Appl
882	101	5.5	489	2	US-09-252-991A-16940	Sequence 16940, A	955	99.5	5.5	440	3	US-10-012-149A-52	Sequence 52, Appl
883	101	5.5	572	2	US-09-252-991A-21105	Sequence 21105, A	956	99.5	5.5	440	3	US-10-007-194A-52	Sequence 52, Appl
884	101	5.5	629	3	US-10-406-832-29	Sequence 29, Appl	957	99.5	5.5	440	3	US-10-013-910A-52	Sequence 52, Appl
885	101	5.5	661	2	US-09-949-016-9121	Sequence 9121, Ap	958	99.5	5.5	440	3	US-10-006-117A-52	Sequence 52, Appl
886	101	5.5	1740	2	US-09-377-285B-40	Sequence 40, Appl	959	99.5	5.5	440	3	US-10-015-480A-52	Sequence 52, Appl
887	101	5.5	1740	2	US-10-192-381-40	Sequence 40, Appl	960	99.5	5.5	440	3	US-10-006-172A-52	Sequence 52, Appl
888	101	5.5	2372	2	US-09-579-181-2	Sequence 2, Appli	961	99.5	5.5	440	3	US-10-063-639A-52	Sequence 52, Appl
889	101	5.5	3118	3	US-09-579-181-1	Sequence 1, Appli	962	99.5	5.5	440	3	US-10-183-305A-52	Sequence 52, Appl
890	100.5	5.5	113	3	US-10-703-032-110824	Sequence 110824,	963	99.5	5.5	440	3	US-10-015-610A-52	Sequence 52, App
891	100.5	5.5	195	3	US-10-703-032-110773	Sequence 110773,	964	99.5	5.5	440	3	US-10-180-998-202	Sequence 202, App
892	100.5	5.5	224	2	US-10-104-047-3343	Sequence 3343, Ap	965	99.5	5.5	440	3	US-10-201-769-202	Sequence 202, App
893	100.5	5.5	239	2	US-09-902-540-10392	Sequence 10392, A	966	99.5	5.5	440	3	US-10-006-130A-52	Sequence 52, Appl
894	100.5	5.5	334	2	US-09-252-991A-18169	Sequence 18169, A	967	99.5	5.5	440	3	US-10-063-638A-52	Sequence 52, Appl
895	100.5	5.5	374	2	US-09-252-991A-30844	Sequence 30844, A	968	99.5	5.5	440	3	US-10-063-638A-52	Sequence 52, Appl
896	100.5	5.5	377	2	US-09-252-991A-31793	Sequence 31793, A	969	99.5	5.5	440	3	US-10-063-510-52	Sequence 52, Appl
897	100.5	5.5	433	2	US-09-046-158A-2	Sequence 2, Appli	970	99.5	5.5	440	3	US-10-223-081-150	Sequence 150, App
898	100.5	5.5	478	2	US-09-252-991A-31455	Sequence 31455, A	971	99.5	5.5	440	3	US-10-063-741-52	Sequence 52, Appl
899	100.5	5.5	495	2	US-09-252-991A-31949	Sequence 31949, A	972	99.5	5.5	440	3	US-10-063-584-52	Sequence 52, Appl
900	100.5	5.5	605	2	US-09-949-016-9305	Sequence 9305, Ap	973	99.5	5.5	440	3	US-10-174-576-202	Sequence 202, App
901	100.5	5.5	615	2	US-09-949-016-9320	Sequence 9320, Ap	974	99.5	5.5	440	3	US-10-219-074-156	Sequence 156, App
902	100.5	5.5	615	2	US-09-949-016-9321	Sequence 9321, Ap	975	99.5	5.5	440	3	US-10-227-873-156	Sequence 156, App

976	99.5	5.5	440	3	US-10-223-087-150	Sequence 150, App	1049	99	5.4	404	2	US-09-252-991A-25762	Sequence 25762, A
977	99.5	5.5	440	3	US-10-218-849-156	Sequence 156, App	1050	99	5.4	436	2	US-09-252-991A-31117	Sequence 31117, A
978	99.5	5.5	440	3	US-10-174-581-202	Sequence 202, App	1051	99	5.4	439	2	US-09-949-016-7372	Sequence 7372, Ap
979	99.5	5.5	440	3	US-10-216-168-156	Sequence 156, App	1052	99	5.4	486	3	US-10-703-032-140650	Sequence 140650, A
980	99.5	5.5	440	3	US-10-006-867-52	Sequence 52, App1	1053	99	5.4	497	2	US-09-252-991A-18725	Sequence 18725, A
981	99.5	5.5	440	3	US-10-223-082-150	Sequence 150, App	1054	99	5.4	570	2	US-09-252-991A-26331	Sequence 26331, A
982	99.5	5.5	440	3	US-10-223-084-150	Sequence 150, App	1055	99	5.4	573	2	US-09-252-991A-30371	Sequence 30371, A
983	99.5	5.5	440	3	US-10-063-659-52	Sequence 52, App1	1056	99	5.4	605	2	US-09-949-016-11347	Sequence 11347, A
984	99.5	5.5	440	3	US-10-015-869A-52	Sequence 52, App1	1057	99	5.4	683	2	US-09-949-016-11117	Sequence 11117, A
985	99.5	5.5	440	3	US-10-063-742-52	Sequence 52, App1	1058	99	5.4	722	2	US-09-252-991A-26839	Sequence 26839, A
986	99.5	5.5	440	3	US-10-063-703-52	Sequence 52, App1	1059	99	5.4	955	2	US-09-252-991A-18882	Sequence 18882, A
987	99.5	5.5	440	3	US-10-063-709-52	Sequence 52, App1	1060	98.5	5.4	955	3	US-10-703-032-115541	Sequence 115541, A
988	99.5	5.5	440	3	US-10-063-581-52	Sequence 52, App1	1061	98.5	5.4	171	2	US-09-252-991A-27570	Sequence 27570, A
989	99.5	5.5	440	3	US-10-063-583-52	Sequence 52, App1	1062	98.5	5.4	230	2	US-10-703-032-138546	Sequence 138546, A
990	99.5	5.5	440	3	US-10-063-593-52	Sequence 52, App1	1063	98.5	5.4	236	3	US-10-703-032-179735	Sequence 179735, A
991	99.5	5.5	440	3	US-10-063-599-52	Sequence 52, App1	1064	98.5	5.4	312	2	US-09-252-991A-21508	Sequence 21508, A
992	99.5	5.5	440	3	US-10-063-646-52	Sequence 52, App1	1065	98.5	5.4	353	2	US-09-252-991A-32071	Sequence 32071, A
993	99.5	5.5	440	3	US-10-063-660-52	Sequence 52, App1	1066	98.5	5.4	381	2	US-09-510-031A-5	Sequence 5, Appli
994	99.5	5.5	440	3	US-10-207-916-202	Sequence 202, App	1067	98.5	5.4	404	2	US-09-949-016-7352	Sequence 7352, Ap
995	99.5	5.5	440	3	US-10-063-647-52	Sequence 52, App1	1068	98.5	5.4	420	1	US-08-845-998-8	Sequence 8, Appli
996	99.5	5.5	440	3	US-10-063-661-52	Sequence 52, App1	1069	98.5	5.4	420	2	US-09-206-537-8	Sequence 8, Appli
997	99.5	5.5	440	3	US-10-063-651-52	Sequence 52, App1	1070	98.5	5.4	420	2	US-09-430-854-8	Sequence 8, Appli
998	99.5	5.5	440	3	US-10-063-530-52	Sequence 52, App1	1071	98.5	5.4	453	2	US-09-605-703B-1228	Sequence 1228, Ap
999	99.5	5.5	440	3	US-10-063-540-52	Sequence 52, App1	1072	98.5	5.4	529	2	US-09-949-016-6944	Sequence 6944, Ap
1000	99.5	5.5	440	3	US-10-063-648-52	Sequence 52, App1	1073	98.5	5.4	535	2	US-09-252-991A-28410	Sequence 28410, A
1001	99.5	5.5	440	3	US-10-063-657-52	Sequence 52, App1	1074	98.5	5.4	550	2	US-09-616-289-47	Sequence 47, Appl
1002	99.5	5.5	440	3	US-10-063-702-52	Sequence 52, App1	1075	98.5	5.4	550	2	US-09-976-740-47	Sequence 47, Appl
1003	99.5	5.5	440	3	US-10-063-529-52	Sequence 52, App1	1076	98.5	5.4	612	2	US-09-949-016-11308	Sequence 11308, A
1004	99.5	5.5	440	3	US-10-063-644-52	Sequence 52, App1	1077	98.5	5.4	917	3	US-10-666-642-1004	Sequence 1004, Ap
1005	99.5	5.5	440	3	US-10-063-585-52	Sequence 52, App1	1078	98.5	5.4	934	2	US-09-252-991A-26779	Sequence 26779, A
1006	99.5	5.5	440	3	US-10-063-591A-52	Sequence 52, App1	1079	98.5	5.4	934	2	US-09-538-092-1171	Sequence 1171, Ap
1007	99.5	5.5	440	3	US-10-063-516-52	Sequence 52, App1	1080	98.5	5.4	1586	3	US-10-386-414A-2	Sequence 2, Appli
1008	99.5	5.5	440	3	US-10-063-532-52	Sequence 52, App1	1081	98	5.4	145	2	US-09-370-838-75	Sequence 75, Appl
1009	99.5	5.5	440	3	US-10-063-654-52	Sequence 52, App1	1082	98	5.4	145	2	US-09-854-133-75	Sequence 75, Appl
1010	99.5	5.5	440	3	US-10-063-582-52	Sequence 52, App1	1083	98	5.4	200	2	US-10-094-749-1762	Sequence 1762, Ap
1011	99.5	5.5	440	3	US-10-063-524-52	Sequence 52, App1	1084	98	5.4	214	3	US-10-703-032-184444	Sequence 184444, A
1012	99.5	5.5	440	3	US-10-972-317-52	Sequence 52, App1	1085	98	5.4	288	3	US-10-703-032-123084	Sequence 123084, A
1013	99.5	5.5	440	3	US-10-174-583-202	Sequence 202, App	1086	98	5.4	289	3	US-10-703-032-137024	Sequence 137024, A
1014	99.5	5.5	440	3	US-10-063-551-52	Sequence 52, App1	1087	98	5.4	294	2	US-09-252-991A-29716	Sequence 29716, A
1015	99.5	5.5	440	3	US-10-063-650-52	Sequence 52, App1	1088	98	5.4	319	2	US-09-252-991A-16622	Sequence 16622, A
1016	99.5	5.5	440	3	US-10-063-523-52	Sequence 52, App1	1089	98	5.4	344	3	US-10-108-260A-4631	Sequence 4631, Ap
1017	99.5	5.5	440	3	US-10-063-592A-52	Sequence 52, App1	1090	98	5.4	395	2	US-09-252-991A-26116	Sequence 26116, A
1018	99.5	5.5	440	3	US-10-063-705-52	Sequence 52, App1	1091	98	5.4	418	2	US-09-252-991A-32035	Sequence 32035, A
1019	99.5	5.5	440	3	US-10-063-598-52	Sequence 52, App1	1092	98	5.4	440	2	US-09-252-991A-26855	Sequence 26855, A
1020	99.5	5.5	440	3	US-10-063-554-52	Sequence 52, App1	1093	98	5.4	441	2	US-09-252-991A-24396	Sequence 24396, A
1021	99.5	5.5	440	3	US-10-063-597-52	Sequence 52, App1	1094	98	5.4	453	2	US-09-252-991A-19516	Sequence 19516, A
1022	99.5	5.5	440	3	US-10-063-600-52	Sequence 52, App1	1095	98	5.4	475	2	US-09-252-991A-25837	Sequence 25837, A
1023	99.5	5.5	440	3	US-10-063-652A-52	Sequence 52, App1	1096	98	5.4	489	2	US-09-949-016-10074	Sequence 10074, A
1024	99.5	5.5	440	3	US-10-063-602-52	Sequence 52, App1	1097	98	5.4	633	3	US-10-168-097A-66	Sequence 66, Appl
1025	99.5	5.5	440	3	US-10-063-560-52	Sequence 52, App1	1098	98	5.4	663	2	US-09-252-991A-30843	Sequence 30843, A
1026	99.5	5.5	440	3	US-10-063-517-52	Sequence 52, App1	1099	98	5.4	684	2	US-09-949-016-8348	Sequence 8348, Ap
1027	99.5	5.5	440	3	US-10-063-548-52	Sequence 52, App1	1100	98	5.4	777	2	US-09-252-991A-27864	Sequence 27864, A
1028	99.5	5.5	440	3	US-10-063-553-52	Sequence 52, App1	1101	98	5.4	11877	2	US-09-105-537-6	Sequence 6, Appli
1029	99.5	5.5	440	3	US-10-063-653A-52	Sequence 52, App1	1102	97.5	5.3	136	2	US-08-990-571-71	Sequence 71, Appl
1030	99.5	5.5	495	3	US-09-958-359-31	Sequence 31, App1	1103	97.5	5.3	136	2	US-08-990-571-73	Sequence 73, Appl
1031	99.5	5.5	570	2	US-09-252-991A-31519	Sequence 31519, A	1104	97.5	5.3	136	2	US-09-528-784A-71	Sequence 71, Appl
1032	99.5	5.5	589	2	US-09-252-991A-18210	Sequence 18210, A	1105	97.5	5.3	136	2	US-09-528-784A-73	Sequence 73, Appl
1033	99.5	5.5	614	2	US-09-252-991A-28630	Sequence 28630, A	1106	97.5	5.3	136	2	US-09-569-098A-71	Sequence 71, Appl
1034	99.5	5.5	615	2	US-09-252-991A-23203	Sequence 23203, A	1107	97.5	5.3	136	2	US-09-569-098A-73	Sequence 73, Appl
1035	99.5	5.5	693	2	US-09-081-385-154	Sequence 154, App	1108	97.5	5.3	175	3	US-09-252-991A-30331	Sequence 30331, A
1036	99.5	5.5	693	2	US-09-752-639-154	Sequence 154, App	1109	97.5	5.3	216	2	US-10-108-260A-2965	Sequence 2965, Ap
1037	99.5	5.5	693	2	US-09-712-813-154	Sequence 154, App	1110	97.5	5.3	234	1	US-08-642-255-51	Sequence 51, Appl
1038	99.5	5.5	693	2	US-09-700-354A-154	Sequence 154, App	1111	97.5	5.3	245	2	US-10-104-047-3466	Sequence 3466, Ap
1039	99.5	5.5	766	2	US-09-902-540-10802	Sequence 10602, A	1112	97.5	5.3	251	2	US-09-710-239-31	Sequence 31, Appl
1040	99.5	5.5	1145	2	US-09-758-759-167	Sequence 167, App	1113	97.5	5.3	326	2	US-09-252-991A-30033	Sequence 30033, A
1041	99.5	5.5	1145	3	US-11-021-825-167	Sequence 167, App	1114	97.5	5.3	326	2	US-09-252-991A-20075	Sequence 20075, A
1042	99.5	5.5	1505	2	US-09-538-092-1102	Sequence 1102, Ap	1115	97.5	5.3	335	2	US-09-252-991A-16882	Sequence 16882, A
1043	99	5.4	162	3	US-10-703-032-199278	Sequence 199278, A	1116	97.5	5.3	339	2	US-09-270-767-44762	Sequence 44762, A
1044	99	5.4	201	3	US-10-703-032-124771	Sequence 124771, A	1117	97.5	5.3	402	2	US-09-252-991A-17143	Sequence 17143, A
1045	99	5.4	242	3	US-10-703-032-136683	Sequence 136683, A	1118	97.5	5.3	407	3	US-10-931-081A-356	Sequence 356, App
1046	99	5.4	269	2	US-09-252-991A-25341	Sequence 25341, A	1119	97.5	5.3	414	2	US-09-252-991A-24714	Sequence 24714, A
1047	99	5.4	356	2	US-09-252-991A-19932	Sequence 19932, A	1120	97.5	5.3	445	2	US-10-094-749-3147	Sequence 3147, Ap
1048	99	5.4	395	2	US-09-252-991A-30497	Sequence 30497, A	1121	97.5	5.3	537	2	US-09-252-991A-22864	Sequence 22864, A

1122	97.5	5.3	560	2	US-09-252-991A-25999	Sequence 25999, A	1195	96.5	5.3	622	2	US-09-502-498C-155	Sequence 155, App
1123	97.5	5.3	582	2	US-09-428-711A-2	Sequence 2, Appli	1196	96.5	5.3	622	2	US-09-502-424C-155	Sequence 155, App
1124	97.5	5.3	626	2	US-09-345-473E-43	Sequence 43, Appli	1197	96.5	5.3	622	3	US-10-108-260A-4703	Sequence 4703, Ap
1125	97.5	5.3	626	2	US-09-862-027-43	Sequence 43, Appli	1198	96.5	5.3	632	2	US-09-859-961-2	Sequence 2, Appli
1126	97.5	5.3	686	2	US-09-252-991A-21221	Sequence 21221, A	1199	96.5	5.3	663	2	US-10-104-047-3473	Sequence 3473, Ap
1127	97.5	5.3	726	2	US-09-252-991A-18271	Sequence 18271, A	1200	96.5	5.3	679	2	US-09-252-991A-18957	Sequence 18957, A
1128	97.5	5.3	776	2	US-09-252-991A-28446	Sequence 28446, A	1201	96.5	5.3	704	2	US-09-502-498C-58	Sequence 58, Appl
1129	97.5	5.3	786	2	US-09-688-188B-23	Sequence 23, Appl	1202	96.5	5.3	704	2	US-09-502-424C-58	Sequence 58, Appl
1130	97.5	5.3	786	2	US-09-291-417D-23	Sequence 23, Appl	1203	96.5	5.3	762	2	US-09-917-378-1	Sequence 1, Appli
1131	97.5	5.3	787	2	US-09-688-188B-151	Sequence 151, App	1204	96.5	5.3	841	2	US-09-502-498C-62	Sequence 62, Appl
1132	97.5	5.3	787	2	US-09-291-417D-151	Sequence 151, App	1205	96.5	5.3	841	2	US-09-502-424C-62	Sequence 62, Appl
1133	97.5	5.3	802	2	US-09-823-240A-2	Sequence 2, Appli	1206	96.5	5.3	877	3	US-10-245-913-90	Sequence 90, Appl
1134	97.5	5.3	875	2	US-09-813-290-2	Sequence 2, Appli	1207	96.5	5.3	877	3	US-10-245-752-90	Sequence 90, Appl
1135	97.5	5.3	1001	2	US-09-688-188B-31	Sequence 31, Appl	1208	96.5	5.3	877	3	US-10-242-095-90	Sequence 90, Appl
1136	97.5	5.3	1001	2	US-09-291-417D-31	Sequence 31, Appl	1209	96.5	5.3	877	3	US-10-242-652-90	Sequence 90, Appl
1137	97.5	5.3	1336	1	US-08-551-356-6	Sequence 6, Appli	1210	96.5	5.3	888	2	US-10-077-940A-4	Sequence 4, Appli
1138	97.5	5.3	1336	1	PCT-US93-12687-6	Sequence 6, Appli	1211	96.5	5.3	888	2	US-10-036-041-35	Sequence 35, Appl
1139	97.5	5.3	1495	2	US-08-522-728B-1	Sequence 1, Appli	1212	96.5	5.3	888	3	US-10-123-292-544	Sequence 544, App
1140	97.5	5.3	1495	2	US-09-337-384-1	Sequence 1, Appli	1213	96.5	5.3	888	3	US-10-152-398-544	Sequence 544, App
1141	97.5	5.3	2517	3	US-10-021-698A-122	Sequence 122, App	1214	96.5	5.3	888	3	US-10-123-907-544	Sequence 544, App
1142	97	5.3	207	3	US-10-703-032-120914	Sequence 120914,	1215	96.5	5.3	888	3	US-10-123-907-544	Sequence 544, App
1143	97	5.3	273	3	US-10-108-260A-3955	Sequence 3955, Ap	1216	96.5	5.3	888	3	US-10-147-512-544	Sequence 544, App
1144	97	5.3	280	2	US-09-252-991A-21650	Sequence 21650, A	1217	96.5	5.3	888	3	US-10-147-485-544	Sequence 544, App
1145	97	5.3	293	2	US-09-252-991A-18793	Sequence 18793, A	1218	96.5	5.3	888	3	US-10-124-814-544	Sequence 544, App
1146	97	5.3	328	2	US-09-252-991A-23205	Sequence 23205, A	1219	96.5	5.3	888	3	US-10-035-855-35	Sequence 35, Appl
1147	97	5.3	387	2	US-09-252-991A-30467	Sequence 30467, A	1220	96.5	5.3	888	3	US-10-124-822-544	Sequence 544, App
1148	97	5.3	405	2	US-09-252-991A-31461	Sequence 31461, A	1221	96.5	5.3	888	3	US-10-223-081-268	Sequence 268, App
1149	97	5.3	469	2	US-09-252-991A-32604	Sequence 32604, A	1222	96.5	5.3	888	3	US-10-036-160-35	Sequence 35, Appl
1150	97	5.3	470	2	US-09-252-991A-19467	Sequence 19467, A	1223	96.5	5.3	888	3	US-10-223-087-268	Sequence 268, App
1151	97	5.3	503	2	US-08-526-136-2	Sequence 2, Appli	1224	96.5	5.3	888	3	US-10-131-833A-544	Sequence 544, App
1152	97	5.3	508	2	US-09-270-767-46233	Sequence 46233, A	1225	96.5	5.3	888	3	US-10-142-419-544	Sequence 544, App
1153	97	5.3	547	1	US-08-494-168-7	Sequence 7, Appli	1226	96.5	5.3	888	3	US-10-152-375-544	Sequence 544, App
1154	97	5.3	553	5	PCT-US94-00658-4	Sequence 4, Appli	1227	96.5	5.3	888	3	US-10-223-082-268	Sequence 268, App
1155	97	5.3	563	3	US-10-703-032-117713	Sequence 117713,	1228	96.5	5.3	888	3	US-10-223-084-268	Sequence 268, App
1156	97	5.3	582	2	US-10-094-749-2543	Sequence 2543, Ap	1229	96.5	5.3	888	3	US-10-131-818A-544	Sequence 544, App
1157	97	5.3	593	3	US-10-479-546-2	Sequence 2, Appli	1230	96.5	5.3	888	3	US-10-145-873-544	Sequence 544, App
1158	97	5.3	696	2	US-09-758-759-125	Sequence 125, App	1231	96.5	5.3	888	3	US-10-152-395-544	Sequence 544, App
1159	97	5.3	696	3	US-11-021-825-125	Sequence 125, App	1232	96.5	5.3	888	3	US-10-131-822A-544	Sequence 544, App
1160	97	5.3	705	2	US-09-252-991A-23298	Sequence 23298, A	1233	96.5	5.3	888	3	US-10-142-763-544	Sequence 544, App
1161	97	5.3	798	2	US-09-252-991A-25309	Sequence 25309, A	1234	96.5	5.3	888	3	US-10-128-694A-544	Sequence 544, App
1162	97	5.3	906	2	US-09-252-991A-32715	Sequence 32715, A	1235	96.5	5.3	888	3	US-10-036-342-35	Sequence 35, Appl
1163	97	5.3	1162	1	US-08-728-323A-2	Sequence 2, Appli	1236	96.5	5.3	888	3	US-10-123-213-544	Sequence 544, App
1164	97	5.3	1162	2	US-09-298-568-2	Sequence 2, Appli	1237	96.5	5.3	888	3	US-10-123-909-544	Sequence 544, App
1165	97	5.3	1162	2	US-09-410-399-2	Sequence 2, Appli	1238	96.5	5.3	888	3	US-10-131-826A-544	Sequence 544, App
1166	97	5.3	1162	2	US-09-894-273-2	Sequence 2, Appli	1239	96.5	5.3	888	3	US-10-147-513-544	Sequence 544, App
1167	97	5.3	1268	2	US-09-252-991A-17764	Sequence 17764, A	1240	96.5	5.3	964	3	US-10-121-043-544	Sequence 544, App
1168	96.5	5.3	138	2	US-08-590-571-74	Sequence 74, Appl	1241	96.5	5.3	970	2	US-10-080-334-70	Sequence 70, Appl
1169	96.5	5.3	138	2	US-09-528-784A-74	Sequence 74, Appl	1242	96.5	5.3	970	2	US-09-502-498C-82	Sequence 82, Appl
1170	96.5	5.3	138	2	US-09-569-098A-74	Sequence 74, Appl	1243	96.5	5.3	982	2	US-09-502-424C-82	Sequence 82, Appl
1171	96.5	5.3	153	3	US-10-703-032-116712	Sequence 116712,	1244	96.5	5.3	982	2	US-09-502-498C-70	Sequence 70, Appl
1172	96.5	5.3	176	3	US-10-703-032-130418	Sequence 130418,	1245	96.5	5.3	1122	2	US-09-502-424C-86	Sequence 86, Appl
1173	96.5	5.3	223	3	US-10-703-032-123047	Sequence 123047,	1246	96.5	5.3	1122	2	US-09-502-424C-86	Sequence 86, Appl
1174	96.5	5.3	263	2	US-09-252-991A-25669	Sequence 25669, A	1247	96.5	5.3	1130	2	US-09-502-498C-74	Sequence 74, Appl
1175	96.5	5.3	280	3	US-10-703-032-138654	Sequence 138654,	1248	96.5	5.3	1130	2	US-09-502-424C-74	Sequence 74, Appl
1176	96.5	5.3	289	2	US-10-094-749-2805	Sequence 2805, Ap	1249	96.5	5.3	1154	2	US-09-502-498C-78	Sequence 78, Appl
1177	96.5	5.3	328	2	US-09-949-016-8858	Sequence 8858, Ap	1250	96.5	5.3	1154	2	US-09-502-424C-78	Sequence 78, Appl
1178	96.5	5.3	350	3	US-10-703-032-121921	Sequence 121921,	1251	96.5	5.3	1155	2	US-09-502-498C-66	Sequence 66, Appl
1179	96.5	5.3	361	2	US-09-252-991A-28125	Sequence 28125, A	1252	96.5	5.3	1155	2	US-09-502-424C-66	Sequence 66, Appl
1180	96.5	5.3	492	2	US-09-252-991A-28339	Sequence 28339, A	1253	96.5	5.3	1487	1	US-08-760-489-2	Sequence 2, Appli
1181	96.5	5.3	500	2	US-09-252-991A-19739	Sequence 19739, A	1254	96.5	5.3	1487	1	US-08-185-373-2	Sequence 2, Appli
1182	96.5	5.3	536	1	US-08-354-456A-2	Sequence 2, Appli	1255	96.5	5.3	1487	1	US-09-185-373-4	Sequence 4, Appli
1183	96.5	5.3	536	1	US-07-999-280A-2	Sequence 2, Appli	1256	96.5	5.3	1487	2	US-09-185-373-4	Sequence 4, Appli
1184	96.5	5.3	536	1	US-08-426-279-2	Sequence 2, Appli	1257	96.5	5.3	1706	2	US-09-452-991A-31760	Sequence 31760, A
1185	96.5	5.3	536	1	US-08-401-013-2	Sequence 2, Appli	1258	96	5.3	181	3	US-10-703-032-201575	Sequence 201575,
1186	96.5	5.3	536	2	US-08-426-570-2	Sequence 2, Appli	1259	96	5.3	188	2	US-09-252-991A-22582	Sequence 22582, A
1187	96.5	5.3	536	2	US-08-425-876-2	Sequence 2, Appli	1260	96	5.3	243	2	US-09-252-991A-19639	Sequence 19639, A
1188	96.5	5.3	536	2	US-08-426-243-2	Sequence 2, Appli	1261	96	5.3	252	3	US-10-703-032-111103	Sequence 111103,
1189	96.5	5.3	536	2	US-08-401-632-2	Sequence 2, Appli	1262	96	5.3	282	3	US-09-252-991A-26399	Sequence 26399, A
1190	96.5	5.3	554	1	US-08-347-254-1	Sequence 1, Appli	1263	96	5.3	285	3	US-10-703-032-120961	Sequence 120961,
1191	96.5	5.3	554	1	US-08-464-463-1	Sequence 1, Appli	1264	96	5.3	386	2	US-09-461-774-10	Sequence 10, Appl
1192	96.5	5.3	554	5	PCT-US93-08282-2	Sequence 2, Appli	1265	96	5.3	456	2	US-09-919-039-66	Sequence 66, Appl
1193	96.5	5.3	609	2	US-09-252-991A-19735	Sequence 19735, A	1266	96	5.3	488	2	US-09-964-899-35	Sequence 35, Appl
1194	96.5	5.3	618	2	US-09-252-991A-23696	Sequence 23696, A	1267	96	5.3	548	2	US-09-252-991A-17591	Sequence 17591, A

1268	96	5.3	555	2	US-10-104-047-3369	Sequence 3369, Ap	1341	95	5.2	456	1	US-08-466-344-2	Sequence 2, Appli
1269	96	5.3	582	2	US-09-252-991A-21510	Sequence 21510, A	1342	95	5.2	472	2	US-09-252-991A-17817	Sequence 17817, A
1270	96	5.3	640	2	US-09-252-991A-27542	Sequence 27542, A	1343	95	5.2	476	2	US-09-538-092-903	Sequence 903, App
1271	96	5.3	656	2	US-09-252-991A-30630	Sequence 30630, A	1344	95	5.2	478	2	US-09-252-991A-20429	Sequence 20429, A
1272	96	5.3	836	2	US-09-491-3560-21	Sequence 21, Appl	1345	95	5.2	486	2	US-09-252-991A-21943	Sequence 21943, A
1273	96	5.3	1002	2	US-09-252-991A-27980	Sequence 27980, A	1346	95	5.2	512	2	US-10-332-795-1	Sequence 1, Appli
1274	96	5.3	1159	2	US-08-956-242-13	Sequence 13, Appl	1347	95	5.2	524	1	US-08-906-713-2	Sequence 2, Appli
1275	96	5.3	1159	2	US-09-351-215-13	Sequence 13, Appl	1348	95	5.2	574	2	US-09-870-574-4	Sequence 4, Appli
1276	96	5.3	1159	2	US-09-226-012-2	Sequence 2, Appli	1349	95	5.2	574	2	US-09-949-016-7006	Sequence 7006, Ap
1277	96	5.3	1159	2	US-09-226-012-4	Sequence 4, Appli	1350	95	5.2	574	2	US-10-090-365-25	Sequence 25, Appl
1278	96	5.3	1159	2	US-09-358-3830-10	Sequence 10, Appl	1351	95	5.2	574	2	US-09-728-911-25	Sequence 25, Appl
1279	96	5.3	1159	2	US-09-275-252A-12	Sequence 12, Appl	1352	95	5.2	574	2	US-10-233-873A-5	Sequence 5, Appli
1280	96	5.3	1744	3	US-09-958-359-22	Sequence 22, Appl	1353	95	5.2	574	3	US-09-925-055D-2	Sequence 2, Appli
1281	96	5.3	2328	3	US-09-619-049-1461	Sequence 1461, Ap	1354	95	5.2	574	3	US-10-063-638A-164	Sequence 164, App
1282	95.5	5.2	148	2	US-09-270-767-60506	Sequence 60506, A	1355	95	5.2	574	3	US-10-063-638A-164	Sequence 164, App
1283	95.5	5.2	185	2	US-09-205-258-623	Sequence 623, App	1356	95	5.2	574	3	US-10-063-510-164	Sequence 164, App
1284	95.5	5.2	185	2	US-10-004-860-623	Sequence 623, App	1357	95	5.2	574	3	US-10-063-741-164	Sequence 164, App
1285	95.5	5.2	201	3	US-10-703-032-108796	Sequence 108796, A	1358	95	5.2	574	3	US-10-063-584-164	Sequence 164, App
1286	95.5	5.2	201	3	US-10-703-032-108424	Sequence 108424, A	1359	95	5.2	574	3	US-10-006-867-164	Sequence 164, App
1287	95.5	5.2	202	3	US-10-703-032-111854	Sequence 111854, A	1360	95	5.2	574	3	US-10-063-659-164	Sequence 164, App
1288	95.5	5.2	237	2	US-09-252-991A-21736	Sequence 21736, A	1361	95	5.2	574	3	US-10-063-742-164	Sequence 164, App
1289	95.5	5.2	245	2	US-09-431-887-15	Sequence 5, Appli	1362	95	5.2	574	3	US-10-063-703-164	Sequence 164, App
1290	95.5	5.2	245	2	US-09-431-887-15	Sequence 15, Appl	1363	95	5.2	574	3	US-10-063-709-164	Sequence 164, App
1291	95.5	5.2	274	3	US-10-080-334-94	Sequence 94, Appl	1364	95	5.2	574	3	US-10-063-581-164	Sequence 164, App
1292	95.5	5.2	295	3	US-10-703-032-106080	Sequence 106080, A	1365	95	5.2	574	3	US-10-063-583-164	Sequence 164, App
1293	95.5	5.2	340	3	US-10-703-032-126421	Sequence 126421, A	1366	95	5.2	574	3	US-10-063-593-164	Sequence 164, App
1294	95.5	5.2	357	2	US-10-104-047-2281	Sequence 2281, Ap	1367	95	5.2	574	3	US-10-063-599-164	Sequence 164, App
1295	95.5	5.2	361	2	US-08-874-569B-21	Sequence 21, Appl	1368	95	5.2	574	3	US-10-063-646-164	Sequence 164, App
1296	95.5	5.2	361	2	US-09-955-518-21	Sequence 21, Appl	1369	95	5.2	574	3	US-10-063-660-164	Sequence 164, App
1297	95.5	5.2	392	2	US-09-252-991A-21863	Sequence 21863, A	1370	95	5.2	574	3	US-10-981-998-25	Sequence 25, Appl
1298	95.5	5.2	425	2	US-09-252-991A-31834	Sequence 31834, A	1371	95	5.2	574	3	US-10-063-647-164	Sequence 164, App
1299	95.5	5.2	460	2	US-09-252-991A-31830	Sequence 31830, A	1372	95	5.2	574	3	US-10-063-661-164	Sequence 164, App
1300	95.5	5.2	508	2	US-09-949-016-9414	Sequence 9414, Ap	1373	95	5.2	574	3	US-10-063-651-164	Sequence 164, App
1301	95.5	5.2	599	2	US-09-746-801A-59	Sequence 59, Appl	1374	95	5.2	574	3	US-10-063-530-164	Sequence 164, App
1302	95.5	5.2	599	2	US-10-719-885-59	Sequence 59, Appl	1375	95	5.2	574	3	US-10-063-540-164	Sequence 164, App
1303	95.5	5.2	599	2	US-11-109-077-59	Sequence 59, Appl	1376	95	5.2	574	3	US-10-063-648-164	Sequence 164, App
1304	95.5	5.2	618	2	US-09-252-991A-28358	Sequence 28358, A	1377	95	5.2	574	3	US-10-063-657-164	Sequence 164, App
1305	95.5	5.2	639	2	US-09-252-991A-20571	Sequence 20571, A	1378	95	5.2	574	3	US-10-063-702-164	Sequence 164, App
1306	95.5	5.2	778	1	US-08-439-818A-5	Sequence 5, Appli	1379	95	5.2	574	3	US-10-063-529-164	Sequence 164, App
1307	95.5	5.2	778	1	US-08-751-965-5	Sequence 5, Appli	1380	95	5.2	574	3	US-10-063-644-164	Sequence 164, App
1308	95.5	5.2	778	1	US-08-738-975-5	Sequence 5, Appli	1381	95	5.2	574	3	US-10-063-585-164	Sequence 164, App
1309	95.5	5.2	778	1	US-08-728-626-5	Sequence 5, Appli	1382	95	5.2	574	3	US-10-063-591A-164	Sequence 164, App
1310	95.5	5.2	778	2	US-08-808-599A-5	Sequence 5, Appli	1383	95	5.2	574	3	US-10-063-516-164	Sequence 164, App
1311	95.5	5.2	787	2	US-09-252-991A-19391	Sequence 19391, A	1384	95	5.2	574	3	US-10-063-532-164	Sequence 164, App
1312	95.5	5.2	799	3	US-10-018-418A-4	Sequence 4, Appli	1385	95	5.2	574	3	US-10-063-654-164	Sequence 164, App
1313	95.5	5.2	799	3	US-10-703-032-110771	Sequence 110771, A	1386	95	5.2	574	3	US-10-063-582-164	Sequence 164, App
1314	95.5	5.2	814	3	US-10-021-698A-136	Sequence 136, App	1387	95	5.2	574	3	US-10-063-524-164	Sequence 164, App
1315	95.5	5.2	823	3	US-10-325-899-9369	Sequence 9369, Ap	1388	95	5.2	574	3	US-10-972-317-164	Sequence 164, App
1316	95.5	5.2	889	2	US-09-949-016-6036	Sequence 6036, Ap	1389	95	5.2	574	3	US-10-063-551-164	Sequence 164, App
1317	95.5	5.2	889	2	US-10-067-457-1	Sequence 1, Appli	1390	95	5.2	574	3	US-10-063-523-164	Sequence 164, App
1318	95	5.2	108	3	US-10-703-032-105686	Sequence 105686, A	1391	95	5.2	574	3	US-10-063-650-164	Sequence 164, App
1319	95	5.2	147	3	US-10-703-032-158442	Sequence 158442, A	1392	95	5.2	574	3	US-10-063-523-164	Sequence 164, App
1320	95	5.2	234	2	US-09-489-038A-13353	Sequence 13353, A	1393	95	5.2	574	3	US-10-063-705-164	Sequence 164, App
1321	95	5.2	239	2	US-10-094-749-2291	Sequence 2291, Ap	1394	95	5.2	574	3	US-10-063-598-164	Sequence 164, App
1322	95	5.2	253	2	US-09-252-991A-29632	Sequence 29632, A	1395	95	5.2	574	3	US-10-063-554-164	Sequence 164, App
1323	95	5.2	272	2	US-09-252-991A-19416	Sequence 19416, A	1396	95	5.2	574	3	US-10-238-565-4	Sequence 4, Appli
1324	95	5.2	297	2	US-09-010-999-2	Sequence 2, Appli	1397	95	5.2	574	3	US-10-063-597-164	Sequence 164, App
1325	95	5.2	297	2	US-10-094-749-2985	Sequence 2985, Ap	1398	95	5.2	574	3	US-10-063-600-164	Sequence 164, App
1326	95	5.2	313	2	US-09-270-767-43688	Sequence 43688, A	1399	95	5.2	574	3	US-10-063-652A-164	Sequence 164, App
1327	95	5.2	327	2	US-09-252-991A-30065	Sequence 30065, A	1400	95	5.2	574	3	US-10-063-602-164	Sequence 164, App
1328	95	5.2	342	2	US-10-094-749-3026	Sequence 3026, Ap	1401	95	5.2	574	3	US-10-063-560-164	Sequence 164, App
1329	95	5.2	343	2	US-09-252-991A-18970	Sequence 18970, A	1402	95	5.2	574	3	US-10-063-517-164	Sequence 164, App
1330	95	5.2	344	2	US-09-252-991A-17842	Sequence 17842, A	1403	95	5.2	574	3	US-10-063-548-164	Sequence 164, App
1331	95	5.2	350	2	US-10-094-749-2790	Sequence 2790, Ap	1404	95	5.2	574	3	US-10-063-553-164	Sequence 164, App
1332	95	5.2	374	2	US-09-489-039A-10451	Sequence 10451, A	1405	95	5.2	574	3	US-10-063-653A-164	Sequence 164, App
1333	95	5.2	377	2	US-09-342-681C-4	Sequence 4, Appli	1406	95	5.2	581	2	US-09-949-016-8522	Sequence 8522, Ap
1334	95	5.2	377	3	US-09-729-658C-4	Sequence 4, Appli	1407	95	5.2	622	3	US-09-949-016-9104	Sequence 9104, Ap
1335	95	5.2	398	2	US-09-252-991A-27517	Sequence 27517, A	1408	95	5.2	663	3	US-10-108-260A-2477	Sequence 2477, Ap
1336	95	5.2	452	2	US-09-205-258-689	Sequence 689, App	1409	95	5.2	716	3	US-10-703-032-117740	Sequence 117740, A
1337	95	5.2	452	2	US-10-004-860-689	Sequence 689, App	1410	95	5.2	742	2	US-09-252-991A-32659	Sequence 32659, A
1338	95	5.2	455	1	US-08-224-482-6	Sequence 6, Appli	1411	95	5.2	763	2	US-09-252-991A-30146	Sequence 30146, A
1339	95	5.2	455	3	US-10-149-310-16	Sequence 16, Appl	1412	95	5.2	770	2	US-09-252-991A-30323	Sequence 30323, A
1340	95	5.2	456	1	US-08-040-548-2	Sequence 2, Appli	1413	95	5.2	980	2	US-09-442-100-8	Sequence 8, Appli


```
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 238
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-201-769-238

Query Match
Best Local Similarity 100.0%; Score 1824; DB 3; Length 325;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQRVAGSCAPGLLLVCLHLPGLFARISGVVEEKVSQNFQTNLPOLGQPSSTGSPNSEH 60
DB 1 MQRVAGSCAPGLLLVCLHLPGLFARISGVVEEKVSQNFQTNLPOLGQPSSTGSPNSEH 60
QY 61 PQALDPRNDLARVPLKLSVPPSDGFPFAGGSVAVORWPPSWGLPAMDSWPPDPQWMA 120
DB 61 PQALDPRNDLARVPLKLSVPPSDGFPFAGGSVAVORWPPSWGLPAMDSWPPDPQWMA 120
QY 121 AAEDRLGEALPEELSYLSAAALAPGSGPLPGCESSPDATGLSPEASLLHQDSERRLPR 180
DB 121 AAEDRLGEALPEELSYLSAAALAPGSGPLPGCESSPDATGLSPEASLLHQDSERRLPR 180
QY 181 SNSLGAGGKILSORPPWSLIHRVLPDPHMGTLNPSVSWGGGPGTGTGTRPMPHPEGIW 240
DB 181 SNSLGAGGKILSORPPWSLIHRVLPDPHMGTLNPSVSWGGGPGTGTGTRPMPHPEGIW 240
QY 241 INNQPPTSGWGNINRYPGGSGWGNINRYPGGSGWGNINRYPGGSGWGNIHLYPGINNPPPGV 300
DB 241 INNQPPTSGWGNINRYPGGSGWGNINRYPGGSGWGNINRYPGGSGWGNIHLYPGINNPPPGV 300
QY 301 LRPPGSSWNPAGFPNPPSPRLQWG 325
DB 301 LRPPGSSWNPAGFPNPPSPRLQWG 325

RESULT 6
US-10-063-510-64
; Sequence 64, Application US/10063510
; Patent No. 7109292
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,510
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 64
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-510-64

Query Match
Best Local Similarity 100.0%; Score 1824; DB 3; Length 325;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQRVAGSCAPGLLLVCLHLPGLFARISGVVEEKVSQNFQTNLPOLGQPSSTGSPNSEH 60
DB 1 MQRVAGSCAPGLLLVCLHLPGLFARISGVVEEKVSQNFQTNLPOLGQPSSTGSPNSEH 60
QY 61 PQALDPRNDLARVPLKLSVPPSDGFPFAGGSVAVORWPPSWGLPAMDSWPPDPQWMA 120
DB 61 PQALDPRNDLARVPLKLSVPPSDGFPFAGGSVAVORWPPSWGLPAMDSWPPDPQWMA 120
QY 121 AAEDRLGEALPEELSYLSAAALAPGSGPLPGCESSPDATGLSPEASLLHQDSERRLPR 180
DB 121 AAEDRLGEALPEELSYLSAAALAPGSGPLPGCESSPDATGLSPEASLLHQDSERRLPR 180
QY 181 SNSLGAGGKILSORPPWSLIHRVLPDPHMGTLNPSVSWGGGPGTGTGTRPMPHPEGIW 240
DB 181 SNSLGAGGKILSORPPWSLIHRVLPDPHMGTLNPSVSWGGGPGTGTGTRPMPHPEGIW 240
QY 241 INNQPPTSGWGNINRYPGGSGWGNINRYPGGSGWGNINRYPGGSGWGNIHLYPGINNPPPGV 300
DB 241 INNQPPTSGWGNINRYPGGSGWGNINRYPGGSGWGNINRYPGGSGWGNIHLYPGINNPPPGV 300
QY 301 LRPPGSSWNPAGFPNPPSPRLQWG 325
DB 301 LRPPGSSWNPAGFPNPPSPRLQWG 325

RESULT 5
US-10-063-638A-64
; Sequence 64, Application US/10063638A
; Patent No. 7101970
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
; FILE REFERENCE: 39780-3230R1C87
; CURRENT APPLICATION NUMBER: US/10/063,638A
; CURRENT FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-063-638A-64

Query Match
Best Local Similarity 100.0%; Score 1824; DB 3; Length 325;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQRVAGSCAPGLLLVCLHLPGLFARISGVVEEKVSQNFQTNLPOLGQPSSTGSPNSEH 60
DB 1 MQRVAGSCAPGLLLVCLHLPGLFARISGVVEEKVSQNFQTNLPOLGQPSSTGSPNSEH 60
QY 61 PQALDPRNDLARVPLKLSVPPSDGFPFAGGSVAVORWPPSWGLPAMDSWPPDPQWMA 120
DB 61 PQALDPRNDLARVPLKLSVPPSDGFPFAGGSVAVORWPPSWGLPAMDSWPPDPQWMA 120
```



```
Db 121 AAAEDRLGEALPEELSYLSAAALAPGSGPLCGESSPDATGLSPEASLLHQDSESRLR 180
Qy 181 SNSLGAGGKILSORPPWSLIHRVLPDHPWGTLNPSVSWGGGGPGTGWGTRPMPHPEGIW 240
Db 181 SNSLGAGGKILSORPPWSLIHRVLPDHPWGTLNPSVSWGGGGPGTGWGTRPMPHPEGIW 240
Qy 241 INNQPPTSGWGNINRYPGGSGWGNINRYPGGSGWGNINRYPGGSGWGNIHLYPGINNPPPGV 300
Db 241 INNQPPTSGWGNINRYPGGSGWGNINRYPGGSGWGNINRYPGGSGWGNIHLYPGINNPPPGV 300
Qy 301 LRPPGSSWNIIPAGFPNPPSRLQW 325
Db 301 LRPPGSSWNIIPAGFPNPPSRLQW 325
```

RESULT 14

US-10-063-703-64

; Sequence 64, Application US/10063703

; Patent No. 7189563

; GENERAL INFORMATION:

; APPLICANT: Eaton, Dan L.

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3230R1C1

; CURRENT APPLICATION NUMBER: US/10/063,703

; CURRENT FILING DATE: 2002-05-08

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 170

; SEQ ID NO 64

; LENGTH: 325

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-063-703-64

```
Query Match 100.0%; Score 1824; DB 3; Length 325;
Best Local Similarity 100.0%; Pred. No. 7.2e-146;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MQGRVAGSCAPLGLLLVCLHPLGLFARSIGVVEEKVSQNFGTNLPLQGGPSSTGSPNSEH 60
Db 1 MQGRVAGSCAPLGLLLVCLHPLGLFARSIGVVEEKVSQNFGTNLPLQGGPSSTGSPNSEH 60
Qy 61 POPALDPRNDLARVPLKLSVPPSDGPPAGGSAVQRPWPSWGLPAMDSWPPDPWQWMA 120
Db 61 POPALDPRNDLARVPLKLSVPPSDGPPAGGSAVQRPWPSWGLPAMDSWPPDPWQWMA 120
Qy 121 AAAEDRLGEALPEELSYLSAAALAPGSGPLCGESSPDATGLSPEASLLHQDSESRLR 180
Db 121 AAAEDRLGEALPEELSYLSAAALAPGSGPLCGESSPDATGLSPEASLLHQDSESRLR 180
Qy 181 SNSLGAGGKILSORPPWSLIHRVLPDHPWGTLNPSVSWGGGGPGTGWGTRPMPHPEGIW 240
Db 181 SNSLGAGGKILSORPPWSLIHRVLPDHPWGTLNPSVSWGGGGPGTGWGTRPMPHPEGIW 240
Qy 241 INNQPPTSGWGNINRYPGGSGWGNINRYPGGSGWGNINRYPGGSGWGNIHLYPGINNPPPGV 300
Db 241 INNQPPTSGWGNINRYPGGSGWGNINRYPGGSGWGNINRYPGGSGWGNIHLYPGINNPPPGV 300
Qy 301 LRPPGSSWNIIPAGFPNPPSRLQW 325
Db 301 LRPPGSSWNIIPAGFPNPPSRLQW 325
```

RESULT 15

US-10-063-709-64

; Sequence 64, Application US/10063709

; Patent No. 7189564

; GENERAL INFORMATION:

; APPLICANT: Eaton, Dan L.

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3230R1C1

; CURRENT APPLICATION NUMBER: US/10/063,709

; CURRENT FILING DATE: 2002-05-08

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 170

; SEQ ID NO 64

; LENGTH: 325

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-063-709-64

```
Query Match 100.0%; Score 1824; DB 3; Length 325;
Best Local Similarity 100.0%; Pred. No. 7.2e-146;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MQGRVAGSCAPLGLLLVCLHPLGLFARSIGVVEEKVSQNFGTNLPLQGGPSSTGSPNSEH 60
Db 1 MQGRVAGSCAPLGLLLVCLHPLGLFARSIGVVEEKVSQNFGTNLPLQGGPSSTGSPNSEH 60
Qy 61 POPALDPRNDLARVPLKLSVPPSDGPPAGGSAVQRPWPSWGLPAMDSWPPDPWQWMA 120
Db 61 POPALDPRNDLARVPLKLSVPPSDGPPAGGSAVQRPWPSWGLPAMDSWPPDPWQWMA 120
Qy 121 AAAEDRLGEALPEELSYLSAAALAPGSGPLCGESSPDATGLSPEASLLHQDSESRLR 180
Db 121 AAAEDRLGEALPEELSYLSAAALAPGSGPLCGESSPDATGLSPEASLLHQDSESRLR 180
Qy 181 SNSLGAGGKILSORPPWSLIHRVLPDHPWGTLNPSVSWGGGGPGTGWGTRPMPHPEGIW 240
Db 181 SNSLGAGGKILSORPPWSLIHRVLPDHPWGTLNPSVSWGGGGPGTGWGTRPMPHPEGIW 240
Qy 241 INNQPPTSGWGNINRYPGGSGWGNINRYPGGSGWGNINRYPGGSGWGNIHLYPGINNPPPGV 300
Db 241 INNQPPTSGWGNINRYPGGSGWGNINRYPGGSGWGNINRYPGGSGWGNIHLYPGINNPPPGV 300
Qy 301 LRPPGSSWNIIPAGFPNPPSRLQW 325
Db 301 LRPPGSSWNIIPAGFPNPPSRLQW 325
```

Search completed: July 30, 2007, 16:40:44

Job time : 86 secs

OM protein - protein search, using sw model
 Run on: July 30, 2007, 16:41:54 ; Search time 154 Seconds
 (without alignments)
 1032.684 Million cell updates/sec

Title: US-10-063-569-64
 Perfect score: 1824
 Sequence: 1 MGRVAGSCAPGLLLVCLH.....SSWNIPAGFPNPPSPRLQWG 325
 Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5
 Total number of hits satisfying chosen parameters: 2782304
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-Processing: Minimum Match 0%
 Maximum Match 100%

Database : Listing first 1500 summaries
 1: Geneseq_200701:*
 2: geneseqp1980s:*
 3: geneseqp1990s:*
 4: geneseqp2000s:*
 5: geneseqp2001s:*
 6: geneseqp2002s:*
 7: geneseqp2003as:*
 8: geneseqp2003bs:*
 11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAU29142	standard; protein; 325 AA.				
DE	Human PRO polypeptide sequence #119.					
PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1824;	DB 4;	Length 325;		
Best Local Similarity	100.0%;	Pred. No. 1.6e-136;				
RESULT 2						
ID	AAB87557	standard; protein; 325 AA.				
DE	Human PRO3566.					
PN	WO200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1824;	DB 4;	Length 325;		
Best Local Similarity	100.0%;	Pred. No. 1.6e-136;				
RESULT 3						
ID	AAE15556	standard; protein; 325 AA.				
DE	Human secreted protein-10 (SECP).					
PN	WO200179291-A2.					
PD	25-OCT-2001.					
PA	(INCY-) INCYTE GENOMICS INC.					
Query Match	100.0%;	Score 1824;	DB 5;	Length 325;		
Best Local Similarity	100.0%;	Pred. No. 1.6e-136;				
RESULT 4						
ID	AAE22555	standard; protein; 325 AA.				
DE	Human ZSfG89 protein.					
PN	US2002042095-A1.					
PD	11-APR-2002.					
PA	(ADLE/) ADLER D A.					
PA	(SHEP/) SHEPPARD P O.					
PA	(NELS/) NELSON A J.					
Query Match	100.0%;	Score 1824;	DB 5;	Length 325;		
Best Local Similarity	100.0%;	Pred. No. 1.6e-136;				
RESULT 5						
ID	ABG95882	standard; protein; 325 AA.				
DE	Human secreted/transmembrane protein PRO3566.					
PN	US2002119130-A1.					
PD	29-AUG-2002.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1824;	DB 5;	Length 325;		
Best Local Similarity	100.0%;	Pred. No. 1.6e-136;				

RESULT 6
 ID ABUS8518 standard; protein; 325 AA.
 DE Human PRO polypeptide #119.
 PN US2003027272-A1.
 PD '06-FEB-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;

RESULT 7
 ID ABUS8066 standard; protein; 325 AA.
 DE Novel human secreted and transmembrane protein PRO3566.
 PN US2003032127-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;

RESULT 8
 ID ABUS4381 standard; protein; 325 AA.
 DE Human secreted/transmembrane protein (PRO) #119.
 PN US2003032112-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;

RESULT 9
 ID ABR66255 standard; protein; 325 AA.
 DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
 PN US2003027278-A1.
 PD 06-FEB-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;

RESULT 10
 ID ABR65645 standard; protein; 325 AA.
 DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
 PN US2003036159-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;

RESULT 11
 ID ABUS9585 standard; protein; 325 AA.
 DE Human secreted/transmembrane protein (PRO) #119.
 PN US2003040070-A1.
 PD 27-FEB-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;

RESULT 12
 ID ABUS2824 standard; protein; 325 AA.
 DE Human PRO polypeptide #119.
 PN US2003032113-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;

RESULT 13
 ID ABUS9945 standard; protein; 325 AA.
 DE Novel human secreted and transmembrane protein PRO3566.
 PN US2003036147-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;

RESULT 14
 ID ABR68194 standard; protein; 325 AA.
 DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
 PN US2003027264-A1.
 PD 06-FEB-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;

RESULT 15
 ID ABUS6247 standard; protein; 325 AA.
 DE Novel human secreted and transmembrane protein PRO3566.
 PN US2003036144-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;

RESULT 16
 ID ABUS2678 standard; protein; 325 AA.
 DE Human secreted/transmembrane protein (PRO) #119.

PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 17
ID ABO08755 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 18
ID ABO02807 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 19
ID ABR74961 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 20
ID ABR94723 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 21
ID ABUS696 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 22
ID ABUS9856 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 23
ID ABUS98071 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 24
ID ABUS91777 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 25
ID ABUS9470 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 26
ID ABUS6311 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003036146-A1.
PD 20-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 27
ID ABUS7524 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 28
ID ABUS0552 standard; protein; 325 AA.
DE Human PRO protein #119.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 29
ID ABUS0907 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 30
ID ABO33966 standard; protein; 325 AA.
DE Human secreted/transmembrane protein PRO3566.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 31
ID ABR99470 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 32
ID ABR98860 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 33
ID ABO16383 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 34
ID ABR92283 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 35
ID ABO18924 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 36
ID ABR78345 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.

```
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1824; DB 6; Length 325;
  Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 37
ID ABU71983 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1824; DB 6; Length 325;
  Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 38
ID ABU85081 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003032114-A1.
PD 13-FEB-2003.
  Query Match      100.0%; Score 1824; DB 6; Length 325;
  Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 39
ID ABO00220 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003032101-A1.
PD 13-FEB-2003.
  Query Match      100.0%; Score 1824; DB 6; Length 325;
  Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 40
ID ABO11552 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003036124-A1.
PD 20-FEB-2003.
  Query Match      100.0%; Score 1824; DB 6; Length 325;
  Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 41
ID ABO02197 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003040054-A1.
PD 27-FEB-2003.
  Query Match      100.0%; Score 1824; DB 6; Length 325;
  Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 42
ID ABU88771 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003036133-A1.
PD 20-FEB-2003.
  Query Match      100.0%; Score 1824; DB 6; Length 325;
  Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 43
ID ABU83466 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003036134-A1.
PD 20-FEB-2003.
  Query Match      100.0%; Score 1824; DB 6; Length 325;
  Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 44
ID ABO06267 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003022294-A1.
PD 30-JAN-2003.
  Query Match      100.0%; Score 1824; DB 6; Length 325;
  Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 45
ID ABR59303 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003027275-A1.
PD 06-FEB-2003.
  Query Match      100.0%; Score 1824; DB 6; Length 325;
  Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 46
ID ABO09365 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003027324-A1.
PD 06-FEB-2003.
  Query Match      100.0%; Score 1824; DB 6; Length 325;
  Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 47
ID ABO19229 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1824; DB 6; Length 325;
  Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 48
ID ABO11247 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003036123-A1.
PD 20-FEB-2003.
  Query Match      100.0%; Score 1824; DB 6; Length 325;
  Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 49
ID ABR66865 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003036148-A1.
PD 20-FEB-2003.
  Query Match      100.0%; Score 1824; DB 6; Length 325;
  Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 50
ID ABO16078 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003040060-A1.
PD 27-FEB-2003.
  Query Match      100.0%; Score 1824; DB 6; Length 325;
  Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 51
ID ABO13784 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003044916-A1.
PD 06-MAR-2003.
  Query Match      100.0%; Score 1824; DB 6; Length 325;
  Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 52
ID ABU71537 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1824; DB 6; Length 325;
  Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 53
ID ABU65687 standard; protein; 325 AA.
DE Human secreted/transmembrane protein, SEQ ID 238.
PN US2003036156-A1.
PD 20-FEB-2003.
  Query Match      100.0%; Score 1824; DB 6; Length 325;
  Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 54
ID ABO07535 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003032117-A1.
PD 13-FEB-2003.
  Query Match      100.0%; Score 1824; DB 6; Length 325;
  Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 55
ID ABO03722 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003036128-A1.
PD 20-FEB-2003.
  Query Match      100.0%; Score 1824; DB 6; Length 325;
  Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 56
ID ABR67170 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003027266-A1.
PD 06-FEB-2003.
```

Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 57
ID ABO15773 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 58
ID ABU56054 standard; protein; 325 AA.
DE Human secreted/transmembrane protein, PRO3566.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 59
ID ABU72318 standard; protein; 325 AA.
DE Human PRO polypeptide #32.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 60
ID ABU65382 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 61
ID ABU95327 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 62
ID ABU71230 standard; protein; 325 AA.
DE Human PRO3566 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 63
ID ABO07840 standard; protein; 325 AA.
DE Human secreted polypeptide #119.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 64
ID ABR70081 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 65
ID ABR69414 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 66
ID ABO01555 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003008353-A1.
PD 09-JAN-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 67
ID ABU81357 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 68
ID ABR60154 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 69
ID ABU90991 standard; protein; 325 AA.
DE Human PRO polypeptide #32.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 70
ID ABR67889 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 71
ID ABR65277 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 72
ID ABR68499 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 73
ID ABR71911 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 74
ID ABU85391 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 75
ID ABU89081 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 76
ID ABU83161 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003032105-A1.
PD 13-FEB-2003.

Query Match
Best Local Similarity 100.0%; Score 1824; DB 6; Length 325;
RESULT 77
ID ABU95017 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 6; Length 325;
RESULT 78
ID ABU90565 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 6; Length 325;
RESULT 79
ID ABU84076 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 6; Length 325;
RESULT 80
ID ABU93727 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 6; Length 325;
RESULT 81
ID ABR64972 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 6; Length 325;
RESULT 82
ID ABO27312 standard; protein; 325 AA.
DE Human secreted/transmembrane polypeptide PRO3566.
PN US200309012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 6; Length 325;
RESULT 83
ID ABR68804 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 6; Length 325;
RESULT 84
ID ABO06620 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 6; Length 325;
RESULT 85
ID ABR99165 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 6; Length 325;
RESULT 86
ID ABUS7049 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 6; Length 325;

Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 87
ID ABUS6001 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 6; Length 325;
RESULT 88
ID ABUS2288 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 6; Length 325;
RESULT 89
ID ABUS7299 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 6; Length 325;
RESULT 90
ID ABUS3771 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 6; Length 325;
RESULT 91
ID ABO08145 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 6; Length 325;
RESULT 92
ID ABUS2507 standard; protein; 325 AA.
DE Human secreted/transmembrane protein PRO3566.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 6; Length 325;
RESULT 93
ID ABUS1856 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 6; Length 325;
RESULT 94
ID ABUS6020 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 6; Length 325;
RESULT 95
ID ABUS1177 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 6; Length 325;
RESULT 96
ID ABR59849 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 6; Length 325;

RESULT 97
ID ABOU4037 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 98
ID ABR99890 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 99
ID ABR66560 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 100
ID ABR90978 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 101
ID ABO53292 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 102
ID ABR94405 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 103
ID ABR9287 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 104
ID ABR6616 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 105
ID ABR6921 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 106
ID ABR94710 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 107
ID ABO04637 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 108
ID ABR70386 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 109
ID ABR98551 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 110
ID ABR65950 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 111
ID ABR64667 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 112
ID ABR9592 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 113
ID ABR92983 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 114
ID ABR95942 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 115
ID ABR91162 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 116
ID ABR90255 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 117
ID ABO09670 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.

PN US2003044931-A1.
 PD 06-MAR-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 118
 ID ABO10942 standard; protein; 325 AA.
 DE Human secreted/transmembrane protein (PRO) #119.
 PN US2003036150-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 119
 ID ABR70996 standard; protein; 325 AA.
 DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
 PN US2003040069-A1.
 PD 27-FEB-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 120
 ID ABU98294 standard; protein; 325 AA.
 DE Novel human secreted and transmembrane protein PRO3566.
 PN US2002183493-A1.
 PD 05-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 121
 ID ABU87604 standard; protein; 325 AA.
 DE Human PRO polypeptide #119.
 PN US2003022293-A1.
 PD 30-JAN-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 122
 ID ABU91472 standard; protein; 325 AA.
 DE Human PRO polypeptide #119.
 PN US2003032128-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 123
 ID ABU89299 standard; protein; 325 AA.
 DE Novel human secreted and transmembrane protein PRO3566.
 PN US2003036634-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 124
 ID ABU84686 standard; protein; 325 AA.
 DE Human secreted/transmembrane protein (PRO) #119.
 PN US2003032116-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 125
 ID ABR69776 standard; protein; 325 AA.
 DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
 PN US2003032122-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 126
 ID ABU80153 standard; protein; 325 AA.
 DE Human PRO protein #119.
 PN US2003036139-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 127
 ID ABU82506 standard; protein; 325 AA.
 DE Novel human secreted and transmembrane protein PRO3566.
 PN US2002183494-A1.

PD 05-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 128
 ID ABU93422 standard; protein; 325 AA.
 DE Human PRO polypeptide #119.
 PN US2003017541-A1.
 PD 23-JAN-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 129
 ID ABO09975 standard; protein; 325 AA.
 DE Human secreted/transmembrane protein (PRO) #119.
 PN US2003017543-A1.
 PD 23-JAN-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 130
 ID ABO09060 standard; protein; 325 AA.
 DE Human secreted/transmembrane protein (PRO) #119.
 PN US2003036152-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 131
 ID ABU96470 standard; protein; 325 AA.
 DE Human PRO polypeptide #32.
 PN US2003027993-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 132
 ID ABU10628 standard; protein; 325 AA.
 DE Human secreted/transmembrane protein #119.
 PN US2002127584-A1.
 PD 12-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 133
 ID ABU72140 standard; protein; 325 AA.
 DE Human PRO polypeptide #32.
 PN US2003023042-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 134
 ID ABU95637 standard; protein; 325 AA.
 DE Human PRO polypeptide #119.
 PN US2003032115-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 135
 ID ABU96846 standard; protein; 325 AA.
 DE Novel human secreted and transmembrane protein PRO3566.
 PN US2003032140-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 136
 ID ABR70691 standard; protein; 325 AA.
 DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
 PN US2003040076-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 137
 ID ABO05042 standard; protein; 325 AA.

DE Novel human secreted and transmembrane protein PRO3566.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 138
ID ABO08450 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 139
ID ABO05657 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 140
ID ABR74046 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US20030356135-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 141
ID ABR95638 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 142
ID ABR80935 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 143
ID ABR81240 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 144
ID ABR00936 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 145
ID ABR88538 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 146
ID ABR77359 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 147
ID ABO28843 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 148
ID ABO31588 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 149
ID ABR08005 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 150
ID ABO40485 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 151
ID ABO35910 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 152
ID ABO44049 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 153
ID ADA77990 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 154
ID ABR24844 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 155
ID ABO03112 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 156
ID ABR77359 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

ID ABR90368 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 157
ID ABR17282 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 158
ID ABR95028 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 159
ID ABR95333 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 160
ID ABR17121 standard; protein; 325 AA.
DE Human transmembrane PRO polypeptide (SeqID 64).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 161
ID ABO21571 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 162
ID ABR97835 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 163
ID ABR87623 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 164
ID ABR77664 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 165
ID ABR27894 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003064440-A1.

PD 03-APR-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 166
ID ABR06175 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 167
ID ABR03681 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 168
ID ABR35132 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 169
ID ABR26369 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 170
ID ABO48151 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 171
ID ABR92893 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 172
ID ABO24654 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 173
ID ABR11665 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 174
ID ABR02766 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 175
ID ABM16062 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 176
ID ABO27623 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 177
ID ABM29114 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 178
ID ABM07090 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 179
ID ABM21184 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 180
ID ABM09530 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 181
ID ABO41400 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 182
ID ABO36215 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 183
ID ABO43744 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;

Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 184
ID ABM76444 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 185
ID ABM76140 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 186
ID ABM25759 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 187
ID ABM26064 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 188
ID ABO3417 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 189
ID ABO2502 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 190
ID ABO44270 standard; protein; 325 AA.
DE Human secreted/transmembrane polypeptide PRO 3566.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 191
ID ABR90673 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 192
ID ABR73741 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 193
ID ABO16993 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 194
ID ABR94418 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 195
ID ABR75925 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 196
ID ABR71301 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 197
ID ABR93198 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 198
ID ABR93503 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 199
ID ABR87928 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 200
ID ABO27928 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 201
ID ABO30063 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 202
ID ABO33272 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 203

ID ABO4960 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 204
ID ABO8920 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 205
ID ABO36520 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 206
ID ABO35605 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 207
ID ABO39570 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 208
ID ABO10445 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 209
ID ABO11970 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 210
ID ABO52116 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 211
ID ABO52421 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 212
ID ADA19926 standard; protein; 325 AA.

DE Novel human secreted and transmembrane protein PRO3566.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 213
ID ABO23739 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 214
ID ADB17309 standard; protein; 325 AA.
DE Human transmembrane PRO polypeptide (SeqID 64).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 215
ID ABR97225 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 216
ID ABR87013 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 217
ID ABM11055 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 218
ID ABM28199 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 219
ID ABO32198 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 220
ID ABM15325 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 221
ID ABM06480 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068709-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 222
ID ABM04291 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 223
ID ABM22404 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 224
ID ABM07700 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 225
ID ABO40790 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 226
ID ABM35437 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 227
ID ABM33200 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 228
ID ABO52726 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 229
ID ABO50286 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 230
ID ABU9280 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;

Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 231
ID ABO04332 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 232
ID ABO5962 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 233
ID ABM18502 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 234
ID ABR97530 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 235
ID ABR80630 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 236
ID ABM01241 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 237
ID ABR88843 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 238
ID ABM13495 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 239
ID ABM20879 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 240
ID ABO42010 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.

PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 241
ID ABO42620 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 242
ID ABM10140 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 243
ID ABO38655 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 244
ID ABM32895 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 245
ID ABM22709 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 246
ID ABM74920 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 247
ID ADA79782 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 248
ID ABR96310 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 249
ID ABM02461 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;

RESULT 250
ID ABR86403 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 251
ID ABR86708 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 252
ID ABM16672 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 253
ID ABM29724 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 254
ID ABO29148 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 255
ID ABM23929 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 256
ID ABM23319 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 257
ID ABM2099 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 258
ID ABO37740 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 259
ID ADA20098 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

ID ABM28504 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 260
ID ABM28809 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 261
ID ABM66453 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 262
ID ABM75935 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 263
ID ABM34115 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 264
ID ABM34420 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 265
ID ABO20351 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 266
ID ABO21266 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 267
ID ABO22181 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 268
ID ADA20098 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 269
ID ABO34198 standard; protein; 325 AA.
DE Human secreted/transmembrane polypeptide PRO 3566.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 270
ID ABR96615 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 271
ID ABR85793 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 272
ID ABR95775 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 273
ID ABM00631 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 274
ID ABM00326 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 275
ID ABO29758 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 276
ID ABM23624 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 277
ID ABM29419 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 278
ID ABR81545 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003049744-A1.
PD 13-MAR-2003.

ID ABO39350 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 279
ID ABO45650 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 280
ID ABM20574 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 281
ID ADA81509 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 282
ID ABO16688 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 283
ID ABO18314 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 284
ID ABO22741 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 285
ID ABO23046 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 286
ID ABR92588 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 287
ID ABR81545 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003049744-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 288
ID ABM77969 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 289
ID ABR89758 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 290
ID ABM26674 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 291
ID ABM13800 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 292
ID ABO28538 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 293
ID ABO30368 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 294
ID ABM07395 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 295
ID ABM03986 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 296
ID ABO37130 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;

RESULT 297
ID ABO41705 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 298
ID ABO35300 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 299
ID ABM25149 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 300
ID ABO47541 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 301
ID ABO47846 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 302
ID ABO48456 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 303
ID ABO51506 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 304
ID ABO51811 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 305
ID ABO50591 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 306
ID ABR79715 standard; protein; 325 AA.

DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 326
ID ABR72216 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 327
ID ABR98555 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 328
ID ABO06925 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 329
ID ABR84878 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 330
ID ABR73436 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 331
ID ABR76530 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 332
ID ABR73131 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 333
ID ABR18197 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 334
ID ABO20656 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 335
ID ABO25399 standard; protein; 325 AA.
DE Human PRO polypeptide #119.

PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 336
ID ABO25704 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 337
ID ABR94113 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 338
ID ABR80020 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 339
ID ABR11360 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 340
ID ABO32967 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 341
ID ABO30673 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 342
ID ABO30978 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 343
ID ABR27284 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 344
ID ABR30029 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068769-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 345
ID ABM05565 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 346
ID ABM15630 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 347
ID ABM08615 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 348
ID ABO42315 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 349
ID ABO38045 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 350
ID ABO45955 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 351
ID ABM66758 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 352
ID ADB20350 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 353
ID ARM19659 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;

Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 354
ID ABO49371 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 355
ID ABO49676 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 356
ID ADA78602 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 357
ID ABR88233 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 358
ID ADA00395 standard; protein; 325 AA.
DE Human secreted/transmembrane polypeptide PRO 3566.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 359
ID ABM26979 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 360
ID ABM03376 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 361
ID ABO39875 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 362
ID ABO49981 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;


```
RESULT 363
ID ABO50896 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 364
ID ABO05352 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 365
ID ABR74656 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 366
ID ABR77135 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 367
ID ABMI7892 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 368
ID ABR95943 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 369
ID ABO21876 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 370
ID ABO20046 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 371
ID ABO24349 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 372
ID ABR86098 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 373
ID ABM10750 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 374
ID ABM76749 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 375
ID ABR89453 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 376
ID ABMI2580 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 377
ID ABM05870 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 378
ID ABO34995 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 379
ID ABM03071 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 380
ID ABM19049 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 381
ID ABM19354 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 382
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
```

ID ABO4565 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 383
ID ABO49066 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 384
ID ABR69109 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 385
ID ABR89148 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 386
ID ABR72521 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 387
ID ABR74351 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 388
ID ABO18619 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 389
ID ABR80325 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 390
ID ABR01546 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 391
ID ABR02156 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 392
ID ABR87318 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 393
ID ABM12885 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 394
ID ABM30639 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 395
ID ABM24539 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003084444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 396
ID ABO29453 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 397
ID ABO31283 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 398
ID ABM14410 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 399
ID ABM09835 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 400
ID ABO38960 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 401
ID ABM34725 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 402
ID ABO51201 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 403
ID ABO04027 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 404
ID ABO10497 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 405
ID ABR7740 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 406
ID ABR78950 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 407
ID ABO24044 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 408
ID ABR93808 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 409
ID ABO1851 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 410
ID ABR78274 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003049764-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 411
ID ABR90063 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 412
ID ABR27589 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 413
ID ABR13190 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 414
ID ABO31893 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 415
ID ABR14105 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 416
ID ABR08310 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 417
ID ABO40180 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 418
ID ABR74615 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 419
ID ABR33810 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;

RESULT 420
ID ABM20269 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 421
ID ABO48761 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 422
ID ABR72826 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 423
ID ABO15468 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 424
ID ABR85183 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 425
ID ABO15163 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 426
ID ABO17298 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 427
ID ABR17587 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 428
ID ABR85488 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 429
ID ABR77054 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 430
ID ABO28233 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 431
ID ABM23014 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 432
ID ABM30334 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 433
ID ABM21794 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 434
ID ABM21489 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 435
ID ABM15020 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 436
ID ABO41095 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 437
ID ABO36825 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 438
ID ABO37435 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 439
ID ABR85488 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 440
ID ABR77054 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 439
ID ABM75225 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 440
ID ABM33505 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 441
ID ABO46260 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 442
ID ADA82673 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 443
ID ADB5637 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 444
ID ABM31859 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 445
ID ABM31249 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 446
ID ADB5981 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 447
ID ABM32164 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 448
ID ADB52392 standard; protein; 325 AA.

ID ABM32469 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 449
ID ADB68316 standard; protein; 325 AA.
DE Human PRO3566 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 450
ID ADB68123 standard; protein; 325 AA.
DE Human PRO3566 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 451
ID ABM31554 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 452
ID ABM30944 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 453
ID ADB0940 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 454
ID ADC07020 standard; protein; 325 AA.
DE Human PRO3566 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 455
ID ADC17199 standard; protein; 325 AA.
DE Mammalian PRO polypeptide (SeqID 64).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 456
ID ADC14897 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 457
ID ADC52392 standard; protein; 325 AA.

DE Novel human secreted and transmembrane protein PRO3566.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 7; Length 325;
RESULT 458
ID ADD05711 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 7; Length 325;
RESULT 459
ID ADD36068 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 7; Length 325;
RESULT 460
ID ADG01069 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 7; Length 325;
RESULT 461
ID ADG08622 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 7; Length 325;
RESULT 462
ID ADG02706 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 7; Length 325;
RESULT 463
ID ADG01413 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 7; Length 325;
RESULT 464
ID ADF95588 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 7; Length 325;
RESULT 465
ID ADF95243 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 7; Length 325;
RESULT 466
ID ADG12403 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 7; Length 325;
RESULT 467
ID ADH24096 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 7; Length 325;
RESULT 468
ID ADH34122 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 7; Length 325;
RESULT 469
ID ADH29955 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 7; Length 325;
RESULT 470
ID ADH23926 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 7; Length 325;
RESULT 471
ID ADH09063 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 7; Length 325;
RESULT 472
ID ADG85330 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 7; Length 325;
RESULT 473
ID ADH24606 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 7; Length 325;
RESULT 474
ID ADH37462 standard; protein; 325 AA.
DE Human secreted and transmembrane protein PRO3566.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1824; DB 7; Length 325;
RESULT 475
ID ADH02051 standard; protein; 325 AA.
DE Human PRO polypeptide #32.
PN US2003180837-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 476
ID ADH37632 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 477
ID ADG85670 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 478
ID ADH24266 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 479
ID ADH38560 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 480
ID ADG3681 standard; protein; 325 AA.
DE Human PRO polypeptide #32.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 481
ID ADH29489 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 482
ID ADH27605 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 483
ID ADH37802 standard; protein; 325 AA.
DE Human secreted and transmembrane protein PRO3566.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 484
ID ADH37979 standard; protein; 325 AA.
DE Human secreted and transmembrane protein PRO3566.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 485
ID ADH57399 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 486
ID ADH53541 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 487
ID ADH53711 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 488
ID ADH52047 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 489
ID ADH49902 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 490
ID ADI25412 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 491
ID ADH90205 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 492
ID ADI25582 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 493
ID ADH97756 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 494
ID ADH37979 standard; protein; 325 AA.
DE Human secreted and transmembrane protein PRO3566.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.


```
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 494
ID ADI03604 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 495
ID ADI11961 standard; protein; 325 AA.
DE Human PRO polypeptide #32.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 496
ID ADH90035 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 497
ID ADH98436 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 498
ID ADI1111 standard; protein; 325 AA.
DE Human PRO polypeptide #32.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 499
ID ADI11621 standard; protein; 325 AA.
DE Human PRO polypeptide #32.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 500
ID ADH98266 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 501
ID ADH98606 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 502
ID ADH98096 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 503
ID ADI05084 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 504
ID ADI03434 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 505
ID ADI04829 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 506
ID ADH78283 standard; protein; 325 AA.
DE Human PRO polypeptide #32.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 507
ID ADI19627 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 508
ID ADH90375 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 509
ID ADI03094 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 510
ID ADH77943 standard; protein; 325 AA.
DE Human PRO polypeptide #32.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 511
ID ADH97926 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 512
ID ADH98096 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
```

ID ADI01311 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 513
ID ADI02006 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 514
ID ADI03264 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 515
ID ADI11451 standard; protein; 325 AA.
DE Human PRO polypeptide #32.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 516
ID ADI02353 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 517
ID ADI11791 standard; protein; 325 AA.
DE Human PRO polypeptide #32.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 518
ID ADI05428 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 519
ID ADH79500 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 520
ID ADI19457 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
ID ADI05258 standard; protein; 325 AA.

DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 522
ID ADH79670 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 523
ID ADI01496 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 524
ID ADI01666 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 525
ID ADI01836 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 526
ID ADH79840 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 527
ID ADI04658 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 528
ID ADI02794 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 529
ID ADH78113 standard; protein; 325 AA.
DE Human PRO polypeptide #32.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
ID ADI25752 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.

PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 531
ID ADL125922 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 532
ID ADK65434 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 533
ID ADH98776 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 534
ID ADH80017 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 535
ID ADL32844 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 536
ID ADM30378 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 537
ID ADL93748 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 538
ID ADC52202 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 7; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 539
ID ADE74375 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003211572-A1

PD 13-NOV-2003.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 540
ID AD874987 standard; protein; 325 AA.
DE Human secreted/transmembrane protein (PRO) #119.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 541
ID ADF96200 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 542
ID ADG04471 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 543
ID ADG06631 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 544
ID ADH06634 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 545
ID ADH06464 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 546
ID ADG68895 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 547
ID ADG68895 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 548
ID ADH27775 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 549
ID ADH25116 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;

RESULT 549
ID ADH33748 standard; protein; 325 AA.
DE Human PRO polypeptide #32.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 550
ID ADG82887 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 551
ID ADH02391 standard; protein; 325 AA.
DE Human PRO polypeptide #32.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 552
ID ADH07998 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 553
ID ADG69395 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 554
ID ADH39216 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 555
ID ADH26168 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 556
ID ADG83956 standard; protein; 325 AA.
DE Human PRO polypeptide #32.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 557
ID ADG85500 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 558

ID ADH06294 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 559
ID ADH30124 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 560
ID ADH24436 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 561
ID ADH33137 standard; protein; 325 AA.
DE Human PRO polypeptide #119.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 562
ID ADG69565 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 563
ID ADH07828 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 564
ID ADG85840 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 565
ID ADH39386 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 566
ID ADH33578 standard; protein; 325 AA.
DE Human PRO polypeptide #32.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 567
ID ADH33918 standard; protein; 325 AA.

DE Human PRO polypeptide #32.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 568
ID ADH01128 standard; protein; 325 AA.
DE Human PRO polypeptide #32.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 569
ID ADG69735 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 570
ID ADH02221 standard; protein; 325 AA.
DE Human PRO polypeptide #32.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 571
ID ADG69225 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 572
ID ADG86010 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 573
ID ADH24946 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 574
ID ADH39563 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 575
ID ADH02561 standard; protein; 325 AA.
DE Human PRO polypeptide #32.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 576
ID ADG69055 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 577
ID ADH07658 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 578
ID ADG86180 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 579
ID ADH24776 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 580
ID ADH25824 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 581
ID ADH38390 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 582
ID ADH57229 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 583
ID ADH52216 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 584
ID ADH49583 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 585
ID ADH90545 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2003181700-A1.

PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 8; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 586
 ID ADI11281 standard; protein; 325 AA.
 DE Human PRO polypeptide #32.
 PN US2003181683-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 8; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 587
 ID ADH99946 standard; protein; 325 AA.
 DE Novel human secreted and transmembrane protein PRO3566.
 PN US2003190698-A1.
 PD 09-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 8; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 588
 ID ADI02176 standard; protein; 325 AA.
 DE Novel human secreted and transmembrane protein PRO3566.
 PN US2003190699-A1.
 PD 09-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 8; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 589
 ID ADH90715 standard; protein; 325 AA.
 DE Novel human secreted and transmembrane protein PRO3566.
 PN US2003181701-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 8; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 590
 ID ADJ54876 standard; protein; 325 AA.
 DE Human PRO polypeptide #119.
 PN US2004023321-A1.
 PD 05-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 8; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 591
 ID ADJ98590 standard; protein; 325 AA.
 DE Novel human secreted and transmembrane protein PRO3566.
 PN US2003181797-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 8; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 592
 ID ADJ98760 standard; protein; 325 AA.
 DE Novel human secreted and transmembrane protein PRO3566.
 PN US2003187228-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 8; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 593
 ID ADH78919 standard; protein; 325 AA.
 DE Novel human secreted and transmembrane protein PRO3566.
 PN US2003181703-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 8; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 594
 ID ADJ99153 standard; protein; 325 AA.
 DE Novel human secreted and transmembrane protein PRO3566.
 PN US2003186408-A1.
 PD 02-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 8; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 595
 ID ADJ99323 standard; protein; 325 AA.
 DE Novel human secreted and transmembrane protein PRO3566.
 PN US2003187196-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 8; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 596
 ID ADJ98941 standard; protein; 325 AA.
 DE Novel human secreted and transmembrane protein PRO3566.
 PN US2003187242-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 8; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 597
 ID ADH79089 standard; protein; 325 AA.
 DE Novel human secreted and transmembrane protein PRO3566.
 PN US2003181702-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 8; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 598
 ID ADK00949 standard; protein; 325 AA.
 DE Human PRO polypeptide #32.
 PN US2003186407-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 8; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 599
 ID ADK14470 standard; protein; 325 AA.
 DE Novel human secreted and transmembrane protein PRO3566.
 PN US2003187229-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 8; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 600
 ID ADJ64647 standard; protein; 325 AA.
 DE Human PRO polypeptide #119.
 PN US2004038337-A1.
 PD 26-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 8; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 601
 ID ADM31543 standard; protein; 325 AA.
 DE Novel human secreted and transmembrane protein PRO3566.
 PN US2004048334-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 8; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 602
 ID ADM36590 standard; protein; 325 AA.
 DE Novel human secreted and transmembrane protein PRO3566.
 PN US2004053358-A1.
 PD 18-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1824; DB 8; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 RESULT 603
 ID ADM40395 standard; protein; 325 AA.
 DE Novel human secreted and transmembrane protein PRO3566.
 PN US2004048335-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 604
ID ADM80919 standard; protein; 325 AA.
DE Human PRO polypeptide #32.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 605
ID ADN38003 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 8; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 606
ID ADY77759 standard; protein; 325 AA.
DE Neoplastic disease detection protein PRO3566.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1824; DB 9; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 607
ID AED50233 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2005163766-A1.
PD 28-JUL-2005.
Query Match 100.0%; Score 1824; DB 9; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 608
ID AEF12590 standard; protein; 325 AA.
DE Human PRO3566 protein SEQ ID NO:64.
PN US2006008901-A1.
PD 12-JAN-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 10; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 609
ID AEF74279 standard; protein; 325 AA.
DE Human PRO3566 protein SEQ ID NO:64.
PN US2005260647-A1.
PD 24-NOV-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W L.
Query Match 100.0%; Score 1824; DB 10; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 610
ID AEG62925 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2006073544-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 10; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;

RESULT 611
ID AEG72748 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2006074226-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 10; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 612
ID AEG62313 standard; protein; 325 AA.
DE Human secreted polypeptide PRO3566, SEQ ID NO:238.
PN US2006073545-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 10; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 613
ID AEG88230 standard; protein; 325 AA.
DE Human PRO protein amino acid sequence - SEQ ID 238.
PN US2006074227-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 10; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 614
ID AEH17546 standard; protein; 325 AA.
DE Human tumor overexpressed cDNA protein product PRO3566 SEQ ID NO: 238.
PN US2006094864-A1.
PD 04-MAY-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1824; DB 10; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 615
ID AEH43617 standard; protein; 325 AA.
DE PRO3566 protein sequence, SEQ ID 64.
PN US2006099657-A1.
PD 11-MAY-2006.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1824; DB 10; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 616
ID AEJ11942 standard; protein; 325 AA.
DE Novel human secreted and transmembrane protein PRO3566.
PN US2006160186-A1.
PD 20-JUL-2006.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1824; DB 10; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
RESULT 617
ID AAE13357 standard; protein; 325 AA.
DE Human REPEATER protein.
PN WO200177292-A2.
PD 18-OCT-2001.
PA (SENO-) SENOMYX INC.
Query Match 99.2%; Score 1810; DB 5; Length 325;
Best Local Similarity 99.4%; Pred. No. 2e-135;
RESULT 618

ID AAU79580 standard; protein; 325 AA.
DE Human STG protein.
PN WO200244375-A2.
PD 06-JUN-2002.
PA (CELL-) CELLTech R & D INC.
Query Match 99.2%; Score 1810; DB 5; Length 325;
Best Local Similarity 99.4%; Pred. No. 2e-135;
RESULT 619
ID AAU79582 standard; protein; 325 AA.
DE Human STG polymorphic protein.
PN WO200244375-A2.
PD 06-JUN-2002.
PA (CELL-) CELLTech R & D INC.
Query Match 98.8%; Score 1802; DB 5; Length 325;
Best Local Similarity 98.8%; Pred. No. 8.8e-135;
RESULT 620
ID ABO58618 standard; protein; 267 AA.
DE Human genome derived single exon protein #4852.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 80.8%; Score 1474; DB 8; Length 267;
Best Local Similarity 98.9%; Pred. No. 8.2e-109;
RESULT 621
ID AAY44869 standard; protein; 388 AA.
DE Rat taste cell specific protein TCP #1 variant #1.
PN WO200006719-A1.
PD 10-FEB-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 39.9%; Score 728; DB 3; Length 388;
Best Local Similarity 45.6%; Pred. No. 2.5e-49;
RESULT 622
ID AAY44854 standard; protein; 388 AA.
DE Rat taste cell specific protein TCP #1.
PN WO200006719-A1.
PD 10-FEB-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 39.7%; Score 724; DB 3; Length 388;
Best Local Similarity 45.4%; Pred. No. 5.2e-49;
RESULT 623
ID AAY44870 standard; protein; 388 AA.
DE Rat taste cell specific protein TCP #1 variant #2.
PN WO200006719-A1.
PD 10-FEB-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 39.6%; Score 723; DB 3; Length 388;
Best Local Similarity 45.4%; Pred. No. 6.3e-49;
RESULT 624
ID AAY44871 standard; protein; 388 AA.
DE Rat taste cell specific protein TCP #1 variant #3.
PN WO200006719-A1.
PD 10-FEB-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 39.5%; Score 721; DB 3; Length 388;
Best Local Similarity 45.1%; Pred. No. 9e-49;
RESULT 625
ID ABO57272 standard; protein; 131 AA.
DE Human genome derived single exon protein #3506.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 38.0%; Score 693; DB 8; Length 131;
Best Local Similarity 99.2%; Pred. No. 4.1e-47;
RESULT 626
ID AAY44855 standard; protein; 349 AA.
DE Mouse taste cell specific protein TCP #1.
PN WO200006719-A1.
PD 10-FEB-2000.
PA (REGC) UNIV CALIFORNIA.

Query Match 37.0%; Score 675.5; DB 3; Length 349;
Best Local Similarity 44.3%; Pred. No. 3.3e-45;
RESULT 627
ID ADL35350 standard; protein; 349 AA.
DE Murine secreted extracellular matrix 31418 protein.
PN JP2004008021-A.
PD 15-JAN-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (RIKA) RIKAGAKU KENKYUSHO.
PA (DANA-) DANAFOMU KK.
Query Match 37.0%; Score 675.5; DB 8; Length 349;
Best Local Similarity 44.3%; Pred. No. 3.3e-45;
RESULT 628
ID ADL35378 standard; protein; 547 AA.
DE Protein related to murine secreted extracellular matrix protein.
PN JP2004008021-A.
PD 15-JAN-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (RIKA) RIKAGAKU KENKYUSHO.
PA (DANA-) DANAFOMU KK.
Query Match 21.6%; Score 394; DB 8; Length 547;
Best Local Similarity 23.2%; Pred. No. 1.3e-22;
RESULT 629
ID ABB70874 standard; protein; 1047 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39414.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.7%; Score 194.5; DB 4; Length 1047;
Best Local Similarity 26.2%; Pred. No. 2.1e-06;
RESULT 630
ID AEL56093 standard; protein; 1348 AA.
DE Mouse SW1/SNF related actin dependent regulator of chromatin a4.
PN US2006216722-A1.
PD 28-SEP-2006.
PA (BETS/) BETSHOLTZ C.
PA (TRYG/) TRYGGVASON K.
PA (TAKE/) TAKEMOTO M.
PA (HELL/) HE L.
PA (PATR/) PATRAKKAS J.
Query Match 9.5%; Score 173; DB 10; Length 1348;
Best Local Similarity 26.3%; Pred. No. 0.00014;
RESULT 631
ID ARG45640 standard; protein; 351 AA.
DE Fusion protein GST-14OR.
PN DE102004043782-A1.
PD 09-MAR-2006.
PA (UYDU-) UNIV DUESSELDORF-HEINRICH-HEINE.
Query Match 9.2%; Score 168.5; DB 10; Length 351;
Best Local Similarity 33.9%; Pred. No. 6.6e-05;
RESULT 632
ID ARG05200 standard; protein; 371 AA.
DE Novel human diagnostic protein #5191.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.2%; Score 168; DB 4; Length 371;
Best Local Similarity 26.2%; Pred. No. 7.7e-05;
RESULT 633
ID ADS98704 standard; protein; 371 AA.
DE Protein factor discovery related human contig polypeptide, SEQ ID 968.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
PA (DRMA/) DRMANAC R T.
Query Match 9.2%; Score 168; DB 8; Length 371;
Best Local Similarity 26.2%; Pred. No. 7.7e-05;
RESULT 634
ID AEG45639 standard; protein; 343 AA.
DE Fusion protein GST-13OR.
PN DE102004043782-A1.
PD 09-MAR-2006.
PA (UYDU-) UNIV DUESSELDORF-HEINRICH-HEINE.

Query Match 9.2%; Score 167.5; DB 10; Length 343;
Best Local Similarity 32.8%; Pred. No. 7.7e-05;
RESULT 635
ID AEG45644 standard; protein; 346 AA.
DE Fusion protein GST-15OR.
PN DE10200403782-A1.
PD 09-MAR-2006.
PA (UYDU-) UNIV DUESSELDORF-HEINRICH-HEINE.
Query Match 9.2%; Score 167.5; DB 10; Length 346;
Best Local Similarity 32.3%; Pred. No. 7.7e-05;
RESULT 636
ID AEG45645 standard; protein; 354 AA.
DE Fusion protein GST-16OR.
PN DE10200403782-A1.
PD 09-MAR-2006.
PA (UYDU-) UNIV DUESSELDORF-HEINRICH-HEINE.
Query Match 9.2%; Score 167.5; DB 10; Length 354;
Best Local Similarity 32.3%; Pred. No. 8e-05;
RESULT 637
ID ABG19238 standard; protein; 265 AA.
DE Novel human diagnostic protein #19229.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.1%; Score 166.5; DB 4; Length 265;
Best Local Similarity 27.6%; Pred. No. 6.8e-05;
RESULT 638
ID ABB63299 standard; protein; 2703 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 16689.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 9.1%; Score 165.5; DB 4; Length 2703;
Best Local Similarity 23.9%; Pred. No. 0.0013;
RESULT 639
ID ABG70019 standard; protein; 2703 AA.
DE Larval viability associated protein #18.
PN WO200257455-A2.
PD 25-JUL-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 9.1%; Score 165.5; DB 5; Length 2703;
Best Local Similarity 23.9%; Pred. No. 0.0013;
RESULT 640
ID AAB27551 standard; protein; 543 AA.
DE Human tumour suppressor BRG1 encoded by cDNA mutated at base 1705.
PN WO200056931-A1.
PD 28-SEP-2000.
PA (MYRI-) MYRIAD GENETICS INC.
Query Match 8.9%; Score 163; DB 3; Length 543;
Best Local Similarity 25.3%; Pred. No. 0.0003;
RESULT 641
ID AAB27550 standard; protein; 577 AA.
DE Human tumour suppressor BRG1 protein from cell lines DUL45 and NCI-H1300.
PN WO200056931-A1.
PD 28-SEP-2000.
PA (MYRI-) MYRIAD GENETICS INC.
Query Match 8.9%; Score 163; DB 3; Length 577;
Best Local Similarity 25.3%; Pred. No. 0.00033;
RESULT 642
ID ADJ80182 standard; protein; 1492 AA.
DE Novel human nucleic acid-associated protein #58.
PN WO2003038052-A2.
PD 08-MAY-2003.
PA (INCYTE) INCYTE GENOMICS INC.
Query Match 8.9%; Score 163; DB 7; Length 1492;
Best Local Similarity 25.3%; Pred. No. 0.001;
RESULT 643
ID AEC20284 standard; protein; 1492 AA.
DE Human nucleic acid-associated protein (NAAP) - SEQ ID 58.
PN US2005186569-A1.
PD 25-AUG-2005.
PA (BECH/) BECHA S D.
PA (BORO/) BOROWSKY M L.

PA (BURE/) BURFORD N.
PA (CHAW/) CHAWLA N K.
PA (ELLI/) ELLIOTT V S.
PA (EMER/) EMERLING B M.
PA (FORS/) FORSYTHE I J.
PA (GIET/) GIETZEN K J.
PA (GORV/) GORVAD A E.
PA (GRIF/) GRIFFIN J A.
PA (HAF/) HAFALIA A J A.
PA (ISON/) ISON C H.
PA (LALP/) LAL P.
PA (LEEE/) LEE E A.
PA (LEES/) LEE S.
PA (MARQ/) MARQUIS J P.
PA (RAMK/) RAMKUMAR J.
PA (SPRA/) SPRAGUE W W.
PA (SWAR/) SWARNAKAR A.
PA (TANG/) TANG Y T.
PA (WARR/) WARREN B A.
PA (YANG/) YANG J.
PA (YUEH/) YUE H.
PA (ZEB/) ZEBARJADIAN Y.
Query Match 8.9%; Score 163; DB 9; Length 1492;
Best Local Similarity 25.3%; Pred. No. 0.001;
RESULT 644
ID AAB27553 standard; protein; 1646 AA.
DE Human tumour suppressor BRG1 splice variant protein #2.
PN WO200056931-A1.
PD 28-SEP-2000.
PA (MYRI-) MYRIAD GENETICS INC.
Query Match 8.9%; Score 163; DB 3; Length 1646;
Best Local Similarity 25.3%; Pred. No. 0.0011;
RESULT 645
ID AAB27549 standard; protein; 1647 AA.
DE Human tumour suppressor BRG1.
PN WO200056931-A1.
PD 28-SEP-2000.
PA (MYRI-) MYRIAD GENETICS INC.
Query Match 8.9%; Score 163; DB 3; Length 1647;
Best Local Similarity 25.3%; Pred. No. 0.0011;
RESULT 646
ID ADF11509 standard; protein; 1647 AA.
DE Human BRG1 polypeptide.
PN US2003077800-A1.
PD 24-APR-2003.
PA (HORN-) HORMOS MEDICAL LTD OY.
Query Match 8.9%; Score 163; DB 7; Length 1647;
Best Local Similarity 25.3%; Pred. No. 0.0011;
RESULT 647
ID ADF76681 standard; protein; 1647 AA.
DE Novel human secreted and transmembrane protein SeqID 356.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 163; DB 7; Length 1647;
Best Local Similarity 25.3%; Pred. No. 0.0011;
RESULT 648
ID ADP22725 standard; protein; 1647 AA.
DE Human SMARCA4 protein, SEQ ID NO:4.
PN WO2004048539-A2.
PD 10-JUN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 8.9%; Score 163; DB 8; Length 1647;
Best Local Similarity 25.3%; Pred. No. 0.0011;
RESULT 649
ID ABM82036 standard; protein; 1647 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO82935, SEQ:5255.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 163; DB 8; Length 1647;
Best Local Similarity 25.3%; Pred. No. 0.0011;

```

RESULT 650
ID ADP54759 standard; protein; 1647 AA.
DE Human PRO protein sequence SEQ ID NO:735.
PN WO200403956-A2.
PD 13-MAY-2004.
PA (GETH ) GENENTECH INC.
Query Match 8.9%; Score 163; DB 8; Length 1647;
Best Local Similarity 25.3%; Pred. No. 0.0011;
RESULT 651
ID ADY19728 standard; protein; 1647 AA.
DE PRO polypeptide SEQ ID NO 5534.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH ) GENENTECH INC.
Query Match 8.9%; Score 163; DB 9; Length 1647;
Best Local Similarity 25.3%; Pred. No. 0.0011;
RESULT 652
ID AEL57003 standard; protein; 1647 AA.
DE Human possible global transcription activator SNF2L4, SEQ ID NO: 1466.
PN US2006216722-A1.
PD 28-SEP-2006.
PA (BETS/) BETSHOLTZ C.
PA (TRYG/) TRYGVASON K.
PA (TAKE/) TAKEMOTO M.
PA (HELL/) HE L.
PA (PATR/) PATRAKXAS J.
Query Match 8.9%; Score 163; DB 10; Length 1647;
Best Local Similarity 25.3%; Pred. No. 0.0011;
RESULT 653
ID AAB27557 standard; protein; 1649 AA.
DE Human tumour suppressor BRG1 splice variant protein #6.
PN WO200056931-A1.
PD 28-SEP-2000.
PA (MYRI-) MYRIAD GENETICS INC.
Query Match 8.9%; Score 163; DB 3; Length 1649;
Best Local Similarity 25.3%; Pred. No. 0.0011;
RESULT 654
ID AAB27555 standard; protein; 1650 AA.
DE Human tumour suppressor BRG1 splice variant protein #4.
PN WO200056931-A1.
PD 28-SEP-2000.
PA (MYRI-) MYRIAD GENETICS INC.
Query Match 8.9%; Score 163; DB 3; Length 1650;
Best Local Similarity 25.3%; Pred. No. 0.0011;
RESULT 655
ID AAB27554 standard; protein; 1678 AA.
DE Human tumour suppressor BRG1 splice variant protein #3.
PN WO200056931-A1.
PD 28-SEP-2000.
PA (MYRI-) MYRIAD GENETICS INC.
Query Match 8.9%; Score 163; DB 3; Length 1678;
Best Local Similarity 25.3%; Pred. No. 0.0012;
RESULT 656
ID AAB27552 standard; protein; 1679 AA.
DE Human tumour suppressor BRG1 splice variant protein #1.
PN WO200056931-A1.
PD 28-SEP-2000.
PA (MYRI-) MYRIAD GENETICS INC.
Query Match 8.9%; Score 163; DB 3; Length 1679;
Best Local Similarity 25.3%; Pred. No. 0.0012;
RESULT 657
ID AEL57005 standard; protein; 1679 AA.
DE Human possible global transcription activator SNF2L4, SEQ ID NO: 1468.
PN US2006216722-A1.
PD 28-SEP-2006.
PA (BETS/) BETSHOLTZ C.
PA (TRYG/) TRYGVASON K.
PA (TAKE/) TAKEMOTO M.
PA (HELL/) HE L.
PA (PATR/) PATRAKXAS J.
Query Match 8.9%; Score 163; DB 10; Length 1679;
Best Local Similarity 25.3%; Pred. No. 0.0012;
RESULT 658
ID AEL57005 standard; protein; 1681 AA.
DE Human tumour suppressor BRG1 splice variant protein #7.
PN WO200056931-A1.
PD 28-SEP-2000.
PA (MYRI-) MYRIAD GENETICS INC.
Query Match 8.9%; Score 163; DB 3; Length 1681;
Best Local Similarity 25.3%; Pred. No. 0.0012;
RESULT 659
ID AAB27556 standard; protein; 1682 AA.
DE Human tumour suppressor BRG1 splice variant protein #5.
PN WO200056931-A1.
PD 28-SEP-2000.
PA (MYRI-) MYRIAD GENETICS INC.
Query Match 8.9%; Score 163; DB 3; Length 1682;
Best Local Similarity 25.3%; Pred. No. 0.0012;
RESULT 660
ID ABM94794 standard; protein; 420 AA.
DE M. xanthus protein sequence, seq id 13993.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS ) MONSANTO TECHNOLOGY LLC.
Query Match 8.9%; Score 161.5; DB 9; Length 420;
Best Local Similarity 27.8%; Pred. No. 0.00029;
RESULT 661
ID ABM85385 standard; protein; 266 AA.
DE Human protein sequence hCF1689982.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 8.7%; Score 159.5; DB 7; Length 266;
Best Local Similarity 27.5%; Pred. No. 0.00024;
RESULT 662
ID ARG03533 standard; protein; 900 AA.
DE Novel human diagnostic protein #3524.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.7%; Score 159; DB 4; Length 900;
Best Local Similarity 24.8%; Pred. No. 0.0012;
RESULT 663
ID ARG45643 standard; protein; 322 AA.
DE Fusion protein GST-120R.
PN DE102004043782-A1.
PD 09-MAR-2006.
PA (UYDU-) UNIV DUESSELDORF-HEINRICH-HEINE.
Query Match 8.7%; Score 158.5; DB 10; Length 322;
Best Local Similarity 30.8%; Pred. No. 0.00037;
RESULT 664
ID ABB57364 standard; protein; 1373 AA.
DE Mouse ischaemic condition related protein sequence SEQ ID NO:1029.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 8.6%; Score 157; DB 5; Length 1373;
Best Local Similarity 27.0%; Pred. No. 0.0028;
RESULT 665
ID ADW44460 standard; protein; 1373 AA.
DE Murine procollagen type I alpha-2 Coll1a2.
PN WO2005001090-A1.
PD 06-JAN-2005.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 8.6%; Score 157; DB 9; Length 1373;
Best Local Similarity 27.0%; Pred. No. 0.0028;
RESULT 666
ID AEF19250 standard; protein; 1373 AA.
DE Mus musculus procollagen, type I, alpha 2 (Colla2).
PN WO2006001396-A1.
PD 05-JAN-2006.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 8.6%; Score 157; DB 10; Length 1373;
Best Local Similarity 27.0%; Pred. No. 0.0028;
RESULT 667
ID AAB36620 standard; protein; 245 AA.

```

DE Human FLEXHT-42 protein sequence SEQ ID NO:42.
PN W200070047-A2.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 8.4%; Score 153.5; DB 4; Length 245;
Best Local Similarity 27.1%; Pred. No. 0.00066;
RESULT 668
ID ADG10502 standard; protein; 245 AA.
DE Human STAT6-activating protein, SEQ ID NO:92.
PN W200296943-A1.
PD 05-DEC-2002.
PA (ASAH) ASAH KASEI KOGYO KK.
Query Match 8.4%; Score 153.5; DB 7; Length 245;
Best Local Similarity 27.1%; Pred. No. 0.00086;
RESULT 669
ID ABO58334 standard; protein; 259 AA.
DE Human genome derived single exon protein #4568.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 8.4%; Score 153.5; DB 8; Length 259;
Best Local Similarity 27.0%; Pred. No. 0.00071;
RESULT 670
ID ABU21936 standard; protein; 300 AA.
DE Protein encoded by Prokaryotic essential gene #7463.
PN W200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 8.4%; Score 153.5; DB 6; Length 300;
Best Local Similarity 29.8%; Pred. No. 0.00085;
RESULT 671
ID ABO52933 standard; protein; 464 AA.
DE Human spliceosome associated protein (SAP) #23.
PN US2003068803-A1.
PD 10-APR-2003.
PA (REED/) REED R.
PA (ZHOU/) ZHOU Z.
Query Match 8.4%; Score 153.5; DB 6; Length 464;
Best Local Similarity 27.0%; Pred. No. 0.0014;
RESULT 672
ID AEM81998 standard; protein; 464 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO82886, SEQ:5153.
PN W2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 153.5; DB 8; Length 464;
Best Local Similarity 27.0%; Pred. No. 0.0014;
RESULT 673
ID ADY70309 standard; protein; 464 AA.
DE Human beta-amyloid precursor protein, SAP-62.
PN W2005023858-A1.
PD 17-MAR-2005.
PA (CELL-) CELLZOME AG.
Query Match 8.4%; Score 153.5; DB 9; Length 464;
Best Local Similarity 27.0%; Pred. No. 0.0014;
RESULT 674
ID AEG59081 standard; protein; 464 AA.
DE Human U2 SAP62 protein.
PN US2006068434-A1.
PD 30-MAR-2006.
PA (STOE/) STOECKER J.
Query Match 8.4%; Score 153.5; DB 10; Length 464;
Best Local Similarity 27.0%; Pred. No. 0.0014;
RESULT 675
ID AEG59129 standard; protein; 464 AA.
DE Human U2 SF3a66 protein.
PN US2006068434-A1.
PD 30-MAR-2006.
PA (STOE/) STOECKER J.
Query Match 8.4%; Score 153.5; DB 10; Length 464;
Best Local Similarity 27.0%; Pred. No. 0.0014;

RESULT 676
ID AEG73471 standard; protein; 464 AA.
DE Human U2 related protein #31.
PN W2006034278-A2.
PD 30-MAR-2006.
PA (MATR-) MATRITECH INC.
Query Match 8.4%; Score 153.5; DB 10; Length 464;
Best Local Similarity 27.0%; Pred. No. 0.0014;
RESULT 677
ID AEG73423 standard; protein; 464 AA.
DE Human U2 related protein #7.
PN W2006034278-A2.
PD 30-MAR-2006.
PA (MATR-) MATRITECH INC.
Query Match 8.4%; Score 153.5; DB 10; Length 464;
Best Local Similarity 27.0%; Pred. No. 0.0014;
RESULT 678
ID AEG45642 standard; protein; 314 AA.
DE Fusion protein GST-110R.
PN DE102004043782-A1.
PD 09-MAR-2006.
PA (VVDU-) UNIV DUESSELDORF-HEINRICH-HEINE.
Query Match 8.4%; Score 152.5; DB 10; Length 314;
Best Local Similarity 29.7%; Pred. No. 0.0011;
RESULT 679
ID AAM80248 standard; protein; 328 AA.
DE Human protein SEQ ID NO 3894.
PN W200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.3%; Score 151.5; DB 4; Length 328;
Best Local Similarity 27.0%; Pred. No. 0.0014;
RESULT 680
ID AAR71702 standard; protein; 1366 AA.
DE Collagen alpha 2 (I) chain precursor.
PN W09508115-A1.
PD 23-MAR-1995.
PA (OSTE-) OSTEOMETER AS.
Query Match 8.3%; Score 151; DB 2; Length 1366;
Best Local Similarity 27.4%; Pred. No. 0.0082;
RESULT 681
ID AAY96123 standard; peptide; 1366 AA.
DE Collagen type I alpha-2.
PN US6110689-A.
PD 29-AUG-2000.
PA (OSTE-) OSTEOMETER AS.
Query Match 8.3%; Score 151; DB 3; Length 1366;
Best Local Similarity 27.4%; Pred. No. 0.0082;
RESULT 682
ID ABB50293 standard; protein; 1366 AA.
DE Collagen type I alpha-2 ovarian tumour marker protein, SEQ ID NO:76.
PN W200175177-A2.
PD 11-OCT-2001.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 8.3%; Score 151; DB 4; Length 1366;
Best Local Similarity 27.4%; Pred. No. 0.0082;
RESULT 683
ID AAE16476 standard; protein; 1366 AA.
DE Human collagen alpha 2-type I protein.
PN US6323314-B1.
PD 27-NOV-2001.
PA (OSTE-) OSTEOMETER AS.
Query Match 8.3%; Score 151; DB 5; Length 1366;
Best Local Similarity 27.4%; Pred. No. 0.0082;
RESULT 684
ID ABB0734 standard; protein; 1366 AA.
DE Protein sequence related to human collagen.
PN US6355442-B1.
PD 12-MAR-2002.
PA (OSTE-) OSTEOMETER BIOTECH AS.
Query Match 8.3%; Score 151; DB 5; Length 1366;
Best Local Similarity 27.4%; Pred. No. 0.0082;
RESULT 685

ID ABB09626 standard; peptide; 1366 AA.
 DE Amino acid sequence of human collagen type I alpha2.
 PN US6342361-B1.
 PD 29-JAN-2002.
 PA (OSTE-) OSTEOMETER BIOTECH AS.
 Query Match 8.3%; Score 151; DB 5; Length 1366;
 Best Local Similarity 27.4%; Pred. No. 0.0082;
 RESULT 686
 ID ADF13076 standard; protein; 1366 AA.
 DE Human procollagen alpha2(I) chain precursor.
 PN US2003119058-A1.
 PD 26-JUN-2003.
 PA (OSTE-) OSTEOMETER AS.
 Query Match 8.3%; Score 151; DB 7; Length 1366;
 Best Local Similarity 27.4%; Pred. No. 0.0082;
 RESULT 687
 ID ADV70234 standard; protein; 1366 AA.
 DE Tumor-associated antigenic target polypeptide TAT473.
 PN WO2004112829-A2.
 PD 29-DEC-2004.
 PA (GETH) GENENTECH INC.
 Query Match 8.3%; Score 151; DB 9; Length 1366;
 Best Local Similarity 27.4%; Pred. No. 0.0082;
 RESULT 688
 ID ABE24257 standard; protein; 1366 AA.
 DE Human type I collagen protein - SEQ ID 3.
 PN US2006100138-A1.
 PD 11-MAY-2006.
 PA (OLSE/) OLSEN D R.
 PA (FOLA/) POLAREK J W.
 PA (YANG/) YANG C.
 Query Match 8.3%; Score 151; DB 10; Length 1366;
 Best Local Similarity 27.4%; Pred. No. 0.0082;
 RESULT 689
 ID ABJ05575 standard; protein; 680 AA.
 DE Breast cancer-associated protein 40.
 PN WO200259377-A2.
 PD 01-AUG-2002.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 8.2%; Score 150; DB 5; Length 680;
 Best Local Similarity 23.9%; Pred. No. 0.0043;
 RESULT 690
 ID ABEU56618 standard; protein; 680 AA.
 DE Lung cancer-associated polypeptide #211.
 PN WO200286443-A2.
 PD 31-OCT-2002.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 8.2%; Score 150; DB 6; Length 680;
 Best Local Similarity 23.9%; Pred. No. 0.0043;
 RESULT 691
 ID ABR47414 standard; protein; 680 AA.
 DE Breast cancer associated protein sequence SEQ ID NO:59.
 PN WO2003004989-A2.
 PD 16-JAN-2003.
 PA (MILL-) MILLENIUM PHARM INC.
 Query Match 8.2%; Score 150; DB 6; Length 680;
 Best Local Similarity 23.9%; Pred. No. 0.0043;
 RESULT 692
 ID ADD46128 standard; protein; 680 AA.
 DE Human Protein Q03692, SEQ ID NO 11803.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GHEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 8.2%; Score 150; DB 7; Length 680;
 Best Local Similarity 23.9%; Pred. No. 0.0043;
 RESULT 693
 ID ADN38792 standard; protein; 680 AA.
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:110.
 PN WO2003042661-A2.
 PD 22-MAY-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 8.2%; Score 150; DB 7; Length 680;

Best Local Similarity 23.9%; Pred. No. 0.0043;
 RESULT 694
 ID ADL06538 standard; protein; 680 AA.
 DE Human tumour-associated antigenic target (TAT) polypeptide #37.
 PN WO2004016225-A2.
 PD 26-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 8.2%; Score 150; DB 8; Length 680;
 Best Local Similarity 23.9%; Pred. No. 0.0043;
 RESULT 695
 ID ADV15274 standard; protein; 680 AA.
 DE Human osteoporosis related protein, seq id 15.
 PN US6825336-B1.
 PD 30-NOV-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 8.2%; Score 150; DB 8; Length 680;
 Best Local Similarity 23.9%; Pred. No. 0.0043;
 RESULT 696
 ID ADV15279 standard; protein; 680 AA.
 DE Human osteoporosis related protein, seq id 20.
 PN US6825336-B1.
 PD 30-NOV-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 8.2%; Score 150; DB 8; Length 680;
 Best Local Similarity 23.9%; Pred. No. 0.0043;
 RESULT 697
 ID ADZ09776 standard; protein; 680 AA.
 DE Human breast cancer marker COL10A1 protein.
 PN EP1522594-A2.
 PD 13-APR-2005.
 PA (FARB-) BAYER HEALTHCARE AG.
 Query Match 8.2%; Score 150; DB 9; Length 680;
 Best Local Similarity 23.9%; Pred. No. 0.0043;
 RESULT 698
 ID AEA00131 standard; protein; 680 AA.
 DE Human TAT158 protein SEQ ID NO:83.
 PN US2005106644-A1.
 PD 19-MAY-2005.
 PA (GETH) GENENTECH INC.
 Query Match 8.2%; Score 150; DB 9; Length 680;
 Best Local Similarity 23.9%; Pred. No. 0.0043;
 RESULT 699
 ID AEA00651 standard; protein; 680 AA.
 DE Human TAT158 protein sequence SeqID83.
 PN US2005107595-A1.
 PD 19-MAY-2005.
 PA (GETH) GENENTECH INC.
 Query Match 8.2%; Score 150; DB 9; Length 680;
 Best Local Similarity 23.9%; Pred. No. 0.0043;
 RESULT 700
 ID ADC86657 standard; protein; 737 AA.
 DE Human GPCR protein SEQ ID NO:1110.
 PN EP1270724-A2.
 PD 02-JAN-2003.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Query Match 8.1%; Score 148.5; DB 7; Length 737;
 Best Local Similarity 28.2%; Pred. No. 0.0062;
 RESULT 701
 ID AAM93401 standard; protein; 740 AA.
 DE Human polypeptide, SEQ ID NO: 3002.
 PN EP1130094-A2.
 PD 05-SEP-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 8.1%; Score 148; DB 4; Length 740;
 Best Local Similarity 24.4%; Pred. No. 0.0068;
 RESULT 702
 ID ADL30969 standard; protein; 740 AA.
 DE Human protein encoded by a full length cDNA clone SeqID 3002.
 PN EP1396543-A2.
 PD 10-MAR-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 8.1%; Score 148; DB 8; Length 740;

```

Best Local Similarity 24.4%; Pred. No. 0.0068;
RESULT 703
ID AAB92725 standard; protein; 278 AA.
DE Human protein sequence SEQ ID NO:11151.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 8.1%; Score 147.5; DB 4; Length 278;
Best Local Similarity 25.9%; Pred. No. 0.0023;
RESULT 704
ID ADY17323 standard; protein; 388 AA.
DE PRO polypeptide SEQ ID NO 3129.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH-) GENENTECH INC.
Query Match 8.1%; Score 147.5; DB 9; Length 388;
Best Local Similarity 25.9%; Pred. No. 0.0035;
RESULT 705
ID ABB65135 standard; protein; 926 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 22197.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 8.1%; Score 147.5; DB 4; Length 926;
Best Local Similarity 22.3%; Pred. No. 0.0098;
RESULT 706
ID ADC31709 standard; protein; 757 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1791.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 8.1%; Score 147; DB 7; Length 757;
Best Local Similarity 24.4%; Pred. No. 0.0084;
RESULT 707
ID ABU63602 standard; protein; 812 AA.
DE Human NF-kappaB associated polypeptide sequence #8.
PN WO200286076-A2.
PD 31-OCT-2002.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match 8.1%; Score 147; DB 6; Length 812;
Best Local Similarity 24.4%; Pred. No. 0.0092;
RESULT 708
ID ADM04988 standard; protein; 812 AA.
DE Human protein of the invention SEQ ID NO:3673.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 8.1%; Score 147; DB 7; Length 812;
Best Local Similarity 24.4%; Pred. No. 0.0092;
RESULT 709
ID ADU83153 standard; protein; 812 AA.
DE Human NFKappaB-associated gene 81, protein.
PN WO2004100886-A2.
PD 25-NOV-2004.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match 8.1%; Score 147; DB 9; Length 812;
Best Local Similarity 24.4%; Pred. No. 0.0092;
RESULT 710
ID AEC87918 standard; protein; 812 AA.
DE Human cDNA clone protein NT2RP70062230, SEQ ID 3673.
PN EP1580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 8.1%; Score 147; DB 9; Length 812;
Best Local Similarity 24.4%; Pred. No. 0.0092;
RESULT 711
ID AEL57313 standard; protein; 812 AA.
DE Human glomerulus-specific marker, SEQ ID NO: 1776.
PN US2006216722-A1.
PD 28-SEP-2006.
PA (BETS-) BETSHOLTZ C.
PA (TRYG-) TRYGGVASON K.
PA (TAKE-) TAKEMOTO M.
PA (PATR/) PATRAKKAS J.
Query Match 8.1%; Score 147; DB 10; Length 812;
Best Local Similarity 24.4%; Pred. No. 0.0092;
RESULT 712
ID ADG42177 standard; protein; 819 AA.
DE Human brain/hippocampus polypeptide #25.
PN JP2002330794-A.
PD 19-NOV-2002.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 8.1%; Score 147; DB 7; Length 819;
Best Local Similarity 24.4%; Pred. No. 0.0092;
RESULT 713
ID AEL57311 standard; protein; 821 AA.
DE Human glomerulus-specific marker, SEQ ID NO: 1774.
PN US2006216722-A1.
PD 28-SEP-2006.
PA (BETS-) BETSHOLTZ C.
PA (TRYG-) TRYGGVASON K.
PA (TAKE-) TAKEMOTO M.
PA (HELI-) HE L.
PA (PATR/) PATRAKKAS J.
Query Match 8.1%; Score 147; DB 10; Length 821;
Best Local Similarity 24.4%; Pred. No. 0.0093;
RESULT 714
ID AEG45641 standard; protein; 306 AA.
DE Fusion protein GST-100R.
PN DE102004043782-A1.
PD 09-MAR-2006.
PA (UYDU-) UNIV DUESSELDORF-HEINRICH-HEINE.
Query Match 8.0%; Score 146.5; DB 10; Length 306;
Best Local Similarity 28.6%; Pred. No. 0.0031;
RESULT 715
ID ABG19237 standard; protein; 333 AA.
DE Novel human diagnostic protein #19228.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.0%; Score 146; DB 4; Length 333;
Best Local Similarity 26.2%; Pred. No. 0.0038;
RESULT 716
ID AAY84548 standard; protein; 1040 AA.
DE A human collagen 1 (alpha2) protein helical region.
PN EP992586-A2.
PD 12-APR-2000.
PA (USSU-) US SURGICAL CORP.
Query Match 8.0%; Score 146; DB 3; Length 1040;
Best Local Similarity 27.0%; Pred. No. 0.015;
RESULT 717
ID AAY84547 standard; protein; 1040 AA.
DE A human collagen 1 (alpha2) protein helical region.
PN EP992586-A2.
PD 12-APR-2000.
PA (USSU-) US SURGICAL CORP.
Query Match 8.0%; Score 146; DB 3; Length 1040;
Best Local Similarity 27.0%; Pred. No. 0.015;
RESULT 718
ID AAY56801 standard; protein; 1366 AA.
DE Human preproalpha 2 (I) collagen.
PN EP967226-A2.
PD 29-DEC-1999.
PA (COHE-) COHESION TECHNOLOGIES INC.
Query Match 8.0%; Score 146; DB 3; Length 1366;
Best Local Similarity 27.0%; Pred. No. 0.02;
RESULT 719
ID ABB90751 standard; protein; 1366 AA.
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 234.
PN WO200210217-A2.
PD 07-FEB-2002.
PA (UYJO-) UNIV JOHNS HOPKINS.
Query Match 8.0%; Score 146; DB 5; Length 1366;
Best Local Similarity 27.0%; Pred. No. 0.02;
RESULT 720

```

ID ABB90766 standard; protein; 1366 AA.
 DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 265.
 PN WO200210217-A2.
 PD 07-FEB-2002.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 8.0%; Score 146; DB 5; Length 1366;
 Best Local Similarity 27.0%; Pred. No. 0.02;
 RESULT 721
 ID ABB90741 standard; protein; 1366 AA.
 DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 214.
 PN WO200210217-A2.
 PD 07-FEB-2002.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 8.0%; Score 146; DB 5; Length 1366;
 Best Local Similarity 27.0%; Pred. No. 0.02;
 RESULT 722
 ID ABU54448 standard; protein; 1366 AA.
 DE Human tumour endothelial marker TEM 10.
 PN WO200283874-A2.
 PD 24-OCT-2002.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 8.0%; Score 146; DB 6; Length 1366;
 Best Local Similarity 27.0%; Pred. No. 0.02;
 RESULT 723
 ID ABU54473 standard; protein; 1366 AA.
 DE Human tumour endothelial marker TEM 40.
 PN WO200283874-A2.
 PD 24-OCT-2002.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 8.0%; Score 146; DB 6; Length 1366;
 Best Local Similarity 27.0%; Pred. No. 0.02;
 RESULT 724
 ID ABU54458 standard; protein; 1366 AA.
 DE Human tumour endothelial marker TEM 20.
 PN WO200283874-A2.
 PD 24-OCT-2002.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 8.0%; Score 146; DB 6; Length 1366;
 Best Local Similarity 27.0%; Pred. No. 0.02;
 RESULT 725
 ID ABR92065 standard; protein; 1366 AA.
 DE Human cervical cancer cell marker protein SEQ ID NO:38.
 PN WO2002101075-A2.
 PD 19-DEC-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 8.0%; Score 146; DB 6; Length 1366;
 Best Local Similarity 27.0%; Pred. No. 0.02;
 RESULT 726
 ID ADK70437 standard; protein; 1366 AA.
 DE Respiratory disease differentially expressed protein #3.
 PN WO2003101283-A2.
 PD 11-DEC-2003.
 PA (INCY-) INCYTE CORP.
 Query Match 8.0%; Score 146; DB 8; Length 1366;
 Best Local Similarity 27.0%; Pred. No. 0.02;
 RESULT 727
 ID ADQ29669 standard; protein; 1366 AA.
 DE Human colorectal cancer-associated protein #24.
 PN EP1439393-A2.
 PD 21-JUL-2004.
 PA (FARB) BAYER HEALTHCARE LLC.
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
 Query Match 8.0%; Score 146; DB 8; Length 1366;
 Best Local Similarity 27.0%; Pred. No. 0.02;
 RESULT 728
 ID ADV87001 standard; protein; 1366 AA.
 DE Collagen type I precursor chain COL1A2.
 PN WO2004110470-A2.
 PD 23-DEC-2004.
 PA (UYBR-) UNIV BRISTOL.
 Query Match 8.0%; Score 146; DB 9; Length 1366;
 Best Local Similarity 27.0%; Pred. No. 0.02;
 RESULT 729

ID ADZ70510 standard; protein; 1366 AA.
 DE Human protein from lung cancer marker gene COL1A2, SEQ ID 195.
 PN WO2005032495-A2.
 PD 14-APR-2005.
 PA (FARB) BAYER PHARM CORP.
 Query Match 8.0%; Score 146; DB 9; Length 1366;
 Best Local Similarity 27.0%; Pred. No. 0.02;
 RESULT 730
 ID ADZ70624 standard; protein; 1366 AA.
 DE Human protein from lung cancer marker gene COL1A2, SEQ ID 309.
 PN WO2005032495-A2.
 PD 14-APR-2005.
 PA (FARB) BAYER PHARM CORP.
 Query Match 8.0%; Score 146; DB 9; Length 1366;
 Best Local Similarity 27.0%; Pred. No. 0.02;
 RESULT 731
 ID AEA04491 standard; protein; 1366 AA.
 DE Human protein from gene overexpressed in cancer, COL1A2.
 PN WO2005044990-A2.
 PD 19-MAY-2005.
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
 Query Match 8.0%; Score 146; DB 9; Length 1366;
 Best Local Similarity 27.0%; Pred. No. 0.02;
 RESULT 732
 ID AED74603 standard; protein; 1366 AA.
 DE Human placental protein SEQ ID NO:1431.
 PN US2005255114-A1.
 PD 17-NOV-2005.
 PA (NUVE-) NUVELO INC.
 Query Match 8.0%; Score 146; DB 9; Length 1366;
 Best Local Similarity 27.0%; Pred. No. 0.02;
 RESULT 733
 ID AEF69981 standard; protein; 1366 AA.
 DE Colorectal cancer-associated marker protein SEQ ID NO:159.
 PN WO2006015047-A2.
 PD 09-FEB-2006.
 PA (FARB) BAYER HEALTHCARE LLC.
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
 Query Match 8.0%; Score 146; DB 10; Length 1366;
 Best Local Similarity 27.0%; Pred. No. 0.02;
 RESULT 734
 ID ADE59683 standard; protein; 1372 AA.
 DE Rat Protein P02466, SEQ ID NO 5579.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 8.0%; Score 146; DB 7; Length 1372;
 Best Local Similarity 26.7%; Pred. No. 0.021;
 RESULT 735
 ID ADD45148 standard; protein; 1372 AA.
 DE Rat Protein P02466, SEQ ID NO 10581.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 8.0%; Score 146; DB 7; Length 1372;
 Best Local Similarity 26.7%; Pred. No. 0.021;
 RESULT 736
 ID ADD45604 standard; protein; 1372 AA.
 DE Rat Protein P02466, SEQ ID NO 11270.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 8.0%; Score 146; DB 7; Length 1372;
 Best Local Similarity 26.7%; Pred. No. 0.021;
 RESULT 737
 ID ADE59687 standard; protein; 1372 AA.
 DE Rat Protein P02466, SEQ ID NO 5583.
 PN WO2003016475-A2.
 PD 27-FEB-2003.

PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 8.0%; Score 146; DB 7; Length 1372;
 Best Local Similarity 26.7%; Pred. No. 0.021;
 RESULT 738
 ID ADD47529 standard; protein; 1372 AA.
 DE Rat Protein AD41775, SEQ ID NO 13225.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 8.0%; Score 146; DB 7; Length 1372;
 Best Local Similarity 26.7%; Pred. No. 0.021;
 RESULT 739
 ID AEG73577 standard; protein; 1389 AA.
 DE Thiol protease aleurain signal sequence/collagen alpha 2 fusion protein.
 PN WO2006035442-A2.
 PD 06-APR-2006.
 PA (COLL-) COLPLANT LTD.
 Query Match 8.0%; Score 146; DB 10; Length 1389;
 Best Local Similarity 27.0%; Pred. No. 0.021;
 RESULT 740
 ID AAE02537 standard; protein; 1466 AA.
 DE Porcine alpha1(III) collagen.
 PN WO200134647-A2.
 PD 17-MAY-2001.
 PA (FIBR-) FIBROGEN INC.
 Query Match 8.0%; Score 146; DB 4; Length 1466;
 Best Local Similarity 25.7%; Pred. No. 0.022;
 RESULT 741
 ID ADO36769 standard; protein; 361 AA.
 DE Murine LAST, SEQ ID 1.
 PN KR2003013970-A.
 PD 15-FEB-2003.
 PA (YUNY/) YUN Y D.
 Query Match 8.0%; Score 145.5; DB 7; Length 361;
 Best Local Similarity 25.3%; Pred. No. 0.0046;
 RESULT 742
 ID AD213217 standard; protein; 481 AA.
 DE Human cancer-associated protein #233.
 PN WO2005031001-A2.
 PD 07-APR-2005.
 PA (CHIR) CHIRON CORP.
 Query Match 8.0%; Score 145.5; DB 9; Length 481;
 Best Local Similarity 24.1%; Pred. No. 0.0064;
 RESULT 743
 ID ABM85681 standard; protein; 533 AA.
 DE Human protein sequence hCP44763.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 8.0%; Score 145.5; DB 7; Length 533;
 Best Local Similarity 24.1%; Pred. No. 0.0073;
 RESULT 744
 ID ADV42115 standard; protein; 914 AA.
 DE Fruitfly resilin homolog.
 PN WO2004104043-A1.
 PD 02-DEC-2004.
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 Query Match 8.0%; Score 145.5; DB 9; Length 914;
 Best Local Similarity 28.2%; Pred. No. 0.014;
 RESULT 745
 ID ADV44212 standard; protein; 914 AA.
 DE Drosophila resilin polypeptide #2.
 PN WO2004104042-A1.
 PD 02-DEC-2004.
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 Query Match 8.0%; Score 145.5; DB 9; Length 914;
 Best Local Similarity 28.2%; Pred. No. 0.014;
 RESULT 746
 ID ABB71513 standard; protein; 950 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 41331.
 PN WO200171042-A2.

PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 8.0%; Score 145.5; DB 4; Length 950;
 Best Local Similarity 28.2%; Pred. No. 0.015;
 RESULT 747
 ID AD213215 standard; protein; 1000 AA.
 DE Human cancer-associated protein #232.
 PN WO2005031001-A2.
 PD 07-APR-2005.
 PA (CHIR) CHIRON CORP.
 Query Match 8.0%; Score 145.5; DB 9; Length 1000;
 Best Local Similarity 24.1%; Pred. No. 0.015;
 RESULT 748
 ID AD213211 standard; protein; 1000 AA.
 DE Human cancer-associated protein #230.
 PN WO2005031001-A2.
 PD 07-APR-2005.
 PA (CHIR) CHIRON CORP.
 Query Match 8.0%; Score 145.5; DB 9; Length 1000;
 Best Local Similarity 24.1%; Pred. No. 0.015;
 RESULT 749
 ID ABM83254 standard; protein; 1359 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:3503.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 8.0%; Score 145.5; DB 8; Length 1359;
 Best Local Similarity 24.1%; Pred. No. 0.022;
 RESULT 750
 ID AD213205 standard; protein; 1374 AA.
 DE Human cancer-associated protein #227.
 PN WO2005031001-A2.
 PD 07-APR-2005.
 PA (CHIR) CHIRON CORP.
 Query Match 8.0%; Score 145.5; DB 9; Length 1374;
 Best Local Similarity 24.1%; Pred. No. 0.023;
 RESULT 751
 ID AD213209 standard; protein; 1388 AA.
 DE Human cancer-associated protein #229.
 PN WO2005031001-A2.
 PD 07-APR-2005.
 PA (CHIR) CHIRON CORP.
 Query Match 8.0%; Score 145.5; DB 9; Length 1388;
 Best Local Similarity 24.1%; Pred. No. 0.023;
 RESULT 752
 ID AD213207 standard; protein; 1388 AA.
 DE Human cancer-associated protein #228.
 PN WO2005031001-A2.
 PD 07-APR-2005.
 PA (CHIR) CHIRON CORP.
 Query Match 8.0%; Score 145.5; DB 9; Length 1388;
 Best Local Similarity 24.1%; Pred. No. 0.023;
 RESULT 753
 ID ABM83253 standard; protein; 1393 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:3502.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 8.0%; Score 145.5; DB 8; Length 1393;
 Best Local Similarity 24.1%; Pred. No. 0.023;
 RESULT 754
 ID ABB12028 standard; peptide; 1684 AA.
 DE Human dJ1042K10.4 homologue, SEQ ID NO:2398.
 PN WO200157188-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 8.0%; Score 145.5; DB 4; Length 1684;
 Best Local Similarity 19.9%; Pred. No. 0.029;
 RESULT 755
 ID AAM79579 standard; protein; 1684 AA.
 DE Human protein SEQ ID NO 3225.
 PN WO200157190-A2.
 PD 09-AUG-2001.

PA (HYSE-) HYSEQ INC.
Query Match 8.0%; Score 145.5; DB 4; Length 1684;
Best Local Similarity 19.9%; Pred. No. 0.029;
RESULT 756
ID AAB94740 standard; protein; 404 AA.
DE Human protein sequence SEQ ID NO:15782.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELT-) HELIX RES INST.
Query Match 7.9%; Score 144.5; DB 4; Length 404;
Best Local Similarity 25.2%; Pred. No. 0.0063;
RESULT 757
ID ADV99535 standard; protein; 508 AA.
DE Human soluble stimulator of endothelial proliferation, sSEP #1.
PN WO2004111085-A1.
PD 23-DEC-2004.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 7.9%; Score 144.5; DB 9; Length 508;
Best Local Similarity 25.2%; Pred. No. 0.0083;
RESULT 758
ID ADM43169 standard; protein; 508 AA.
DE Human soluble SEP (sSEP) protein fragment - SEQ ID 7.
PN WO2004111088-A2.
PD 23-DEC-2004.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 7.9%; Score 144.5; DB 9; Length 508;
Best Local Similarity 25.2%; Pred. No. 0.0083;
RESULT 759
ID ADV99546 standard; protein; 510 AA.
DE Human soluble stimulator of endothelial proliferation, sSEP #12.
PN WO2004111085-A1.
PD 23-DEC-2004.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 7.9%; Score 144.5; DB 9; Length 510;
Best Local Similarity 25.2%; Pred. No. 0.0083;
RESULT 760
ID ADM43180 standard; protein; 510 AA.
DE Human soluble SEP (sSEP) protein fragment - SEQ ID 18.
PN WO2004111088-A2.
PD 23-DEC-2004.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 7.9%; Score 144.5; DB 9; Length 510;
Best Local Similarity 25.2%; Pred. No. 0.0083;
RESULT 761
ID AAM39963 standard; protein; 540 AA.
DE Human polypeptide SEQ ID NO 3108.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.9%; Score 144.5; DB 4; Length 540;
Best Local Similarity 25.2%; Pred. No. 0.0089;
RESULT 762
ID ASP61508 standard; protein; 540 AA.
DE Human NF-kB activating protein SEQ ID NO 170.
PN WO200253737-A1.
PD 11-JUL-2002.
PA (ASAH) ASahi Kasei Kogyo KK.
Query Match 7.9%; Score 144.5; DB 5; Length 540;
Best Local Similarity 25.2%; Pred. No. 0.0089;
RESULT 763
ID ADC37213 standard; protein; 540 AA.
DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 46.
PN WO2003048202-A2.
PD 12-JUN-2003.
PA (ASAH) ASahi Kasei KK.
Query Match 7.9%; Score 144.5; DB 7; Length 540;
Best Local Similarity 25.2%; Pred. No. 0.0089;
RESULT 764
ID ADR89526 standard; protein; 540 AA.
DE Apoptosis-inducing protein, SEQ ID 50.
PN WO2004078112-A2.
PD 16-SEP-2004.
PA (ASAH-) ASahi Kasei Pharma Corp.

Query Match 7.9%; Score 144.5; DB 8; Length 540;
Best Local Similarity 25.2%; Pred. No. 0.0089;
RESULT 765
ID ADV99532 standard; protein; 540 AA.
DE Human membrane-bound stimulator of endothelial proliferation, SEP #1.
PN WO2004111085-A1.
PD 23-DEC-2004.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 7.9%; Score 144.5; DB 9; Length 540;
Best Local Similarity 25.2%; Pred. No. 0.0089;
RESULT 766
ID ADV99534 standard; protein; 540 AA.
DE Human membrane-bound stimulator of endothelial proliferation, SEP #2.
PN WO2004111085-A1.
PD 23-DEC-2004.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 7.9%; Score 144.5; DB 9; Length 540;
Best Local Similarity 25.2%; Pred. No. 0.0089;
RESULT 767
ID ADM43168 standard; protein; 540 AA.
DE Human membrane-bound angiogenic factor SEP protein - SEQ ID 6.
PN WO2004111088-A2.
PD 23-DEC-2004.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 7.9%; Score 144.5; DB 9; Length 540;
Best Local Similarity 25.2%; Pred. No. 0.0089;
RESULT 768
ID ADM43166 standard; protein; 540 AA.
DE Human membrane-bound angiogenic factor SEP protein - SEQ ID 4.
PN WO2004111088-A2.
PD 23-DEC-2004.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 7.9%; Score 144.5; DB 9; Length 540;
Best Local Similarity 25.2%; Pred. No. 0.0089;
RESULT 769
ID AAU33195 standard; protein; 2153 AA.
DE Novel human secreted protein #3686.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.9%; Score 144.5; DB 4; Length 2153;
Best Local Similarity 21.5%; Pred. No. 0.046;
RESULT 770
ID ADQ66000 standard; protein; 631 AA.
DE Novel human protein sequence #973.
PN EPI440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.9%; Score 143.5; DB 8; Length 631;
Best Local Similarity 24.4%; Pred. No. 0.013;
RESULT 771
ID AAB41839 standard; protein; 494 AA.
DE Human ORFX ORF1603 polypeptide sequence SEQ ID NO:3206.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 7.8%; Score 142.5; DB 3; Length 494;
Best Local Similarity 23.2%; Pred. No. 0.012;
RESULT 772
ID AEJ56558 standard; protein; 1735 AA.
DE Gene isolation method-related human protein - SEQ ID 1.
PN US20041115659-A1.
PD 17-JUN-2004.
PA (GEIG/) GEIGER B.
PA (KAMZ/) KAM Z.
PA (ZAMI/) ZAMIR E.
PA (BERS/) BERSHADSKY A.
PA (SHTU/) SHTUTMAN M.
PA (BENZ/) BEN-ZE'EV A.
Query Match 7.8%; Score 142.5; DB 5; Length 1735;
Best Local Similarity 22.9%; Pred. No. 0.052;
RESULT 773
ID ADE62371 standard; protein; 1735 AA.

DE Human Protein NP_072174, SEQ ID NO 8300.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 7.8%; Score 142.5; DB 7; Length 1735;
 Best Local Similarity 22.9%; Pred. No. 0.052;
 RESULT 774
 ID ADD46185 standard; protein; 1735 AA.
 DE Human Protein NP_072174, SEQ ID NO 11860.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 7.8%; Score 142.5; DB 7; Length 1735;
 Best Local Similarity 22.9%; Pred. No. 0.052;
 RESULT 775
 ID ADN05947 standard; protein; 1735 AA.
 DE Antipsoriatic protein sequence #1134.
 PN WO2004028479-A2.
 PD 08-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 7.8%; Score 142.5; DB 8; Length 1735;
 Best Local Similarity 22.9%; Pred. No. 0.052;
 RESULT 776
 ID ADQ07986 standard; protein; 1735 AA.
 DE Human tensin (TNS).
 PN WO2004061123-A2.
 PD 22-JUL-2004.
 PA (EXEL-) EXELIXIS INC.
 Query Match 7.8%; Score 142.5; DB 8; Length 1735;
 Best Local Similarity 22.9%; Pred. No. 0.052;
 RESULT 777
 ID ADP25231 standard; protein; 1735 AA.
 DE PRO polypeptide SEQ ID NO:2409.
 PN WO2004041170-A2.
 PD 21-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 7.8%; Score 142.5; DB 8; Length 1735;
 Best Local Similarity 22.9%; Pred. No. 0.052;
 RESULT 778
 ID AAY33497 standard; protein; 1185 AA.
 DE Human atrophin I protein.
 PN WO9945944-A1.
 PD 16-SEP-1999.
 PA (BURN-) BURNHAM INST.
 Query Match 7.8%; Score 142; DB 2; Length 1185;
 Best Local Similarity 23.8%; Pred. No. 0.036;
 RESULT 779
 ID ABB60516 standard; protein; 1190 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 8340.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 7.8%; Score 142; DB 4; Length 1190;
 Best Local Similarity 25.1%; Pred. No. 0.036;
 RESULT 780
 ID AEL95564 standard; protein; 1190 AA.
 DE Drosophila melanogaster survival essential protein, SEQ:456.
 PN US713558-B1.
 PD 14-NOV-2006.
 PA (APPL-) APPLERA CORP.
 Query Match 7.8%; Score 142; DB 11; Length 1190;
 Best Local Similarity 25.1%; Pred. No. 0.036;
 RESULT 781
 ID ADU20559 standard; protein; 1006 AA.
 DE A. thaliana Atlg15825 homologue #1.
 PN WO2004092349-A2.
 PD 28-OCT-2004.
 PA (BADI) BASF PLANT SCI GMBH.
 Query Match 7.8%; Score 141.5; DB 8; Length 1006;
 Best Local Similarity 26.4%; Pred. No. 0.032;
 RESULT 782

ID ADU20561 standard; protein; 1006 AA.
 DE A. thaliana Atlg15825 homologue #2.
 PN WO2004092349-A2.
 PD 28-OCT-2004.
 PA (BADI) BASF PLANT SCI GMBH.
 Query Match 7.8%; Score 141.5; DB 8; Length 1006;
 Best Local Similarity 26.4%; Pred. No. 0.032;
 RESULT 783
 ID ADJ70466 standard; protein; 1189 AA.
 DE Human heat mitochondrial protein as a therapeutic target SeqID2272.
 PN WO2003087768-A2.
 PD 23-OCT-2003.
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 Query Match 7.8%; Score 141.5; DB 7; Length 1189;
 Best Local Similarity 23.5%; Pred. No. 0.04;
 RESULT 784
 ID ABB62882 standard; protein; 362 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 15438.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 7.7%; Score 141; DB 4; Length 362;
 Best Local Similarity 23.2%; Pred. No. 0.01;
 RESULT 785
 ID AAR91204 standard; protein; 539 AA.
 DE Human BPGF-1.
 PN WO9604379-A1.
 PD 15-FEB-1996.
 PA (TEXA) UNIV TEXAS SYSTEM.
 Query Match 7.7%; Score 141; DB 2; Length 539;
 Best Local Similarity 24.0%; Pred. No. 0.017;
 RESULT 786
 ID ABB70499 standard; protein; 815 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 38289.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 7.7%; Score 141; DB 4; Length 815;
 Best Local Similarity 24.6%; Pred. No. 0.028;
 RESULT 787
 ID ABP54340 standard; protein; 815 AA.
 DE Drosophila melanogaster daughter of legless (Doll) protein SEQ ID NO:6.
 PN WO200277023-A2.
 PD 03-OCT-2002.
 PA (UYZU-) UNIV ZUERICH.
 Query Match 7.7%; Score 141; DB 6; Length 815;
 Best Local Similarity 24.6%; Pred. No. 0.028;
 RESULT 788
 ID AAW26328 standard; protein; 1288 AA.
 DE Mouse alpha-1 collagen (XVIII).
 PN US5643783-A.
 PD 01-JUL-1997.
 PA (HARD) HARVARD COLLEGE.
 Query Match 7.7%; Score 141; DB 2; Length 1288;
 Best Local Similarity 28.0%; Pred. No. 0.048;
 RESULT 789
 ID AAW92297 standard; peptide; 1288 AA.
 DE Mouse alpha-1 (XVIII) collagen chain common sequence MO18(common)28.
 PN WO9856399-A1.
 PD 17-DEC-1998.
 PA (FIBR-) FIBROGEN INC.
 PA (FIFI-) ACAD FINLAND.
 PA (INRM) INST NAT SANTE & RECH MEDICALE.
 Query Match 7.7%; Score 141; DB 2; Length 1288;
 Best Local Similarity 28.0%; Pred. No. 0.048;
 RESULT 790
 ID AB084585 standard; protein; 1315 AA.
 DE Mouse cancer-associated protein MPI7-008.2.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 7.7%; Score 141; DB 8; Length 1315;

Best Local Similarity 28.0%; Pred. No. 0.049;
RESULT 791
ID ADR16801 standard; protein; 1366 AA.
DE Human collagen I alpha2 (I) chain protein.
PN US2004151731-A1.
PD 05-AUG-2004.
PA (JICH/) JICHA D L.
Query Match 7.7%; Score 141; DB 8; Length 1366;
Best Local Similarity 27.0%; Pred. No. 0.051;
RESULT 792
ID ADR16426 standard; protein; 1366 AA.
DE Human collagen I alpha2 (I) chain protein.
PN US2004151732-A1.
PD 05-AUG-2004.
PA (JICH/) JICHA D L.
PA (PELU/) PELUSE S.
Query Match 7.7%; Score 141; DB 8; Length 1366;
Best Local Similarity 27.0%; Pred. No. 0.051;
RESULT 793
ID ADR99147 standard; protein; 1366 AA.
DE Collagen, type I, alpha 2, COL1A2, SEQ ID 153.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Query Match 7.7%; Score 141; DB 8; Length 1366;
Best Local Similarity 27.0%; Pred. No. 0.051;
RESULT 794
ID ABO84584 standard; protein; 1527 AA.
DE Mouse cancer-associated protein MP17-008.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 7.7%; Score 141; DB 8; Length 1527;
Best Local Similarity 28.0%; Pred. No. 0.058;
RESULT 795
ID ADM02023 standard; protein; 1740 AA.
DE Human MPTEN protein, eyelid/Osa protein.
PN WO2005002418-A2.
PD 13-JAN-2005.
PA (EXEL-) EXELIXIS INC.
Query Match 7.7%; Score 141; DB 9; Length 1740;
Best Local Similarity 27.1%; Pred. No. 0.068;
RESULT 796
ID ADJ69868 standard; protein; 2060 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1674.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 7.7%; Score 141; DB 7; Length 2060;
Best Local Similarity 21.3%; Pred. No. 0.084;
RESULT 797
ID AEM80768 standard; protein; 2145 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81398, SEQ:1980.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 141; DB 8; Length 2145;
Best Local Similarity 21.3%; Pred. No. 0.088;
RESULT 798
ID ADX06181 standard; protein; 2145 AA.
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 746.
PN WO2005012875-A2.
PD 10-FEB-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 7.7%; Score 141; DB 9; Length 2145;
Best Local Similarity 21.3%; Pred. No. 0.088;
RESULT 799
ID AEM80769 standard; protein; 2157 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81399, SEQ:1982.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.

Query Match 7.7%; Score 141; DB 8; Length 2157;
Best Local Similarity 21.3%; Pred. No. 0.088;
RESULT 800
ID ADX06183 standard; protein; 2157 AA.
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 748.
PN WO2005012875-A2.
PD 10-FEB-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 7.7%; Score 141; DB 9; Length 2157;
Best Local Similarity 21.3%; Pred. No. 0.088;
RESULT 801
ID AEG45646 standard; protein; 298 AA.
DE Fusion protein GST-9OR.
PN DE10204043782-A1.
PD 09-MAR-2006.
PA (UYDU-) UNIV DUESSELDORF-HEINRICH-HEINE.
Query Match 7.7%; Score 140.5; DB 10; Length 298;
Best Local Similarity 27.6%; Pred. No. 0.0091;
RESULT 802
ID ADM16778 standard; protein; 448 AA.
DE N. patriciarum xylanase #1.
PN US2004053238-A1.
PD 18-MAR-2004.
PA (HSEU/) HSEU R.
PA (HUAN/) HUANG Y.
Query Match 7.7%; Score 140.5; DB 8; Length 448;
Best Local Similarity 21.5%; Pred. No. 0.015;
RESULT 803
ID AAO30817 standard; protein; 478 AA.
DE Human cell adhesion and extracellular matrix protein (CADECM)-7.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.7%; Score 140.5; DB 7; Length 478;
Best Local Similarity 25.0%; Pred. No. 0.016;
RESULT 804
ID AAM41749 standard; protein; 484 AA.
DE Human polypeptide SEQ ID NO 6680.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.7%; Score 140.5; DB 4; Length 484;
Best Local Similarity 22.8%; Pred. No. 0.016;
RESULT 805
ID AAW65462 standard; protein; 485 AA.
DE Neocallimastix patriciarum endo-xylanase.
PN CA2190194-A.
PD 13-MAY-1998.
PA (LIUJ/) LIU J H.
PA (SELI/) SELINGER L B.
PA (MOLO/) MOLONEY M M.
PA (FORS/) FORSBERG C W.
PA (CHEN/) CHENG K.
PA (HUYU/) HU Y.
Query Match 7.7%; Score 140.5; DB 2; Length 485;
Best Local Similarity 21.5%; Pred. No. 0.016;
RESULT 806
ID AAY27283 standard; protein; 485 AA.
DE N. patriciarum xylanase.
PN US5948667-A.
PD 07-SEP-1999.
PA (MIAC) CANADA DEPT AGRICULTURE.
Query Match 7.7%; Score 140.5; DB 2; Length 485;
Best Local Similarity 21.5%; Pred. No. 0.016;
RESULT 807
ID AAB35588 standard; protein; 485 AA.
DE N. patriciarum endo-xylanase xynC.
PN US6137032-A.
PD 24-OCT-2000.
PA (MIAC) CANADA DEPT AGRICULTURE.
Query Match 7.7%; Score 140.5; DB 4; Length 485;
Best Local Similarity 21.5%; Pred. No. 0.016;
RESULT 808

ID ABM83255 standard; protein; 1178 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3504.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.7%; Score 140.5; DB 8; Length 1178;
Best Local Similarity 24.1%; Pred. No. 0.047;
RESULT 809
ID AAM78595 standard; protein; 1723 AA.
DE Human protein SEQ ID NO 1257.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.7%; Score 140.5; DB 4; Length 1723;
Best Local Similarity 20.0%; Pred. No. 0.074;
RESULT 810
ID AEF41874 standard; protein; 1723 AA.
DE Human modifier of IGF (MIGF) K1AA1093.
PN WO2006009947-A2.
PD 26-JAN-2006.
PA (EXEL-) EXELIXIS INC.
Query Match 7.7%; Score 140.5; DB 10; Length 1723;
Best Local Similarity 20.0%; Pred. No. 0.074;
RESULT 811
ID ADJ70007 standard; protein; 1727 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1813.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 7.7%; Score 140.5; DB 7; Length 1727;
Best Local Similarity 20.0%; Pred. No. 0.074;
RESULT 812
ID ADJ78498 standard; protein; 1727 AA.
DE K1AA1093 protein fragment for anti-cancer protein complex.
PN WO2004009619-A2.
PD 29-JAN-2004.
PA (CELL-) CELLZOME AG.
Query Match 7.7%; Score 140.5; DB 8; Length 1727;
Best Local Similarity 20.0%; Pred. No. 0.074;
RESULT 813
ID ADV99538 standard; protein; 232 AA.
DE Human soluble stimulator of endothelial proliferation, sSEP #4.
PN WO2004111085-A1.
PD 23-DEC-2004.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 7.7%; Score 140; DB 9; Length 232;
Best Local Similarity 25.1%; Pred. No. 0.0074;
RESULT 814
ID ADW43172 standard; protein; 232 AA.
DE Human soluble SEP (sSEP) protein fragment - SEQ ID 10.
PN WO2004111088-A2.
PD 23-DEC-2004.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 7.7%; Score 140; DB 9; Length 232;
Best Local Similarity 25.1%; Pred. No. 0.0074;
RESULT 815
ID ADV99537 standard; protein; 236 AA.
DE Human soluble stimulator of endothelial proliferation, sSEP #3.
PN WO2004111085-A1.
PD 23-DEC-2004.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 7.7%; Score 140; DB 9; Length 236;
Best Local Similarity 25.1%; Pred. No. 0.0075;
RESULT 816
ID ADW43171 standard; protein; 236 AA.
DE Human soluble SEP (sSEP) protein fragment - SEQ ID 9.
PN WO2004111088-A2.
PD 23-DEC-2004.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 7.7%; Score 140; DB 9; Length 236;
Best Local Similarity 25.1%; Pred. No. 0.0075;

ID ADV99536 standard; protein; 239 AA.
DE Human soluble stimulator of endothelial proliferation, sSEP #2.
PN WO2004111085-A1.
PD 23-DEC-2004.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 7.7%; Score 140; DB 9; Length 239;
Best Local Similarity 25.1%; Pred. No. 0.0076;
RESULT 818
ID ADW43170 standard; protein; 239 AA.
DE Human soluble SEP (sSEP) protein fragment - SEQ ID 8.
PN WO2004111088-A2.
PD 23-DEC-2004.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 7.7%; Score 140; DB 9; Length 239;
Best Local Similarity 25.1%; Pred. No. 0.0076;
RESULT 819
ID ADQ66121 standard; protein; 924 AA.
DE Novel human protein sequence #1094.
PN EPI440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.7%; Score 140; DB 8; Length 924;
Best Local Similarity 26.1%; Pred. No. 0.038;
RESULT 820
ID AAR86875 standard; protein; 623 AA.
DE Cancer suppressor transfer factor protein.
PN JP07289297-A.
PD 07-NOV-1995.
PA (EISA) EISAI CO LTD.
PA (GANK-) ZH GAN KENYUKAI.
Query Match 7.6%; Score 139.5; DB 2; Length 623;
Best Local Similarity 28.0%; Pred. No. 0.026;
RESULT 821
ID ADS11814 standard; protein; 363 AA.
DE Human therapeutic contig protein - SEQ ID 2051.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 7.6%; Score 139; DB 8; Length 363;
Best Local Similarity 25.1%; Pred. No. 0.015;
RESULT 822
ID ADC32833 standard; protein; 626 AA.
DE Human novel contig-encoded polypeptide sequence, SEQ ID NO:2915.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 7.6%; Score 139; DB 7; Length 626;
Best Local Similarity 24.3%; Pred. No. 0.029;
RESULT 823
ID ADQ39949 standard; protein; 1823 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1612.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.6%; Score 139; DB 8; Length 1823;
Best Local Similarity 21.5%; Pred. No. 0.1;
RESULT 824
ID ADQ39951 standard; protein; 2102 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1614.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.6%; Score 139; DB 8; Length 2102;
Best Local Similarity 21.5%; Pred. No. 0.12;
RESULT 825
ID ADQ39950 standard; protein; 2108 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1613.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.6%; Score 139; DB 8; Length 2108;
Best Local Similarity 21.5%; Pred. No. 0.12;
RESULT 826

ID ADQ39952 standard; protein; 2157 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1615.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.6%; Score 139; DB 8; Length 2157;
Best Local Similarity 21.5%; Pred. No. 0.13;
RESULT 827
ID AAY32202 standard; protein; 361 AA.
DE Human receptor molecule (REC) encoded by Incyte clone 2121924.
PN WO9957270-A2.
PD 11-NOV-1999.
PA (INCY-) INCYTE PHARM INC.
Query Match 7.6%; Score 138.5; DB 3; Length 361;
Best Local Similarity 25.7%; Pred. No. 0.016;
RESULT 828
ID ADE09337 standard; protein; 534 AA.
DE Novel protein-related contig polypeptide sequence #403.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 7.6%; Score 138.5; DB 7; Length 534;
Best Local Similarity 26.1%; Pred. No. 0.026;
RESULT 829
ID ADS12261 standard; protein; 534 AA.
DE Human therapeutic contig protein - SEQ ID 2498.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 7.6%; Score 138.5; DB 8; Length 534;
Best Local Similarity 26.1%; Pred. No. 0.026;
RESULT 830
ID ADZ85050 standard; protein; 1003 AA.
DE Full-length FHO5 interacting protein, SEQ ID 99.
PN US2005100966-A1.
PD 12-MAY-2005.
PA (SAXA/) SAKAMOTO T.
PA (TAKE/) TAKEDA S.
Query Match 7.6%; Score 138.5; DB 9; Length 1003;
Best Local Similarity 26.5%; Pred. No. 0.056;
RESULT 831
ID ABJ38695 standard; protein; 1902 AA.
DE Human nucleic acid-associated protein (NAAP) #25.
PN WO2003010329-A2.
PD 06-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.6%; Score 138.5; DB 6; Length 1902;
Best Local Similarity 20.9%; Pred. No. 0.12;
RESULT 832
ID ADM02024 standard; protein; 2285 AA.
DE Human MPTEN protein, SMARCF1.
PN WO2005002418-A2.
PD 13-JAN-2005.
PA (EXEL-) EXELIXIS INC.
Query Match 7.6%; Score 138.5; DB 9; Length 2285;
Best Local Similarity 20.9%; Pred. No. 0.15;
RESULT 833
ID AEB94379 standard; protein; 2285 AA.
DE Human SMT/SNF related/OSA-1 nuclear protein (AMBP-2), SEQ ID NO: 101.
PN US2005176662-A1.
PD 11-AUG-2005.
PA (UYMI-) UNIV MIAMI.
Query Match 7.6%; Score 138.5; DB 9; Length 2285;
Best Local Similarity 20.9%; Pred. No. 0.15;
RESULT 834
ID AAW40720 standard; protein; 408 AA.
DE Human polypeptide SEQ ID NO 5651.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.6%; Score 138; DB 4; Length 408;
Best Local Similarity 26.8%; Pred. No. 0.021;
RESULT 835
ID ADN21309 standard; protein; 639 AA.
DE Bacterial polypeptide #3962.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.6%; Score 138; DB 8; Length 639;
Best Local Similarity 24.2%; Pred. No. 0.036;
RESULT 836
ID AUA32115 standard; protein; 390 AA.
DE Novel human secreted protein #2606.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.5%; Score 137.5; DB 4; Length 390;
Best Local Similarity 25.7%; Pred. No. 0.022;
RESULT 837
ID ADZ13213 standard; protein; 826 AA.
DE Human cancer-associated protein #231.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR-) CHIRON CORP.
Query Match 7.5%; Score 137.5; DB 9; Length 826;
Best Local Similarity 23.4%; Pred. No. 0.053;
RESULT 838
ID AAR28916 standard; protein; 1196 AA.
DE Type III procollagen (prior art).
PN WO9219754-A1.
PD 12-NOV-1992.
PA (UYJE-) UNIV JEFFERSON THOMAS.
Query Match 7.5%; Score 137.5; DB 2; Length 1196;
Best Local Similarity 25.7%; Pred. No. 0.083;
RESULT 839
ID AAM39077 standard; protein; 1672 AA.
DE Human polypeptide SEQ ID NO 2222.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.5%; Score 137.5; DB 4; Length 1672;
Best Local Similarity 24.5%; Pred. No. 0.12;
RESULT 840
ID ADL35838 standard; protein; 368 AA.
DE Human single-stranded DNA binding protein-1 (SSBPl) protein.
PN WO2004019893-A2.
PD 11-MAR-2004.
PA (RIGE-) RIGEL PHARM INC.
Query Match 7.5%; Score 137; DB 8; Length 368;
Best Local Similarity 26.7%; Pred. No. 0.022;
RESULT 841
ID ARM80095 standard; protein; 368 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO80587, SEQ:240.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 7.5%; Score 137; DB 8; Length 368;
Best Local Similarity 26.7%; Pred. No. 0.022;
RESULT 842
ID ADF94310 standard; protein; 1071 AA.
DE Human collagen-like protein, SEQ ID 1.
PN WO2003106494-A1.
PD 24-DEC-2003.
PA (FAND/) FAN D.
Query Match 7.5%; Score 136.5; DB 7; Length 1071;
Best Local Similarity 29.5%; Pred. No. 0.087;
RESULT 843
ID ABB57334 standard; protein; 1669 AA.
DE Mouse ischaemic condition related protein sequence SEQ ID NO:933.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

Query Match 7.5%; Score 136.5; DB 5; Length 1669;
 Best Local Similarity 24.6%; Pred. No. 0.15;
 RESULT 844
 ID ADY25053 standard; protein; 510 AA.
 DE Plant full length insert polypeptide seqid 72837.
 PN US2004034888-A1.
 PD 19-FEB-2004.
 PA (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVU/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABR/) TABASKA J E.
 PA (CAOX/) CAO Y.
 Query Match 7.5%; Score 136; DB 8; Length 510;
 Best Local Similarity 20.7%; Pred. No. 0.039;
 RESULT 845
 ID ABG14126 standard; protein; 684 AA.
 DE Novel human diagnostic protein #14117.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 7.5%; Score 136; DB 4; Length 684;
 Best Local Similarity 23.7%; Pred. No. 0.056;
 RESULT 846
 ID AAE02534 standard; protein; 1466 AA.
 DE Bovine alpha1(III) collagen #2.
 PN WO200134647-A2.
 PD 17-MAY-2001.
 PA (FIBR-) FIBROGEN INC.
 Query Match 7.5%; Score 136; DB 4; Length 1466;
 Best Local Similarity 25.6%; Pred. No. 0.14;
 RESULT 847
 ID AAE02533 standard; protein; 1466 AA.
 DE Bovine alpha1(III) collagen #1.
 PN WO200134647-A2.
 PD 17-MAY-2001.
 PA (FIBR-) FIBROGEN INC.
 Query Match 7.5%; Score 136; DB 4; Length 1466;
 Best Local Similarity 25.6%; Pred. No. 0.14;
 RESULT 848
 ID ABG93944 standard; protein; 1496 AA.
 DE Human polypeptide orthologous to DACC-10.
 PN WO200264625-A1.
 PD 22-AUG-2002.
 PA (ADPP-) ADP PHARM PTY LTD.
 PA (UNSY) UNIV SYDNEY.
 Query Match 7.5%; Score 136; DB 5; Length 1496;
 Best Local Similarity 26.6%; Pred. No. 0.14;
 RESULT 849
 ID ABR47419 standard; protein; 1496 AA.
 DE Breast cancer associated protein sequence SEQ ID NO:70.
 PN WO2003004989-A2.
 PD 16-JAN-2003.
 PA (MILL-) MILLENIUM PHARM INC.
 Query Match 7.5%; Score 136; DB 6; Length 1496;
 Best Local Similarity 26.6%; Pred. No. 0.14;
 RESULT 850
 ID ADB70382 standard; protein; 1496 AA.
 DE Procollagen alpha 2(V) SEQ ID NO:74.
 PN WO2003021229-A2.
 PD 13-MAR-2003.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 Query Match 7.5%; Score 136; DB 7; Length 1496;
 Best Local Similarity 26.6%; Pred. No. 0.14;
 RESULT 851
 ID ADE61180 standard; protein; 1496 AA.
 DE Human Protein NP_000384, SEQ ID NO 7098.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 7.5%; Score 136; DB 7; Length 1496;
 Best Local Similarity 26.6%; Pred. No. 0.14;

RESULT 852
 ID ADP65253 standard; protein; 1496 AA.
 DE Human alpha 2 type V collagen preproprotein, collagen V, alpha-2.
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match 7.5%; Score 136; DB 7; Length 1496;
 Best Local Similarity 26.6%; Pred. No. 0.14;
 RESULT 853
 ID ADJ37161 standard; protein; 1496 AA.
 DE Human malignant pleural mesothelioma (MPM) protein #33.
 PN US2003219760-A1.
 PD 27-NOV-2003.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 Query Match 7.5%; Score 136; DB 8; Length 1496;
 Best Local Similarity 26.6%; Pred. No. 0.14;
 RESULT 854
 ID ADR9242 standard; protein; 1496 AA.
 DE Collagen, type V, alpha 2, COL5A2, SEQ ID 248.
 PN WO2004078035-A2.
 PD 16-SEP-2004.
 PA (FARB) BAYER PHARM CORP.
 Query Match 7.5%; Score 136; DB 8; Length 1496;
 Best Local Similarity 26.6%; Pred. No. 0.14;
 RESULT 855
 ID ADZ09865 standard; protein; 1496 AA.
 DE Human breast cancer marker COL5A2 protein.
 PN EP1522594-A2.
 PD 13-APR-2005.
 PA (FARB) BAYER HEALTHCARE AG.
 Query Match 7.5%; Score 136; DB 9; Length 1496;
 Best Local Similarity 26.6%; Pred. No. 0.14;
 RESULT 856
 ID AEA04459 standard; protein; 1496 AA.
 DE Human protein from gene overexpressed in cancer, COL5A2.
 PN WO2005044990-A2.
 PD 19-MAY-2005.
 PA (FARB) BAYER HEALTHCARE LLC.
 Query Match 7.5%; Score 136; DB 9; Length 1496;
 Best Local Similarity 26.6%; Pred. No. 0.14;
 RESULT 857
 ID AAG50494 standard; protein; 1559 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 63997.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 7.5%; Score 136; DB 3; Length 1559;
 Best Local Similarity 20.7%; Pred. No. 0.15;
 RESULT 858
 ID AAG50493 standard; protein; 1596 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 63996.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 7.5%; Score 136; DB 3; Length 1596;
 Best Local Similarity 20.7%; Pred. No. 0.15;
 RESULT 859
 ID AAG50492 standard; protein; 1752 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 63995.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 7.5%; Score 136; DB 3; Length 1752;
 Best Local Similarity 20.7%; Pred. No. 0.17;
 RESULT 860
 ID ABO14694 standard; protein; 494 AA.
 DE Novel human protein #67.
 PN WO2003023002-A2.
 PD 20-MAR-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 7.4%; Score 135.5; DB 6; Length 494;
 Best Local Similarity 27.3%; Pred. No. 0.041;
 RESULT 861
 ID AAB42049 standard; protein; 551 AA.
 DE Human ORFX ORF1813 polypeptide sequence SEQ ID NO:3626.

PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 7.4%; Score 135.5; DB 3; Length 551;
Best Local Similarity 27.3%; Pred. No. 0.047;
RESULT 862
ID ABO14693 standard; protein; 551 AA.
DE Novel human protein #66.
PN WO2003023002-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 7.4%; Score 135.5; DB 6; Length 551;
Best Local Similarity 27.3%; Pred. No. 0.047;
RESULT 863
ID ABM82177 standard; protein; 551 AA.
DE Tumour-associated antigenic target (TAR) polypeptide PRO83099, SEQ:5618.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 135.5; DB 8; Length 551;
Best Local Similarity 27.3%; Pred. No. 0.047;
RESULT 864
ID AAB24234 standard; protein; 576 AA.
DE Human vesicle associated protein 13 SEQ ID NO:13.
PN WO200060082-A2.
PD 12-OCT-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 7.4%; Score 135.5; DB 3; Length 576;
Best Local Similarity 27.3%; Pred. No. 0.05;
RESULT 865
ID AAB95100 standard; protein; 576 AA.
DE Human protein sequence SEQ ID NO:17064.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 7.4%; Score 135.5; DB 4; Length 576;
Best Local Similarity 27.3%; Pred. No. 0.05;
RESULT 866
ID ADC31465 standard; protein; 806 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1547.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 7.4%; Score 135.5; DB 7; Length 806;
Best Local Similarity 26.4%; Pred. No. 0.074;
RESULT 867
ID ABR82254 standard; protein; 1786 AA.
DE Human nucleic acid-associated protein (NAAP)-Id 3056408CD1.
PN WO2003052048-A2.
PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.4%; Score 135.5; DB 6; Length 1786;
Best Local Similarity 26.4%; Pred. No. 0.19;
RESULT 868
ID ABR58606 standard; protein; 1030 AA.
DE Human cancer related protein SEQ ID NO:263.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 7.4%; Score 135; DB 6; Length 1030;
Best Local Similarity 23.4%; Pred. No. 0.11;
RESULT 869
ID ADF55479 standard; protein; 1070 AA.
DE Human novel polypeptide #43.
PN JP2003245081-A.
PD 02-SEP-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 7.4%; Score 135; DB 7; Length 1070;
Best Local Similarity 23.4%; Pred. No. 0.11;
RESULT 870
ID AEE72798 standard; protein; 1070 AA.
DE Novel human protein amino acid sequence - SEQ ID 60.
PN JP2003116575-A.
PD 22-APR-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 7.4%; Score 135; DB 7; Length 1070;
Best Local Similarity 23.4%; Pred. No. 0.11;
RESULT 871
ID AAE02536 standard; protein; 1366 AA.
DE Porcine alpha2(I) collagen.
PN WO200134647-A2.
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match 7.4%; Score 135; DB 4; Length 1366;
Best Local Similarity 26.6%; Pred. No. 0.15;
RESULT 872
ID ADT07495 standard; protein; 690 AA.
DE Human colon-specific polypeptide (CSP) #12.
PN WO2004089301-A2.
PD 21-OCT-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 7.4%; Score 134.5; DB 8; Length 690;
Best Local Similarity 23.7%; Pred. No. 0.074;
RESULT 873
ID AAB71230 standard; protein; 1115 AA.
DE Human legless homologue hlgs-1 partial protein.
PN US2002086986-A1.
PD 04-JUL-2002.
PA (BASL/) BASLER K.
PA (BRUN/) BRUNNER E.
PA (FROE/) FROESCH B.
PA (KRAM/) KRAMPS T.
PA (PETE/) PETER O.
Query Match 7.4%; Score 134.5; DB 5; Length 1115;
Best Local Similarity 25.4%; Pred. No. 0.13;
RESULT 874
ID ABW01535 standard; protein; 1115 AA.
DE Human lgs-1 protein.
PN US2003114413-A1.
PD 19-JUN-2003.
PA (UYZU-) UNIV ZURICH.
Query Match 7.4%; Score 134.5; DB 7; Length 1115;
Best Local Similarity 25.4%; Pred. No. 0.13;
RESULT 875
ID ADJ71905 standard; protein; 1115 AA.
DE Human lgs/Bcl9 partial polypeptide.
PN US2004038901-A1.
PD 26-FEB-2004.
PA (UYZU-) UNIV ZURICH.
Query Match 7.4%; Score 134.5; DB 8; Length 1115;
Best Local Similarity 25.4%; Pred. No. 0.13;
RESULT 876
ID ABB65293 standard; protein; 1192 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 22671.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.4%; Score 134.5; DB 4; Length 1192;
Best Local Similarity 25.9%; Pred. No. 0.14;
RESULT 877
ID ABG93945 standard; protein; 1497 AA.
DE Mouse polypeptide orthologous to DACC-10.
PN WO200264625-A1.
PD 22-AUG-2002.
PA (ADPP-) ADP PHARM PTY LTD.
PA (UNSY) UNIV SYDNEY.
Query Match 7.4%; Score 134.5; DB 5; Length 1497;
Best Local Similarity 25.9%; Pred. No. 0.19;
RESULT 878
ID ADN17284 standard; protein; 262 AA.
DE Chicken galectin-3 protein.
PN US2004071684-A1.
PD 15-APR-2004.
PA (PANJ/) PANJWANI N.
PA (CAOZ/) CAO Z.
Query Match 7.3%; Score 134; DB 8; Length 262;

Best Local Similarity 25.5%; Pred. No. 0.026;
 RESULT 879
 ID AEF80637 standard; protein; 262 AA.
 DE Chicken galectin-3.
 PN US2006035817-A1.
 PD 16-FEB-2006.
 PA (TUFT) TUFTS COLLEGE.
 Query Match 7.3%; Score 134; DB 10; Length 262;
 Best Local Similarity 25.5%; Pred. No. 0.026;
 RESULT 880
 ID ADV42114 standard; protein; 314 AA.
 DE Honey bee resilin homolog SEQ ID NO 6.
 PN WO2004104043-A1.
 PD 02-DEC-2004.
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 Query Match 7.3%; Score 134; DB 9; Length 314;
 Best Local Similarity 24.6%; Pred. No. 0.032;
 RESULT 881
 ID ADV44211 standard; protein; 314 AA.
 DE Honey bee resilin polypeptide #2.
 PN WO2004104042-A1.
 PD 02-DEC-2004.
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 Query Match 7.3%; Score 134; DB 9; Length 314;
 Best Local Similarity 24.6%; Pred. No. 0.032;
 RESULT 882
 ID ABP54344 standard; protein; 406 AA.
 DE Mouse daughter of legless (Doll) mDoll-2 protein SEQ ID NO:10.
 PN WO200277023-A2.
 PD 03-OCT-2002.
 PA (UYZU) UNIV ZUERICH.
 Query Match 7.3%; Score 134; DB 6; Length 406;
 Best Local Similarity 22.4%; Pred. No. 0.043;
 RESULT 883
 ID ABO84441 standard; protein; 842 AA.
 DE Mouse cancer-associated protein MP7-221.1.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 7.3%; Score 134; DB 8; Length 842;
 Best Local Similarity 23.4%; Pred. No. 0.1;
 RESULT 884
 ID ADQ39813 standard; protein; 1767 AA.
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1476.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 7.3%; Score 134; DB 8; Length 1767;
 Best Local Similarity 26.3%; Pred. No. 0.25;
 RESULT 885
 ID ADQ39817 standard; protein; 1767 AA.
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1480.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 7.3%; Score 134; DB 8; Length 1767;
 Best Local Similarity 26.3%; Pred. No. 0.25;
 RESULT 886
 ID AEL75482 standard; protein; 1767 AA.
 DE Human collagen XI alpha 1, SEQ ID NO: 50.
 PN KR2005092659-A.
 PD 22-SEP-2005.
 PA (UYKY-) UNIV KYUNGPOOK NAT IND ACADEMIC COOP.
 Query Match 7.3%; Score 134; DB 10; Length 1767;
 Best Local Similarity 26.3%; Pred. No. 0.25;
 RESULT 887
 ID AAU84266 standard; protein; 1806 AA.
 DE Human endometrial cancer related protein, COL11A1.
 PN WO200209573-A2.
 PD 07-FEB-2002.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 Query Match 7.3%; Score 134; DB 5; Length 1806;
 Best Local Similarity 26.3%; Pred. No. 0.26;

RESULT 888
 ID ABJ05596 standard; protein; 1806 AA.
 DE Breast cancer-associated protein 61.
 PN WO200259377-A2.
 PD 01-AUG-2002.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 7.3%; Score 134; DB 5; Length 1806;
 Best Local Similarity 26.3%; Pred. No. 0.26;
 RESULT 889
 ID ABR58545 standard; protein; 1806 AA.
 DE Human cancer related protein SEQ ID NO:202.
 PN WO2003025138-A2.
 PD 27-MAR-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 7.3%; Score 134; DB 6; Length 1806;
 Best Local Similarity 26.3%; Pred. No. 0.26;
 RESULT 890
 ID ABU56581 standard; protein; 1806 AA.
 DE Lung cancer-associated polypeptide #174.
 PN WO200286443-A2.
 PD 31-OCT-2002.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 7.3%; Score 134; DB 6; Length 1806;
 Best Local Similarity 26.3%; Pred. No. 0.26;
 RESULT 891
 ID ADP65251 standard; protein; 1806 AA.
 DE Human alpha 1 type XI collagen, isoform A preproprotein.
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match 7.3%; Score 134; DB 7; Length 1806;
 Best Local Similarity 26.3%; Pred. No. 0.26;
 RESULT 892
 ID ADQ39816 standard; protein; 1806 AA.
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1479.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 7.3%; Score 134; DB 8; Length 1806;
 Best Local Similarity 26.3%; Pred. No. 0.26;
 RESULT 893
 ID ADQ39815 standard; protein; 1806 AA.
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1478.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 7.3%; Score 134; DB 8; Length 1806;
 Best Local Similarity 26.3%; Pred. No. 0.26;
 RESULT 894
 ID ADZ09764 standard; protein; 1806 AA.
 DE Human breast cancer marker COL11A1 protein.
 PN EPI522594-A2.
 PD 13-APR-2005.
 PA (FARB) BAYER HEALTHCARE AG.
 Query Match 7.3%; Score 134; DB 9; Length 1806;
 Best Local Similarity 26.3%; Pred. No. 0.26;
 RESULT 895
 ID AEC04181 standard; protein; 1806 AA.
 DE Human breast cancer marker protein SEQ ID NO 348.
 PN WO2005072050-A2.
 PD 11-AUG-2005.
 PA (COMP-) COMPUGEN USA INC.
 Query Match 7.3%; Score 134; DB 9; Length 1806;
 Best Local Similarity 26.3%; Pred. No. 0.26;
 RESULT 896
 ID AEC04182 standard; protein; 1806 AA.
 DE Human breast cancer marker protein SEQ ID NO 349.
 PN WO2005072050-A2.
 PD 11-AUG-2005.
 PA (COMP-) COMPUGEN USA INC.
 Query Match 7.3%; Score 134; DB 9; Length 1806;
 Best Local Similarity 26.3%; Pred. No. 0.26;
 RESULT 897

ID AEC79074 standard; protein; 1806 AA.
DE Human collagen alpha 1, CA1B.
PN WO2005072053-A2.
PD 11-AUG-2005.
PA (COMP-) COMPUGEN LTD. 7.3%; Score 134; DB 9; Length 1806;
Best Local Similarity 26.3%; Pred. No. 0.26;
Query Match
RESULT 898
ID AEC79075 standard; protein; 1806 AA.
DE Human collagen alpha 1, CA1B V5.
PN WO2005072053-A2.
PD 11-AUG-2005.
PA (COMP-) COMPUGEN LTD. 7.3%; Score 134; DB 9; Length 1806;
Best Local Similarity 26.3%; Pred. No. 0.26;
Query Match
RESULT 899
ID AEG12882 standard; protein; 1806 AA.
DE Human collagen alpha 1 protein.
PN US2006046257-A1.
PD 02-MAR-2006.
PA (POLL/) POLLOCK S.
PA (LEVI/) LEVINE Z.
PA (NOVI/) NOVIK A.
PA (DARA/) DAHARY D.
PA (SORE/) SOREK R.
PA (TOPO/) TOPORIK A.
PA (SAME/) SAMEAH-GREENWALD S.
PA (SELL/) SELLA-TAVOR O.
PA (DIBE/) DIBER A.
PA (COJO/) COJOCARU G S.
PA (AYAL/) AYALON-SOFFER M.
PA (WALA/) WALACH S.
PA (AKIV/) AKIVA P.
PA (KERE/) KEREN N.
PA (SHEM/) SHEMESH R.
Query Match
Best Local Similarity 7.3%; Score 134; DB 10; Length 1806;
Best Local Similarity 26.3%; Pred. No. 0.26;
ID AEG12883 standard; protein; 1806 AA.
DE Human collagen alpha 1 protein V5.
PN US2006046257-A1.
PD 02-MAR-2006.
PA (POLL/) POLLOCK S.
PA (LEVI/) LEVINE Z.
PA (NOVI/) NOVIK A.
PA (DARA/) DAHARY D.
PA (SORE/) SOREK R.
PA (TOPO/) TOPORIK A.
PA (SAME/) SAMEAH-GREENWALD S.
PA (SELL/) SELLA-TAVOR O.
PA (DIBE/) DIBER A.
PA (COJO/) COJOCARU G S.
PA (AYAL/) AYALON-SOFFER M.
PA (WALA/) WALACH S.
PA (AKIV/) AKIVA P.
PA (KERE/) KEREN N.
PA (SHEM/) SHEMESH R.
Query Match
Best Local Similarity 7.3%; Score 134; DB 10; Length 1806;
Best Local Similarity 26.3%; Pred. No. 0.26;
ID ADQ39812 standard; protein; 1818 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1475.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP. 7.3%; Score 134; DB 8; Length 1818;
Best Local Similarity 26.3%; Pred. No. 0.26;
Query Match
RESULT 902
ID ADQ39814 standard; protein; 1818 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1477.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.

Query Match 7.3%; Score 134; DB 8; Length 1818;
Best Local Similarity 26.3%; Pred. No. 0.26;
RESULT 903
ID ABR58607 standard; protein; 616 AA.
DE Human cancer related protein SEQ ID NO:264.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 7.3%; Score 133.5; DB 6; Length 616;
Best Local Similarity 22.5%; Pred. No. 0.078;
RESULT 904
ID ADG42171 standard; protein; 624 AA.
DE Human brain/hippocampus polypeptide #19.
PN JF2002330794-A.
PD 19-NOV-2002.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 7.3%; Score 133.5; DB 7; Length 624;
Best Local Similarity 22.5%; Pred. No. 0.079;
RESULT 905
ID ADJ69967 standard; protein; 624 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1773.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 7.3%; Score 133.5; DB 7; Length 624;
Best Local Similarity 22.5%; Pred. No. 0.079;
RESULT 906
ID AAG91922 standard; protein; 1004 AA.
DE C glutamicum protein fragment SEQ ID NO: 5676.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 7.3%; Score 133.5; DB 4; Length 1004;
Best Local Similarity 23.3%; Pred. No. 0.14;
RESULT 907
ID ABO68795 standard; protein; 332 AA.
DE Pseudomonas aeruginosa polypeptide #970.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 7.3%; Score 133; DB 7; Length 332;
Best Local Similarity 26.9%; Pred. No. 0.041;
RESULT 908
ID ADA55521 standard; protein; 404 AA.
DE Human protein, SEQ ID 3089.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.3%; Score 133; DB 6; Length 404;
Best Local Similarity 24.0%; Pred. No. 0.051;
RESULT 909
ID ABG14285 standard; protein; 489 AA.
DE Novel human diagnostic protein #14276.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.3%; Score 133; DB 4; Length 489;
Best Local Similarity 26.0%; Pred. No. 0.065;
RESULT 910
ID ABG14111 standard; protein; 547 AA.
DE Novel human diagnostic protein #14102.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.3%; Score 133; DB 4; Length 547;
Best Local Similarity 26.4%; Pred. No. 0.074;
RESULT 911
ID ADE87051 standard; protein; 1536 AA.
DE Human pancreatic cell protein sequence SeqID511.
PN WO2003060145-A2.
PD 24-JUL-2003.

PA (DIAD-) DIADEXUS INC. 7.3%; Score 133; DB 7; Length 1536;
 Query Match 25.3%; Pred. No. 0.25;
 RESULT 912
 ID AAM23916 standard; protein; 1690 AA.
 DE Human EST encoded protein SEQ ID NO: 1441.
 PN WO200154477-A2.
 PD 02-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 7.3%; Score 133; DB 4; Length 1690;
 Best Local Similarity 25.7%; Pred. No. 0.29;
 RESULT 913
 ID AAR21707 standard; protein; 338 AA.
 DE HSV-1 (MGH-10) ICP34.5.
 PN WO2004050-A.
 PD 19-MAR-1992.
 PA (ROI2/) ROI2MAN B.
 Query Match 7.3%; Score 132.5; DB 2; Length 338;
 Best Local Similarity 26.3%; Pred. No. 0.046;
 RESULT 914
 ID AAU10544 standard; protein; 704 AA.
 DE Rat synapsin 1A (YSG8) polypeptide.
 PN WO200175440-A2.
 PD 11-OCT-2001.
 PA (WELF-) WELFIDE CORP.
 Query Match 7.3%; Score 132.5; DB 5; Length 704;
 Best Local Similarity 22.3%; Pred. No. 0.11;
 RESULT 915
 ID ADE57712 standard; protein; 704 AA.
 DE Rat Protein P09951, SEQ ID NO 3575.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 7.3%; Score 132.5; DB 7; Length 704;
 Best Local Similarity 22.3%; Pred. No. 0.11;
 RESULT 916
 ID ABB71759 standard; protein; 2061 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 42069.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 7.3%; Score 132.5; DB 4; Length 2061;
 Best Local Similarity 21.6%; Pred. No. 0.4;
 RESULT 917
 ID ADL61309 standard; protein; 417 AA.
 DE Human protein tyrosine kinase biomarker iroquois homeobox protein 5.
 PN WO2004020583-A2.
 PD 11-MAR-2004.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match 7.2%; Score 132; DB 8; Length 417;
 Best Local Similarity 26.4%; Pred. No. 0.064;
 RESULT 918
 ID ADQ21366 standard; protein; 417 AA.
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4186.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 7.2%; Score 132; DB 8; Length 417;
 Best Local Similarity 26.4%; Pred. No. 0.064;
 RESULT 919
 ID ADQ16005 standard; protein; 417 AA.
 DE Human Irx-2 splice variant Irx-2A.
 PN WO2004060302-A2.
 PD 22-JUL-2004.
 PA (CEMI-) CEMINES LLC.
 Query Match 7.2%; Score 132; DB 8; Length 417;
 Best Local Similarity 26.4%; Pred. No. 0.064;
 RESULT 920
 ID ADF94875 standard; protein; 458 AA.
 DE Human gene 2-encoded ACRP30-like protein, SEQ ID NO:78.
 PN WO2003031586-A2.
 PD 17-APR-2003.

PA (HUMA-) HUMAN GENOME SCI INC.
 PA (BLON/) BLONDEL O.
 PA (RUBE/) RUBEN S M.
 Query Match 7.2%; Score 132; DB 7; Length 458;
 Best Local Similarity 24.5%; Pred. No. 0.072;
 RESULT 921
 ID ADB65210 standard; protein; 652 AA.
 DE Human protein encoded by clone TEST110000190.
 PN EPI308459-A2.
 PD 07-MAY-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 7.2%; Score 132; DB 7; Length 652;
 Best Local Similarity 24.0%; Pred. No. 0.11;
 RESULT 922
 ID ADJ69477 standard; protein; 2161 AA.
 DE Human heat mitochondrial protein as a therapeutic target SeqID1283.
 PN WO2003087768-A2.
 PD 23-OCT-2003.
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 Query Match 7.2%; Score 132; DB 7; Length 2161;
 Best Local Similarity 27.2%; Pred. No. 0.46;
 RESULT 923
 ID ADX98562 standard; protein; 2161 AA.
 DE Human SH3 and multiple ankyrin repeat domains 1 (SHANK1) protein.
 PN WO2005017121-A2.
 PD 24-FEB-2005.
 PA (EXEL-) EXELIXIS INC.
 Query Match 7.2%; Score 132; DB 9; Length 2161;
 Best Local Similarity 27.2%; Pred. No. 0.46;
 RESULT 924
 ID ABP76680 standard; protein; 19938 AA.
 DE Streptomyces viridochromogenes Avi gene cluster polypeptide frame 4.
 PN WO200268436-A1.
 PD 06-SEP-2002.
 PA (COMB-) COMBINATURE BIOPHARM AG.
 Query Match 7.2%; Score 132; DB 6; Length 19938;
 Best Local Similarity 22.2%; Pred. No. 6.5;
 RESULT 925
 ID AEG04840 standard; protein; 547 AA.
 DE Novel human diagnostic protein #4831.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 7.2%; Score 131.5; DB 4; Length 547;
 Best Local Similarity 25.3%; Pred. No. 0.097;
 RESULT 926
 ID AEL57499 standard; protein; 960 AA.
 DE Human collagen alpha 3(IV) chain precursor, SEQ ID NO: 1962.
 PN US2006216722-A1.
 PD 28-SEP-2006.
 PA (BETS/) BETSHOLTZ C.
 PA (TRYG/) TRYGGVASON K.
 PA (TAKE/) TAKEMOTO M.
 PA (HELL/) HE L.
 PA (PATR/) PATRAKKAS J.
 Query Match 7.2%; Score 131.5; DB 10; Length 960;
 Best Local Similarity 25.1%; Pred. No. 0.19;
 RESULT 927
 ID ABP69842 standard; protein; 1419 AA.
 DE Human polypeptide SEQ ID NO 1889.
 PN WO200270539-A2.
 PD 12-SEP-2002.
 PA (HYSE-) HYSEQ INC.
 Query Match 7.2%; Score 131.5; DB 5; Length 1419;
 Best Local Similarity 18.6%; Pred. No. 0.3;
 RESULT 928
 ID ABP69841 standard; protein; 1477 AA.
 DE Human polypeptide SEQ ID NO 1888.
 PN WO200270539-A2.
 PD 12-SEP-2002.
 PA (HYSE-) HYSEQ INC.

Query Match 7.2%; Score 131.5; DB 5; Length 1477;
 Best Local Similarity 18.6%; Pred. No. 0.32;
 RESULT 929
 ID AAE37932 standard; protein; 1488 AA.
 DE Human CGDD-21 protein.
 PN WO2003050253-A2.
 PD 19-JUN-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 7.2%; Score 131.5; DB 7; Length 1488;
 Best Local Similarity 18.6%; Pred. No. 0.32;
 RESULT 930
 ID ABP69840 standard; protein; 1516 AA.
 DE Human polypeptide SEQ ID NO 1887.
 PN WO200270539-A2.
 PD 12-SEP-2002.
 PA (HYSE-) HYSEQ INC.
 Query Match 7.2%; Score 131.5; DB 5; Length 1516;
 Best Local Similarity 18.6%; Pred. No. 0.33;
 RESULT 931
 ID AEF41875 standard; protein; 1690 AA.
 DE Human modifier of IGF (MIGF) KIAA1582.
 PN WO2006009947-A2.
 PD 26-JAN-2006.
 PA (EXEL-) EXELIXIS INC.
 Query Match 7.2%; Score 131.5; DB 10; Length 1690;
 Best Local Similarity 18.6%; Pred. No. 0.38;
 RESULT 932
 ID ADT71535 standard; protein; 1905 AA.
 DE Human CGDD polypeptide 7525307CD1, seq id 9.
 PN WO2004085625-A2.
 PD 07-OCT-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 7.2%; Score 131.5; DB 8; Length 1905;
 Best Local Similarity 18.6%; Pred. No. 0.43;
 RESULT 933
 ID ABB62231 standard; protein; 2441 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 13485.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 7.2%; Score 131.5; DB 4; Length 2441;
 Best Local Similarity 22.6%; Pred. No. 0.58;
 RESULT 934
 ID ADF69307 standard; protein; 553 AA.
 DE Human lung specific protein sequence SEQ ID NO:64.
 PN WO2003102137-A2.
 PD 11-DEC-2003.
 PA (DIAD-) DIADEXUS INC.
 Query Match 7.2%; Score 131; DB 8; Length 553;
 Best Local Similarity 26.7%; Pred. No. 0.11;
 RESULT 935
 ID AEB04222 standard; protein; 585 AA.
 DE Human KSRP protein127 to 711 SEQ ID NO:3.
 PN WO2005054181-A1.
 PD 16-JUN-2005.
 PA (REVE-) REVERSE PROTEOMICS RES INST CO LTD.
 Query Match 7.2%; Score 131; DB 9; Length 585;
 Best Local Similarity 23.2%; Pred. No. 0.12;
 RESULT 936
 ID AEB04221 standard; protein; 711 AA.
 DE Tumour-associated antigenic target (TAT) polypeptide PRO82910, SEQ:5204.
 PN WO2004030615-A2.
 PD 15-APR-2004.
 PA (GETH-) GENENTECH INC.
 Query Match 7.2%; Score 131; DB 8; Length 711;
 Best Local Similarity 23.2%; Pred. No. 0.15;
 RESULT 937
 ID AEB04221 standard; protein; 711 AA.
 DE Human KSRP protein SEQ ID NO:2.
 PN WO2005054181-A1.
 PD 16-JUN-2005.
 PA (REVE-) REVERSE PROTEOMICS RES INST CO LTD.
 Query Match 7.2%; Score 131; DB 9; Length 711;

Best Local Similarity 23.2%; Pred. No. 0.15;
 RESULT 938
 ID ADZ21366 standard; protein; 734 AA.
 DE Androgen receptor.
 PN WO2005033291-A2.
 PD 14-APR-2005.
 PA (UYRP) UNIV ROCHESTER.
 Query Match 7.2%; Score 131; DB 9; Length 734;
 Best Local Similarity 25.8%; Pred. No. 0.15;
 RESULT 939
 ID ADT02206 standard; protein; 902 AA.
 DE Variant human androgen receptor protein - SEQ ID 3.
 PN JP2004254600-A.
 PD 16-SEP-2004.
 PA (SUMO) SUMITOMO CHEM CO LTD.
 Query Match 7.2%; Score 131; DB 8; Length 902;
 Best Local Similarity 25.8%; Pred. No. 0.19;
 RESULT 940
 ID AAY33491 standard; protein; 918 AA.
 DE Human androgen receptor protein.
 PN WO9945944-A1.
 PD 16-SEP-1999.
 PA (BURN-) BURNHAM INST.
 Query Match 7.2%; Score 131; DB 2; Length 918;
 Best Local Similarity 25.8%; Pred. No. 0.2;
 RESULT 941
 ID ABR82983 standard; protein; 918 AA.
 DE Human androgen receptor polypeptide.
 PN WO2003072700-A2.
 PD 04-SEP-2003.
 PA (PFIZ) PFIZER PROD INC.
 Query Match 7.2%; Score 131; DB 7; Length 918;
 Best Local Similarity 25.8%; Pred. No. 0.2;
 RESULT 942
 ID ADL18566 standard; protein; 918 AA.
 DE Human androgen receptor variant protein.
 PN JP2004008140-A.
 PD 15-JAN-2004.
 PA (SUMO) SUMITOMO CHEM CO LTD.
 Query Match 7.2%; Score 131; DB 8; Length 918;
 Best Local Similarity 25.8%; Pred. No. 0.2;
 RESULT 943
 ID ADL18565 standard; protein; 918 AA.
 DE Human androgen receptor wild-type protein.
 PN JP2004008140-A.
 PD 15-JAN-2004.
 PA (SUMO) SUMITOMO CHEM CO LTD.
 Query Match 7.2%; Score 131; DB 8; Length 918;
 Best Local Similarity 25.8%; Pred. No. 0.2;
 RESULT 944
 ID ADL34483 standard; protein; 918 AA.
 DE Wild-type human androgen receptor protein.
 PN JP2004008141-A.
 PD 15-JAN-2004.
 PA (SUMO) SUMITOMO CHEM CO LTD.
 Query Match 7.2%; Score 131; DB 8; Length 918;
 Best Local Similarity 25.8%; Pred. No. 0.2;
 RESULT 945
 ID ADL34485 standard; protein; 918 AA.
 DE Variant human androgen receptor protein, SEQ ID 3.
 PN JP2004008141-A.
 PD 15-JAN-2004.
 PA (SUMO) SUMITOMO CHEM CO LTD.
 Query Match 7.2%; Score 131; DB 8; Length 918;
 Best Local Similarity 25.8%; Pred. No. 0.2;
 RESULT 946
 ID ADL34484 standard; protein; 918 AA.
 DE Variant human androgen receptor protein, SEQ ID 2.
 PN JP2004008141-A.
 PD 15-JAN-2004.
 PA (SUMO) SUMITOMO CHEM CO LTD.
 Query Match 7.2%; Score 131; DB 8; Length 918;
 Best Local Similarity 25.8%; Pred. No. 0.2;

RESULT 947
ID ADL34486 standard; protein; 918 AA.
DE Variant human androgen receptor protein, SEQ ID 4.
PN JP2004008141-A.
PD 15-JAN-2004.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 7.2%; Score 131; DB 8; Length 918;
Best Local Similarity 25.8%; Pred. No. 0.2;
RESULT 948
ID ADL34487 standard; protein; 918 AA.
DE Variant human androgen receptor protein, SEQ ID 5.
PN JP2004008141-A.
PD 15-JAN-2004.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 7.2%; Score 131; DB 8; Length 918;
Best Local Similarity 25.8%; Pred. No. 0.2;
RESULT 949
ID ADL96729 standard; protein; 918 AA.
DE Human variant androgen receptor protein, SEQ ID No 11.
PN JP2004008142-A.
PD 15-JAN-2004.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 7.2%; Score 131; DB 8; Length 918;
Best Local Similarity 25.8%; Pred. No. 0.2;
RESULT 950
ID ADL96720 standard; protein; 918 AA.
DE Human variant androgen receptor protein, SEQ ID No 2.
PN JP2004008142-A.
PD 15-JAN-2004.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 7.2%; Score 131; DB 8; Length 918;
Best Local Similarity 25.8%; Pred. No. 0.2;
RESULT 951
ID ADL96719 standard; protein; 918 AA.
DE Human variant androgen receptor protein, SEQ ID No 1.
PN JP2004008142-A.
PD 15-JAN-2004.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 7.2%; Score 131; DB 8; Length 918;
Best Local Similarity 25.8%; Pred. No. 0.2;
RESULT 952
ID ADL96730 standard; protein; 918 AA.
DE Human variant androgen receptor protein, SEQ ID No 12.
PN JP2004008142-A.
PD 15-JAN-2004.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 7.2%; Score 131; DB 8; Length 918;
Best Local Similarity 25.8%; Pred. No. 0.2;
RESULT 953
ID ADT02204 standard; protein; 918 AA.
DE Human androgen receptor protein - SEQ ID 1.
PN JP2004254600-A.
PD 16-SEP-2004.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 7.2%; Score 131; DB 8; Length 918;
Best Local Similarity 25.8%; Pred. No. 0.2;
RESULT 954
ID ADT02205 standard; protein; 918 AA.
DE Variant human androgen receptor protein - SEQ ID 2.
PN JP2004254600-A.
PD 16-SEP-2004.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 7.2%; Score 131; DB 8; Length 918;
Best Local Similarity 25.8%; Pred. No. 0.2;
RESULT 955
ID ADS15261 standard; protein; 918 AA.
DE Human variant androgen receptor protein sequence SeqID3.
PN JP2004254602-A.
PD 16-SEP-2004.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 7.2%; Score 131; DB 8; Length 918;
Best Local Similarity 25.8%; Pred. No. 0.2;
RESULT 956
ID ADS09608 standard; protein; 918 AA.

ADSI5262 standard; protein; 918 AA.
Human variant androgen receptor protein sequence SeqID4.
JP2004254602-A.
16-SEP-2004.
(SUMO) SUMITOMO CHEM CO LTD.
Query Match 7.2%; Score 131; DB 8; Length 918;
Best Local Similarity 25.8%; Pred. No. 0.2;
RESULT 957
ID ADS15263 standard; protein; 918 AA.
DE Human variant androgen receptor protein sequence SeqID5.
PN JP2004254602-A.
PD 16-SEP-2004.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 7.2%; Score 131; DB 8; Length 918;
Best Local Similarity 25.8%; Pred. No. 0.2;
RESULT 958
ID ADS15260 standard; protein; 918 AA.
DE Human variant androgen receptor protein sequence SeqID2.
PN JP2004254602-A.
PD 16-SEP-2004.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 7.2%; Score 131; DB 8; Length 918;
Best Local Similarity 25.8%; Pred. No. 0.2;
RESULT 959
ID ADS15259 standard; protein; 918 AA.
DE Human androgen receptor protein sequence SeqID1.
PN JP2004254602-A.
PD 16-SEP-2004.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 7.2%; Score 131; DB 8; Length 918;
Best Local Similarity 25.8%; Pred. No. 0.2;
RESULT 960
ID ADS15264 standard; protein; 918 AA.
DE Human variant androgen receptor protein sequence SeqID6.
PN JP2004254602-A.
PD 16-SEP-2004.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 7.2%; Score 131; DB 8; Length 918;
Best Local Similarity 25.8%; Pred. No. 0.2;
RESULT 961
ID ADS09610 standard; protein; 918 AA.
DE Variant human androgen receptor protein #4.
PN JP2004254601-A.
PD 16-SEP-2004.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 7.2%; Score 131; DB 8; Length 918;
Best Local Similarity 25.8%; Pred. No. 0.2;
RESULT 962
ID ADS09609 standard; protein; 918 AA.
DE Variant human androgen receptor protein #3.
PN JP2004254601-A.
PD 16-SEP-2004.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 7.2%; Score 131; DB 8; Length 918;
Best Local Similarity 25.8%; Pred. No. 0.2;
RESULT 963
ID ADS09606 standard; protein; 918 AA.
DE Wild type human androgen receptor protein.
PN JP2004254601-A.
PD 16-SEP-2004.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 7.2%; Score 131; DB 8; Length 918;
Best Local Similarity 25.8%; Pred. No. 0.2;
RESULT 964
ID ADS09607 standard; protein; 918 AA.
DE Variant human androgen receptor protein #1.
PN JP2004254601-A.
PD 16-SEP-2004.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 7.2%; Score 131; DB 8; Length 918;
Best Local Similarity 25.8%; Pred. No. 0.2;
RESULT 965
ID ADS09608 standard; protein; 918 AA.

DE Variant human androgen receptor protein #2.
 PN JP2004254601-A.
 PD 16-SEP-2004.
 PA (SUMO) SUMITOMO CHEM CO LTD.
 Query Match 7.2%; Score 131; DB 8; Length 918;
 Best Local Similarity 25.8%; Pred. No. 0.2;
 RESULT 966
 ID AEB88131 standard; protein; 918 AA.
 DE Human neprilysin related protein #1.
 PN WO2005073395-A1.
 PD 11-AUG-2005.
 PA (SUMO) SUMITOMO CHEM CO LTD.
 Query Match 7.2%; Score 131; DB 9; Length 918;
 Best Local Similarity 25.8%; Pred. No. 0.2;
 RESULT 967
 ID ADN05775 standard; protein; 920 AA.
 DE Antipsoriatic protein sequence #1051.
 PN WO2004028479-A2.
 PD 08-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 7.2%; Score 131; DB 8; Length 920;
 Best Local Similarity 25.2%; Pred. No. 0.2;
 RESULT 968
 ID AEB25751 standard; protein; 920 AA.
 DE Human androgen receptor mutant R614H, SEQ ID NO 21.
 PN WO2005062760-A2.
 PD 14-JUL-2005.
 PA (UYRP) UNIV ROCHESTER.
 Query Match 7.2%; Score 131; DB 9; Length 920;
 Best Local Similarity 25.2%; Pred. No. 0.2;
 RESULT 969
 ID AEB68270 standard; protein; 920 AA.
 DE Nuclear hormone receptor polypeptide #8.
 PN WO2005073396-A1.
 PD 11-AUG-2005.
 PA (CERE-) CERES INC.
 PA (BOBZ/) BOEZIN S C.
 Query Match 7.2%; Score 131; DB 9; Length 920;
 Best Local Similarity 25.2%; Pred. No. 0.2;
 RESULT 970
 ID AEB88131 standard; protein; 920 AA.
 DE Human nuclear receptor SEQ ID NO 108.
 PN WO2006055786-A2.
 PD 26-MAY-2006.
 PA (ACAD-) ACADIA PHARM INC.
 Query Match 7.2%; Score 131; DB 10; Length 920;
 Best Local Similarity 25.2%; Pred. No. 0.2;
 RESULT 971
 ID ADF12119 standard; protein; 924 AA.
 DE Androgen receptor #SEQ ID 2.
 PN WO2003102188-A1.
 PD 11-DEC-2003.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 7.2%; Score 131; DB 8; Length 924;
 Best Local Similarity 25.2%; Pred. No. 0.2;
 RESULT 972
 ID ABO71662 standard; protein; 957 AA.
 DE Pseudomonas aeruginosa polypeptide #3837.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 7.2%; Score 131; DB 7; Length 957;
 Best Local Similarity 23.0%; Pred. No. 0.21;
 RESULT 973
 ID ADW99579 standard; protein; 1014 AA.
 DE Human gelatin protein - SEQ ID 12.
 PN WO2005012356-A2.
 PD 10-FEB-2005.
 PA (FIBR-) FIBROGEN INC.
 Query Match 7.2%; Score 131; DB 9; Length 1014;
 Best Local Similarity 26.7%; Pred. No. 0.22;
 RESULT 974
 ID ADJ11666 standard; protein; 1198 AA.

DE Rice protein modulated by post-transcriptional gene silencing SeqID 302.
 PN US2003135888-A1.
 PD 17-JUL-2003.
 PA (ZHUT/) ZHU T.
 PA (WANG/) WANG X.
 PA (CHAN/) CHANG H.
 PA (BRIG/) BRIGGS S P.
 PA (COOP/) COOPER B.
 PA (GLAZ/) GLAZEBROOK J.
 PA (GOFF/) GOFF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (MOUG/) MOUGHAMER T.
 PA (PROV/) PROVANT N.
 PA (RICK/) RICKE D.
 Query Match 7.2%; Score 131; DB 7; Length 1198;
 Best Local Similarity 26.0%; Pred. No. 0.27;
 RESULT 975
 ID AAB72370 standard; peptide; 258 AA.
 DE Marsupial prion protein cellular form (PrPc) amino acid sequence.
 PN WO200107479-A2.
 PD 01-FEB-2001.
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 Query Match 7.2%; Score 130.5; DB 4; Length 258;
 Best Local Similarity 37.4%; Pred. No. 0.048;
 RESULT 976
 ID ADC55552 standard; protein; 675 AA.
 DE Mutant human androgen receptor #4.
 PN JP2003102333-A.
 PD 08-APR-2003.
 PA (YAMA) YAMANOUCHI PHARM CO LTD.
 Query Match 7.2%; Score 130.5; DB 7; Length 675;
 Best Local Similarity 25.2%; Pred. No. 0.15;
 RESULT 977
 ID ADC55546 standard; protein; 690 AA.
 DE Mutant human androgen receptor #2.
 PN JP2003102333-A.
 PD 08-APR-2003.
 PA (YAMA) YAMANOUCHI PHARM CO LTD.
 Query Match 7.2%; Score 130.5; DB 7; Length 690;
 Best Local Similarity 25.2%; Pred. No. 0.15;
 RESULT 978
 ID ADC55550 standard; protein; 722 AA.
 DE Mutant human androgen receptor #3.
 PN JP2003102333-A.
 PD 08-APR-2003.
 PA (YAMA) YAMANOUCHI PHARM CO LTD.
 Query Match 7.2%; Score 130.5; DB 7; Length 722;
 Best Local Similarity 25.2%; Pred. No. 0.16;
 RESULT 979
 ID ADK71139 standard; protein; 898 AA.
 DE 12S/AR-TAD chimeric protein.
 PN WO2004015086-A2.
 PD 19-FEB-2004.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 7.2%; Score 130.5; DB 8; Length 898;
 Best Local Similarity 25.2%; Pred. No. 0.21;
 RESULT 980
 ID AAP93109 standard; protein; 919 AA.
 DE Human androgen receptor.
 PN WO8909791-A.
 PD 19-OCT-1989.
 PA (UYNC-) UNIV OF N CAROLINA.
 Query Match 7.2%; Score 130.5; DB 1; Length 919;
 Best Local Similarity 25.2%; Pred. No. 0.22;
 RESULT 981
 ID AAW14783 standard; protein; 919 AA.
 DE Androgen receptor.
 PN WO9711170-A1.
 PD 27-MAR-1997.
 PA (WORC-) WORCESTER FOUND BIOMEDICAL RES.
 Query Match 7.2%; Score 130.5; DB 2; Length 919;
 Best Local Similarity 25.2%; Pred. No. 0.22;

RESULT 982
ID AAY78914 standard; protein; 919 AA.
DE Human androgen receptor (AR) amino acid sequence.
PN WO200001813-A2.
PD 13-JAN-2000.
PA (UYBR-) UNIV BRITISH COLUMBIA.
Query Match 7.2%; Score 130.5; DB 3; Length 919;
Best Local Similarity 25.2%; Pred. No. 0.22;
RESULT 983
ID AAE19061 standard; protein; 919 AA.
DE Human androgen receptor (AR).
PN WO200210452-A2.
PD 07-FEB-2002.
PA (UYRP-) UNIV ROCHESTER.
Query Match 7.2%; Score 130.5; DB 5; Length 919;
Best Local Similarity 25.2%; Pred. No. 0.22;
RESULT 984
ID ABJ05582 standard; protein; 919 AA.
DE Breast cancer-associated protein 47.
PN WO200259377-A2.
PD 01-AUG-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 7.2%; Score 130.5; DB 5; Length 919;
Best Local Similarity 25.2%; Pred. No. 0.22;
RESULT 985
ID ABJ19809 standard; protein; 919 AA.
DE Androgen-independent prostate cancer-related protein - SEQ ID NO 25.
PN WO200298358-A2.
PD 12-DEC-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 7.2%; Score 130.5; DB 6; Length 919;
Best Local Similarity 25.2%; Pred. No. 0.22;
RESULT 986
ID ADB75212 standard; protein; 919 AA.
DE Prostate cancer marker protein.
PN WO2003009814-A2.
PD 06-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.2%; Score 130.5; DB 7; Length 919;
Best Local Similarity 25.2%; Pred. No. 0.22;
RESULT 987
ID ADC55542 standard; protein; 919 AA.
DE Human androgen receptor.
PN JP2003102333-A.
PD 08-APR-2003.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
Query Match 7.2%; Score 130.5; DB 7; Length 919;
Best Local Similarity 25.2%; Pred. No. 0.22;
RESULT 988
ID ADF72327 standard; protein; 919 AA.
DE Human androgen receptor protein sequence SEQ ID NO:23.
PN WO2003103595-A2.
PD 18-DEC-2003.
PA (UYRP-) UNIV ROCHESTER.
Query Match 7.2%; Score 130.5; DB 8; Length 919;
Best Local Similarity 25.2%; Pred. No. 0.22;
RESULT 989
ID ADJ78488 standard; protein; 919 AA.
DE Androgen receptor for anti-cancer protein complex.
PN WO2004009619-A2.
PD 29-JAN-2004.
PA (CELL-) CELLZOME AG.
Query Match 7.2%; Score 130.5; DB 8; Length 919;
Best Local Similarity 25.2%; Pred. No. 0.22;
RESULT 990
ID ADP05627 standard; protein; 919 AA.
DE Human nuclear receptor protein SeqID1.
PN WO2004045369-A2.
PD 03-JUN-2004.
PA (NURA-) NURA INC.
Query Match 7.2%; Score 130.5; DB 8; Length 919;
Best Local Similarity 25.2%; Pred. No. 0.22;
RESULT 991
ID ADR45375 standard; protein; 919 AA.
DE Human androgen receptor protein SeqID31.
PN WO2004071461-A2.
PD 26-AUG-2004.
PA (UYRP-) UNIV ROCHESTER.
Query Match 7.2%; Score 130.5; DB 8; Length 919;
Best Local Similarity 25.2%; Pred. No. 0.22;
RESULT 992
ID AEB25733 standard; protein; 919 AA.
DE Human androgen receptor protein sequence, seqid 3.
PN WO2005062760-A2.
PD 14-JUL-2005.
PA (UYRP-) UNIV ROCHESTER.
Query Match 7.2%; Score 130.5; DB 9; Length 919;
Best Local Similarity 25.2%; Pred. No. 0.22;
RESULT 993
ID AED03747 standard; protein; 919 AA.
DE Androgen receptor ligand binding domain.
PN US2005202440-A1.
PD 15-SEP-2005.
PA (FLET/) FLETTERICK R.
PA (ESTE/) ESTEBANEZ-PERPINA E.
PA (HURE/) HUR E. S. J.
PA (PFAE/) PFAFF S. J.
PA (BUEH/) BUEHRER B. M.
Query Match 7.2%; Score 130.5; DB 9; Length 919;
Best Local Similarity 25.2%; Pred. No. 0.22;
RESULT 994
ID AEJ93234 standard; protein; 919 AA.
DE Human Androgen receptor transcript variant 1.
PN WO2006074378-A2.
PD 13-JUL-2006.
PA (UYRP-) UNIV ROCHESTER.
Query Match 7.2%; Score 130.5; DB 10; Length 919;
Best Local Similarity 25.2%; Pred. No. 0.22;
RESULT 995
ID ADC55544 standard; protein; 951 AA.
DE Mutant human androgen receptor #1.
PN JP2003102333-A.
PD 08-APR-2003.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
Query Match 7.2%; Score 130.5; DB 7; Length 951;
Best Local Similarity 25.2%; Pred. No. 0.23;
RESULT 996
ID ADC32758 standard; protein; 1090 AA.
DE Human novel contig-encoded polypeptide sequence, SEQ ID NO:2840.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 7.2%; Score 130.5; DB 7; Length 1090;
Best Local Similarity 25.3%; Pred. No. 0.27;
RESULT 997
ID ADC33247 standard; protein; 1090 AA.
DE Human novel contig-encoded polypeptide sequence, SEQ ID NO:3329.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 7.2%; Score 130.5; DB 7; Length 1090;
Best Local Similarity 25.3%; Pred. No. 0.27;
RESULT 998
ID ADD89022 standard; protein; 1212 AA.
DE TAT262.
PN WO2003057160-A2.
PD 17-JUL-2003.
PA (GETH-) GENENTECH INC.
Query Match 7.2%; Score 130.5; DB 7; Length 1212;
Best Local Similarity 27.0%; Pred. No. 0.3;
RESULT 999
ID ADV70231 standard; protein; 1212 AA.
DE Tumor-associated antigenic target polypeptide TAT262.
PN WO2004112829-A2.
PD 29-DEC-2004.
PA (GETH-) GENENTECH INC.

Query Match 7.2%; Score 130.5; DB 9; Length 1212;
 Best Local Similarity 27.0%; Pred. No. 0.3; /
 RESULT 1000
 ID ABG93948 standard; protein; 1453 AA.
 DE Mouse polypeptide orthologous to DACC-11.
 PN WO200264625-A1.
 PD 22-AUG-2002.
 PA (ADPP-) ADP PHARM PTY LTD.
 PA (UNSY) UNIV SYDNEY.
 Query Match 7.2%; Score 130.5; DB 5; Length 1453;
 Best Local Similarity 25.0%; Pred. No. 0.38;
 RESULT 1001
 ID ADM44458 standard; protein; 1453 AA.
 DE Murine FVB/N collagen pro-alpha-1 type I chain.
 PN WO2005001090-A1.
 PD 06-JAN-2005.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 Query Match 7.2%; Score 130.5; DB 9; Length 1453;
 Best Local Similarity 25.0%; Pred. No. 0.38;
 RESULT 1002
 ID AEF19248 standard; protein; 1453 AA.
 DE Mouse FVB/N pro-alpha-1 collagen.
 PN WO2006001396-A1.
 PD 05-JAN-2006.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 Query Match 7.2%; Score 130.5; DB 10; Length 1453;
 Best Local Similarity 25.0%; Pred. No. 0.38;
 RESULT 1003
 ID AAM40863 standard; protein; 1669 AA.
 DE Human polypeptide SEQ ID NO 5794.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 7.2%; Score 130.5; DB 4; Length 1669;
 Best Local Similarity 27.0%; Pred. No. 0.44;
 RESULT 1004
 ID ABB90760 standard; protein; 1669 AA.
 DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 252.
 PN WO200210217-A2.
 PD 07-FEB-2002.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 7.2%; Score 130.5; DB 5; Length 1669;
 Best Local Similarity 27.0%; Pred. No. 0.44;
 RESULT 1005
 ID ABU54467 standard; protein; 1669 AA.
 DE Human tumour endothelial marker TEM 31.
 PN WO200283874-A2.
 PD 24-OCT-2002.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 7.2%; Score 130.5; DB 6; Length 1669;
 Best Local Similarity 27.0%; Pred. No. 0.44;
 RESULT 1006
 ID ADF90900 standard; protein; 1669 AA.
 DE Human hepatic-fibrosis disease marker protein SEQ ID 362.
 PN JP2003259877-A.
 PD 16-SEP-2003.
 PA (SUMU) SUMITOMO SEIYAKU KK.
 Query Match 7.2%; Score 130.5; DB 7; Length 1669;
 Best Local Similarity 27.0%; Pred. No. 0.44;
 RESULT 1007
 ID ADR87604 standard; protein; 1669 AA.
 DE Human Type IV collagen alpha 1, SEQ ID 8.
 PN WO2004075835-A2.
 PD 10-SEP-2004.
 PA (GETH) GENENTECH INC.
 Query Match 7.2%; Score 130.5; DB 8; Length 1669;
 Best Local Similarity 27.0%; Pred. No. 0.44;
 RESULT 1008
 ID ABB90754 standard; protein; 1732 AA.
 DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 240.
 PN WO200210217-A2.
 PD 07-FEB-2002.
 PA (UYJO) UNIV JOHNS HOPKINS.

Query Match 7.2%; Score 130.5; DB 5; Length 1732;
 Best Local Similarity 22.9%; Pred. No. 0.46;
 RESULT 1009
 ID ABU54461 standard; protein; 1732 AA.
 DE Human tumour endothelial marker TEM 24.
 PN WO200283874-A2.
 PD 24-OCT-2002.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 7.2%; Score 130.5; DB 6; Length 1732;
 Best Local Similarity 22.9%; Pred. No. 0.46;
 RESULT 1010
 ID ADD18778 standard; protein; 1735 AA.
 DE Human disease related protein SeqID209.
 PN WO2003018621-A2.
 PD 06-MAR-2003.
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 Query Match 7.2%; Score 130.5; DB 7; Length 1735;
 Best Local Similarity 22.9%; Pred. No. 0.46;
 RESULT 1011
 ID ADY65376 standard; protein; 477 AA.
 DE S. mansoni protein SEQ ID 794.
 PN WO2005023979-A2.
 PD 17-MAR-2005.
 PA (AMPA-) FUNDACAO AMPARO A PESQUISA DO ESTADO.
 Query Match 7.1%; Score 130; DB 9; Length 477;
 Best Local Similarity 27.0%; Pred. No. 0.11;
 RESULT 1012
 ID ADX94266 standard; protein; 845 AA.
 DE Plant full length insert polypeptide seqid 56930.
 PN US2004034888-A1.
 PD 19-FEB-2004.
 PA (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 Query Match 7.1%; Score 130; DB 8; Length 845;
 Best Local Similarity 22.0%; Pred. No. 0.22;
 RESULT 1013
 ID AAR12223 standard; protein; 918 AA.
 DE Human androgen receptor.
 PN WO9107423-A.
 PD 30-MAY-1991.
 PA (ARCH-) ARCH DEV CORP.
 Query Match 7.1%; Score 130; DB 2; Length 918;
 Best Local Similarity 25.8%; Pred. No. 0.24;
 RESULT 1014
 ID ADL34489 standard; protein; 918 AA.
 DE Variant human androgen receptor protein, SEQ ID 7.
 PN JP2004008141-A.
 PD 15-JAN-2004.
 PA (SUMO) SUMITOMO CHEM CO LTD.
 Query Match 7.1%; Score 130; DB 8; Length 918;
 Best Local Similarity 25.8%; Pred. No. 0.24;
 RESULT 1015
 ID AAP90996 standard; protein; 919 AA.
 DE Human androgen receptor DNA clone.
 PN WO8909223-A.
 PD 05-OCT-1989.
 PA (ARCH-) ARCH DEV CORP.
 Query Match 7.1%; Score 130; DB 1; Length 919;
 Best Local Similarity 25.8%; Pred. No. 0.24;
 RESULT 1016
 ID ADP65203 standard; protein; 1629 AA.
 DE Human alpha 2 type XI collagen, isoform 3 preproprotein.
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match 7.1%; Score 130; DB 7; Length 1629;
 Best Local Similarity 25.9%; Pred. No. 0.47;
 RESULT 1017
 ID AAG77793 standard; protein; 1745 AA.

DE Human pro-alpha-3(V) fibrillar procollagen polypeptide.
 PN WO200164871-A2.
 PD 07-SEP-2001.
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 Query Match 7.1%; Score 130; DB 4; Length 1745;
 Best Local Similarity 27.1%; Pred. No. 0.51;
 RESULT 1018
 ID ABB97234 standard; protein; 1745 AA.
 DE Novel human protein SEQ ID NO: 502.
 PN WO200222660-A2.
 PD 21-MAR-2002.
 PA (HYSE-) HYSEQ INC.
 Query Match 7.1%; Score 130; DB 5; Length 1745;
 Best Local Similarity 27.1%; Pred. No. 0.51;
 RESULT 1019
 ID ADQ19841 standard; protein; 1745 AA.
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2660.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 7.1%; Score 130; DB 8; Length 1745;
 Best Local Similarity 27.1%; Pred. No. 0.51;
 RESULT 1020
 ID AAB87356 standard; protein; 459 AA.
 DE Human gene 15 encoded secreted protein HUFQHS3, SEQ ID NO:97.
 PN WO200118022-A1.
 PD 15-MAR-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 7.1%; Score 129.5; DB 4; Length 459;
 Best Local Similarity 24.1%; Pred. No. 0.11;
 RESULT 1021
 ID ABG65357 standard; protein; 459 AA.
 DE Human albumin fusion protein #2032.
 PN WO20017137-A1.
 PD 18-OCT-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 7.1%; Score 129.5; DB 5; Length 459;
 Best Local Similarity 24.1%; Pred. No. 0.11;
 RESULT 1022
 ID ADF94869 standard; protein; 459 AA.
 DE Human gene 2-encoded ACRP30-like protein, SEQ ID NO:72.
 PN WO2003031586-A2.
 PD 17-APR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (BLON/) BLONDEL O.
 PA (RUBE/) RUBEN S M.
 Query Match 7.1%; Score 129.5; DB 7; Length 459;
 Best Local Similarity 24.1%; Pred. No. 0.11;
 RESULT 1023
 ID ADL78624 standard; protein; 459 AA.
 DE Albumin fusion protein related therapeutic protein X, SEQ ID No 2106.
 PN US2004010134-A1.
 PD 15-JAN-2004.
 PA (ROSE/) ROSEN C A.
 PA (HASE/) HASELTINE W A.
 Query Match 7.1%; Score 129.5; DB 8; Length 459;
 Best Local Similarity 24.1%; Pred. No. 0.11;
 RESULT 1024
 ID AEH08897 standard; protein; 459 AA.
 DE Therapeutic protein HUFQHS3, SEQ ID 2106.
 PN US2006084794-A1.
 PD 20-APR-2006.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 7.1%; Score 129.5; DB 10; Length 459;
 Best Local Similarity 24.1%; Pred. No. 0.11;
 RESULT 1025
 ID ABG15617 standard; protein; 546 AA.
 DE Novel human diagnostic protein #15608.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 7.1%; Score 129.5; DB 4; Length 546;
 Best Local Similarity 24.5%; Pred. No. 0.14;

RESULT 1026
 ID ABB58971 standard; protein; 1020 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 3705.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 7.1%; Score 129.5; DB 4; Length 1020;
 Best Local Similarity 25.1%; Pred. No. 0.3;
 RESULT 1027
 ID ABG14734 standard; protein; 1040 AA.
 DE Novel human diagnostic protein #14725.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 7.1%; Score 129.5; DB 4; Length 1040;
 Best Local Similarity 23.7%; Pred. No. 0.3;
 RESULT 1028
 ID AAB31516 standard; protein; 2087 AA.
 DE Amino acid sequence of the rat Shankla polypeptide.
 PN WO200078921-A2.
 PD 28-DEC-2000.
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 PA (MASS-) MASSACHUSETTS GEN HOSPITAL.
 Query Match 7.1%; Score 129.5; DB 4; Length 2087;
 Best Local Similarity 26.0%; Pred. No. 0.7;
 RESULT 1029
 ID AAB12000 standard; protein; 2091 AA.
 DE Rat p3103 protein.
 PN JP2000184884-A.
 PD 04-JUL-2000.
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 Query Match 7.1%; Score 129.5; DB 3; Length 2091;
 Best Local Similarity 26.0%; Pred. No. 0.7;
 RESULT 1030
 ID ABG70269 standard; protein; 577 AA.
 DE Human Epsin-like protein.
 PN WO200255702-A2.
 PD 18-JUL-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 7.1%; Score 129; DB 5; Length 577;
 Best Local Similarity 26.9%; Pred. No. 0.16;
 RESULT 1031
 ID ABB11527 standard; peptide; 1008 AA.
 DE Human apolipoprotein B receptor homologue, SEQ ID NO:1897.
 PN WO200157188-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 7.1%; Score 129; DB 4; Length 1008;
 Best Local Similarity 22.7%; Pred. No. 0.32;
 RESULT 1032
 ID ABG08112 standard; protein; 1013 AA.
 DE Novel human diagnostic protein #8103.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 7.1%; Score 129; DB 4; Length 1013;
 Best Local Similarity 22.7%; Pred. No. 0.32;
 RESULT 1033
 ID AEL57493 standard; protein; 1263 AA.
 DE Human collagen alpha 3(IV) chain precursor, SEQ ID NO: 1956.
 PN US2006216722-A1.
 PD 28-SEP-2006
 PA (BETS/) BETSHOLTZ C.
 PA (TRYG/) TRYGGVASON K.
 PA (TAKE/) TAKEMOTO M.
 PA (HELL/) HE L.
 PA (PATR/) PATRAKKAS J.
 Query Match 7.1%; Score 129; DB 10; Length 1263;
 Best Local Similarity 25.3%; Pred. No. 0.42;
 RESULT 1034
 ID ADJ70656 standard; protein; 2527 AA.
 DE Human heat mitochondrial protein as a therapeutic target SeqID2462.
 PN WO2003087768-A2.

PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 7.1%; Score 129; DB 7; Length 2527;
Best Local Similarity 24.9%; Pred. No. 0.96;
RESULT 1035
ID ADJ69060 standard; protein; 2715 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID866.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 7.1%; Score 129; DB 7; Length 2715;
Best Local Similarity 24.9%; Pred. No. 1;
RESULT 1036
ID ADQ18982 standard; protein; 3530 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1801.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 7.1%; Score 129; DB 8; Length 3530;
Best Local Similarity 24.4%; Pred. No. 1.4;
RESULT 1037
ID ABP76679 standard; protein; 19938 AA.
DE Streptomyces viridochromogenes Avi gene cluster polypeptide frame 3.
PN WO200268436-A1.
PD 06-SEP-2002.
PA (COMB-) COMBINATURE BIOPHARM AG.
Query Match 7.1%; Score 129; DB 6; Length 19938;
Best Local Similarity 23.2%; Pred. No. 11;
RESULT 1038
ID AEG09026 standard; protein; 370 AA.
DE Novel human diagnostic protein #9017.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 128.5; DB 4; Length 370;
Best Local Similarity 26.5%; Pred. No. 0.11;
RESULT 1039
ID ADC31490 standard; protein; 682 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1572.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 128.5; DB 7; Length 682;
Best Local Similarity 26.2%; Pred. No. 0.22;
RESULT 1040
ID ABL1397 standard; peptide; 686 AA.
DE Human secreted protein homologue, SEQ ID NO:1767.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 128.5; DB 4; Length 686;
Best Local Similarity 24.8%; Pred. No. 0.22;
RESULT 1041
ID ABG03868 standard; protein; 760 AA.
DE Novel human diagnostic protein #3859.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 128.5; DB 4; Length 760;
Best Local Similarity 27.8%; Pred. No. 0.25;
RESULT 1042
ID ABR82984 standard; protein; 906 AA.
DE Human androgen receptor polypeptide.
PN WO2003072700-A2.
PD 04-SEP-2003.
PA (PFIZ) PFIZER PROD INC.
Query Match 7.0%; Score 128.5; DB 7; Length 906;
Best Local Similarity 25.7%; Pred. No. 0.31;
RESULT 1043
ID ADN04533 standard; protein; 906 AA.
DE Antipsoriatic protein sequence #459.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 128.5; DB 8; Length 906;
Best Local Similarity 25.7%; Pred. No. 0.31;
RESULT 1044
ID ADA54960 standard; protein; 1003 AA.
DE Human protein, SEQ ID 2528.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.0%; Score 128.5; DB 6; Length 1003;
Best Local Similarity 26.2%; Pred. No. 0.35;
RESULT 1045
ID ABP58226 standard; protein; 1003 AA.
DE Human cell adhesion and extracellular matrix protein 3.
PN WO200288322-A2.
PD 07-NOV-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.0%; Score 128.5; DB 6; Length 1003;
Best Local Similarity 26.2%; Pred. No. 0.35;
RESULT 1046
ID ADC31335 standard; protein; 1452 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1417.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 128.5; DB 7; Length 1452;
Best Local Similarity 24.6%; Pred. No. 0.54;
RESULT 1047
ID ABO75574 standard; protein; 247 AA.
DE Pseudomonas aeruginosa polypeptide #7749.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 7.0%; Score 128; DB 7; Length 247;
Best Local Similarity 22.3%; Pred. No. 0.071;
RESULT 1048
ID AEB31354 standard; protein; 525 AA.
DE Human SFPQ protein #2.
PN WO2005068501-A1.
PD 28-JUL-2005.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 7.0%; Score 128; DB 9; Length 525;
Best Local Similarity 24.7%; Pred. No. 0.18;
RESULT 1049
ID ADP56334 standard; protein; 583 AA.
DE Human PRO protein sequence SEQ ID NO:2310.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 128; DB 8; Length 583;
Best Local Similarity 24.5%; Pred. No. 0.2;
RESULT 1050
ID AEB31352 standard; protein; 669 AA.
DE Human PSF short form, PSF-F.
PN WO2005068501-A1.
PD 28-JUL-2005.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 7.0%; Score 128; DB 9; Length 669;
Best Local Similarity 24.7%; Pred. No. 0.24;
RESULT 1051
ID AAM39141 standard; protein; 707 AA.
DE Human polypeptide SEQ ID NO 2286.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 128; DB 4; Length 707;
Best Local Similarity 24.7%; Pred. No. 0.25;
RESULT 1052
ID ADE54941 standard; protein; 707 AA.
DE Human Protein P23246, SEQ ID NO 746.

```

PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
  Query Match      7.0%; Score 128; DB 7; Length 707;
  Best Local Similarity 24.7%; Pred. No. 0.25;
RESULT 1053
ID ADE54938 standard; protein; 707 AA.
DE Human Protein P23246, SEQ ID NO 743.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
  Query Match      7.0%; Score 128; DB 7; Length 707;
  Best Local Similarity 24.7%; Pred. No. 0.25;
RESULT 1054
ID ADE54944 standard; protein; 707 AA.
DE Human Protein P23246, SEQ ID NO 749.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
  Query Match      7.0%; Score 128; DB 7; Length 707;
  Best Local Similarity 24.7%; Pred. No. 0.25;
RESULT 1055
ID ADE54947 standard; protein; 707 AA.
DE Human Protein P23246, SEQ ID NO 752.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
  Query Match      7.0%; Score 128; DB 7; Length 707;
  Best Local Similarity 24.7%; Pred. No. 0.25;
RESULT 1056
ID ADE54935 standard; protein; 707 AA.
DE Human Protein P23246, SEQ ID NO 740.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
  Query Match      7.0%; Score 128; DB 7; Length 707;
  Best Local Similarity 24.7%; Pred. No. 0.25;
RESULT 1057
ID ADE54950 standard; protein; 707 AA.
DE Human Protein P23246, SEQ ID NO 755.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
  Query Match      7.0%; Score 128; DB 7; Length 707;
  Best Local Similarity 24.7%; Pred. No. 0.25;
RESULT 1058
ID ADE77113 standard; protein; 707 AA.
DE Human protein expressed in a liver disorder #73.
PN US2003108871-A1.
PD 12-JUN-2003.
PA (KASE/) KASER M R.
  Query Match      7.0%; Score 128; DB 8; Length 707;
  Best Local Similarity 24.7%; Pred. No. 0.25;
RESULT 1059
ID ADP54263 standard; protein; 707 AA.
DE Human PRO protein sequence SEQ ID NO:239.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH ) GENENTECH INC.
  Query Match      7.0%; Score 128; DB 8; Length 707;
  Best Local Similarity 24.7%; Pred. No. 0.25;
RESULT 1060
ID ADZ44698 standard; protein; 707 AA.
DE NFK-B protein #4.
PN WO2005033284-A2.
PD 14-APR-2005.
PA (REGC ) UNIV CALIFORNIA.
  Query Match      7.0%; Score 128; DB 10; Length 1588;
  Best Local Similarity 23.6%; Pred. No. 0.66;

  Query Match      7.0%; Score 128; DB 9; Length 707;
  Best Local Similarity 24.7%; Pred. No. 0.25;
RESULT 1061
ID AEB31351 standard; protein; 707 AA.
DE Human PGF proline/glutamine rich polypeptide.
PN WO2005068501-A1.
PD 28-JUL-2005.
PA (MOUN ) MOUNT SINAI HOSPITAL.
  Query Match      7.0%; Score 128; DB 9; Length 707;
  Best Local Similarity 24.7%; Pred. No. 0.25;
RESULT 1062
ID AEB31350 standard; protein; 707 AA.
DE Human PGF long form, PSF-A.
PN WO2005068501-A1.
PD 28-JUL-2005.
PA (MOUN ) MOUNT SINAI HOSPITAL.
  Query Match      7.0%; Score 128; DB 9; Length 707;
  Best Local Similarity 24.7%; Pred. No. 0.25;
RESULT 1063
ID AEC12876 standard; protein; 707 AA.
DE Human biomarker of neurotrophic agent protein SEQ ID NO 1222.
PN WO2005083125-A2.
PD 09-SEP-2005.
PA (BIOJ ) BIOGEN IDEC MA INC.
  Query Match      7.0%; Score 128; DB 9; Length 707;
  Best Local Similarity 24.7%; Pred. No. 0.25;
RESULT 1064
ID ABG74229 standard; protein; 907 AA.
DE Canine Androgen receptor.
PN US2002161194-A1.
PD 31-OCT-2002.
PA (CAST/) CASTLEBERRY T A.
PA (LUBB/) LU B.
PA (OWEN/) OWEN T A.
PA (SMOC/) SMOCK S L.
  Query Match      7.0%; Score 128; DB 6; Length 907;
  Best Local Similarity 24.9%; Pred. No. 0.34;
RESULT 1065
ID ABO67909 standard; protein; 977 AA.
DE Pseudomonas aeruginosa polypeptide #84.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
  Query Match      7.0%; Score 128; DB 7; Length 977;
  Best Local Similarity 26.9%; Pred. No. 0.37;
RESULT 1066
ID ABP96226 standard; protein; 1003 AA.
DE Human nucleic-acid associated protein 9 SEQ ID NO:9.
PN WO2003016549-A2.
PD 27-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
  Query Match      7.0%; Score 128; DB 6; Length 1003;
  Best Local Similarity 22.6%; Pred. No. 0.38;
RESULT 1067
ID ADE09399 standard; protein; 1470 AA.
DE Novel protein-related contig polypeptide sequence #465.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
  Query Match      7.0%; Score 128; DB 7; Length 1470;
  Best Local Similarity 24.9%; Pred. No. 0.6;
RESULT 1068
ID AEL57323 standard; protein; 1588 AA.
DE Mouse procollagen, type IV, alpha 3, SEQ ID NO: 1786.
PN US2006216722-A1.
PD 28-SEP-2006.
PA (BETS/) BETSHOLTZ C.
PA (TRYG/) TRYGVASON K.
PA (TAKE/) TAKEMOTO M.
PA (HELL/) HE L.
PA (PATR/) PATRAKKAS J.
  Query Match      7.0%; Score 128; DB 10; Length 1588;
  Best Local Similarity 23.6%; Pred. No. 0.66;

```

RESULT 1069
 ID ADM44466 standard; protein; 1669 AA.
 DE Murine procollagen, type IV, alpha 3 (Col4a3).
 PN W02005001090-A1.
 PD 06-JAN-2005.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 Query Match 7.0%; Score 128; DB 9; Length 1669;
 Best Local Similarity 23.6%; Pred. No. 0.7;
 RESULT 1070
 ID AEF19256 standard; protein; 1669 AA.
 DE Mus musculus procollagen, type IV, alpha 3 (Col4a3).
 PN W02006001396-A1.
 PD 03-JAN-2006.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 Query Match 7.0%; Score 128; DB 10; Length 1669;
 Best Local Similarity 23.6%; Pred. No. 0.7;
 RESULT 1071
 ID AAR53257 standard; protein; 1838 AA.
 DE Human collagen (Type V).
 PN JP06105687-A.
 PD 19-APR-1994.
 PA (TAKI) TAKARA SHUZO CO LTD.
 Query Match 7.0%; Score 128; DB 2; Length 1838;
 Best Local Similarity 24.0%; Pred. No. 0.79;
 RESULT 1072
 ID ADE55566 standard; protein; 1838 AA.
 DE Human Protein P20908, SEQ ID NO 1383.
 PN W02003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 7.0%; Score 128; DB 7; Length 1838;
 Best Local Similarity 24.0%; Pred. No. 0.79;
 RESULT 1073
 ID ADE55570 standard; protein; 1838 AA.
 DE Human Protein P20908, SEQ ID NO 1387.
 PN W02003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 7.0%; Score 128; DB 7; Length 1838;
 Best Local Similarity 24.0%; Pred. No. 0.79;
 RESULT 1074
 ID ADP65220 standard; protein; 1838 AA.
 DE Human alpha 1 type V collagen preproprotein.
 PN W02003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match 7.0%; Score 128; DB 7; Length 1838;
 Best Local Similarity 24.0%; Pred. No. 0.79;
 RESULT 1075
 ID ADV70238 standard; protein; 1838 AA.
 DE Tumor-associated antigenic target polypeptide TAT477.
 PN W02004112829-A2.
 PD 29-DEC-2004.
 PA (GETH) GENENTECH INC.
 Query Match 7.0%; Score 128; DB 9; Length 1838;
 Best Local Similarity 24.0%; Pred. No. 0.79;
 RESULT 1076
 ID ADZ09822 standard; protein; 1838 AA.
 DE Human breast cancer marker COL5A1 protein.
 PN EPI522594-A2.
 PD 13-APR-2005.
 PA (FARB) BAYER HEALTHCARE AG.
 Query Match 7.0%; Score 128; DB 9; Length 1838;
 Best Local Similarity 24.0%; Pred. No. 0.79;
 RESULT 1077
 ID ADZ70492 standard; protein; 1838 AA.
 DE Human protein from lung cancer marker gene COL5A1.
 PN W02005032495-A2.
 PD 14-APR-2005.
 PA (FARB) BAYER PHARM CORP.
 Query Match 7.0%; Score 128; DB 9; Length 1838;

Best Local Similarity 24.0%; Pred. No. 0.79;
 RESULT 1078
 ID ARD74354 standard; protein; 1874 AA.
 DE Human placental protein SEQ ID NO:1182.
 PN US2005255114-A1.
 PD 17-NOV-2005.
 PA (NUVE-) NUVELO INC.
 Query Match 7.0%; Score 128; DB 9; Length 1874;
 Best Local Similarity 24.0%; Pred. No. 0.81;
 RESULT 1079
 ID ABB63068 standard; protein; 445 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 15996.
 PN W0200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 7.0%; Score 127.5; DB 4; Length 445;
 Best Local Similarity 25.3%; Pred. No. 0.16;
 RESULT 1080
 ID ADS96700 standard; protein; 445 AA.
 DE Drosophila melanogaster protein, SEQ ID 321.
 PN W02004039999-A2.
 PD 13-MAY-2004.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 7.0%; Score 127.5; DB 8; Length 445;
 Best Local Similarity 25.3%; Pred. No. 0.16;
 RESULT 1081
 ID AEL95903 standard; protein; 445 AA.
 DE Drosophila melanogaster survival essential protein, SEQ:795.
 PN US7135558-B1.
 PD 14-NOV-2006.
 PA (APPL-) APPLERA CORP.
 Query Match 7.0%; Score 127.5; DB 11; Length 445;
 Best Local Similarity 25.3%; Pred. No. 0.16;
 RESULT 1082
 ID AM82061 standard; protein; 884 AA.
 DE Tumor-associated antigenic target (TAT) polypeptide PRO82963, SEQ:5320.
 PN W02004030615-A2.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 7.0%; Score 127.5; DB 8; Length 884;
 Best Local Similarity 22.2%; Pred. No. 0.36;
 RESULT 1083
 ID ADY91609 standard; protein; 884 AA.
 DE Human prostatic cancer marker, calcium (ca2+) homeostasis ER protein.
 PN JP2005080524-A.
 PD 31-MAR-2005.
 PA (DOKU-) DOKURITSU GYOSHI HOJIN KAGAKU GIJUTSU SH.
 Query Match 7.0%; Score 127.5; DB 9; Length 884;
 Best Local Similarity 22.2%; Pred. No. 0.36;
 RESULT 1084
 ID AEG59107 standard; protein; 884 AA.
 DE Human U2 CHERP protein.
 PN US2006068434-A1.
 PD 30-MAR-2006.
 PA (STOE/) STOECKER J.
 Query Match 7.0%; Score 127.5; DB 10; Length 884;
 Best Local Similarity 22.2%; Pred. No. 0.36;
 RESULT 1085
 ID AEG73449 standard; protein; 884 AA.
 DE Human U2 related protein #20.
 PN W02006034278-A2.
 PD 30-MAR-2006.
 PA (MATR-) MATRITECH INC.
 Query Match 7.0%; Score 127.5; DB 10; Length 884;
 Best Local Similarity 22.2%; Pred. No. 0.36;
 RESULT 1086
 ID ABG03340 standard; protein; 1149 AA.
 DE Novel human diagnostic protein #3331.
 PN W0200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 7.0%; Score 127.5; DB 4; Length 1149;
 Best Local Similarity 21.5%; Pred. No. 0.49;

RESULT 1087
ID ADK71138 standard; protein; 1164 AA.
DE 12S/AR chimeric protein.
PN WO2004015086-A2.
PD 19-FEB-2004.
PA (UYUO) UNIV JOHNS HOPKINS.
Query Match 7.0%; Score 127.5; DB 8; Length 1164;
Best Local Similarity 25.2%; Pred. No. 0.5;
RESULT 1088
ID AED74136 standard; protein; 1166 AA.
DE Human placental protein SEQ ID NO:964.
PN US2005255114-A1.
PD 17-NOV-2005.
PA (NUVE-) NUVELO INC.
Query Match 7.0%; Score 127.5; DB 9; Length 1166;
Best Local Similarity 25.4%; Pred. No. 0.5;
RESULT 1089
ID ADQ14315 standard; protein; 1424 AA.
DE Human collagen type IV alpha 3 (Goodpasture antigen).
PN WO2004060262-A2.
PD 22-JUL-2004.
PA (LORA-) LORANTIS LTD.
Query Match 7.0%; Score 127.5; DB 8; Length 1424;
Best Local Similarity 26.6%; Pred. No. 0.64;
RESULT 1090
ID ADR41697 standard; protein; 1424 AA.
DE Human collagen (aa sequence), type IV, alpha 3 (Goodpasture antigen).
PN WO2004064863-A1.
PD 05-AUG-2004.
PA (LORA-) LORANTIS LTD.
Query Match 7.0%; Score 127.5; DB 8; Length 1424;
Best Local Similarity 26.6%; Pred. No. 0.64;
RESULT 1091
ID ADU06693 standard; protein; 1424 AA.
DE Novel bronchial cancer-associated human protein SeqID919.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERW/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 7.0%; Score 127.5; DB 8; Length 1424;
Best Local Similarity 26.6%; Pred. No. 0.64;
RESULT 1092
ID AEB77777 standard; protein; 1424 AA.
DE Human Goodpasture antigen, collagen, type IV, alpha 3.
PN WO2005073250-A2.
PD 11-AUG-2005.
PA (LORA-) LORANTIS LTD.
Query Match 7.0%; Score 127.5; DB 9; Length 1424;
Best Local Similarity 26.6%; Pred. No. 0.64;
RESULT 1093
ID ADD45053 standard; protein; 1453 AA.
DE Rat Protein CAB01633, SEQ ID NO 10485.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.0%; Score 127.5; DB 7; Length 1453;
Best Local Similarity 24.7%; Pred. No. 0.65;
RESULT 1094
ID ADD45057 standard; protein; 1453 AA.
DE Rat Protein CAB01633, SEQ ID NO 10489.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.0%; Score 127.5; DB 7; Length 1453;
Best Local Similarity 24.7%; Pred. No. 0.65;
RESULT 1095
ID ADD48341 standard; protein; 1453 AA.
DE Rat Protein CAB01633, SEQ ID NO 14041.
PN WO2003016475-A2.
PD 27-FEB-2003.

PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.0%; Score 127.5; DB 7; Length 1453;
Best Local Similarity 24.7%; Pred. No. 0.65;
RESULT 1096
ID ADD45049 standard; protein; 1453 AA.
DE Rat Protein CAB01633, SEQ ID NO 10481.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.0%; Score 127.5; DB 7; Length 1453;
Best Local Similarity 24.7%; Pred. No. 0.65;
RESULT 1097
ID ADD48337 standard; protein; 1453 AA.
DE Rat Protein CAB01633, SEQ ID NO 14037.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.0%; Score 127.5; DB 7; Length 1453;
Best Local Similarity 24.7%; Pred. No. 0.65;
RESULT 1098
ID ADD48345 standard; protein; 1453 AA.
DE Rat Protein CAB01633, SEQ ID NO 14045.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.0%; Score 127.5; DB 7; Length 1453;
Best Local Similarity 24.7%; Pred. No. 0.65;
RESULT 1099
ID AEC11998 standard; protein; 1453 AA.
DE Rat surrogate marker of neuropathic pain protein SEQ ID NO 344.
PN WO2005083125-A2.
PD 09-SEP-2005.
PA (BIOJ) BIOGEN IDEC MA INC.
Query Match 7.0%; Score 127.5; DB 9; Length 1453;
Best Local Similarity 24.7%; Pred. No. 0.65;
RESULT 1100
ID AEC12088 standard; protein; 1453 AA.
DE Rat surrogate marker of neuropathic pain protein SEQ ID NO 434.
PN WO2005083125-A2.
PD 09-SEP-2005.
PA (BIOJ) BIOGEN IDEC MA INC.
Query Match 7.0%; Score 127.5; DB 9; Length 1453;
Best Local Similarity 24.7%; Pred. No. 0.65;
RESULT 1101
ID AEC12604 standard; protein; 1453 AA.
DE Rat surrogate marker of neurotrophic activity protein SEQ ID NO 950.
PN WO2005083125-A2.
PD 09-SEP-2005.
PA (BIOJ) BIOGEN IDEC MA INC.
Query Match 7.0%; Score 127.5; DB 9; Length 1453;
Best Local Similarity 24.7%; Pred. No. 0.65;
RESULT 1102
ID AEC12572 standard; protein; 1453 AA.
DE Rat surrogate marker of neurotrophic activity protein SEQ ID NO 918.
PN WO2005083125-A2.
PD 09-SEP-2005.
PA (BIOJ) BIOGEN IDEC MA INC.
Query Match 7.0%; Score 127.5; DB 9; Length 1453;
Best Local Similarity 24.7%; Pred. No. 0.65;
RESULT 1103
ID ADE87048 standard; protein; 1464 AA.
DE Human pancreatic cell protein sequence SeqID508.
PN WO2003060145-A2.
PD 24-JUL-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 7.0%; Score 127.5; DB 7; Length 1464;
Best Local Similarity 24.4%; Pred. No. 0.66;
RESULT 1104
ID ABB50291 standard; protein; 1466 AA.

DE Collagen type III alpha-1 ovarian tumour marker protein, SEQ ID NO:72.
FN WO200175177-A2.
PD 11-OCT-2001.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 7.0%; Score 127.5; DB 4; Length 1466;
Best Local Similarity 25.4%; Pred. No. 0.66;
RESULT 1105
ID ABB90747 standard; protein; 1466 AA.
DE Human Tumour Endothelial Marker polypeptide SRQ ID NO 226.
FN WO200210217-A2.
PD 07-FEB-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 7.0%; Score 127.5; DB 5; Length 1466;
Best Local Similarity 25.4%; Pred. No. 0.66;
RESULT 1106
ID ABU54454 standard; protein; 1466 AA.
DE Human tumour endothelial marker TEM 15.
FN WO200283874-A2.
PD 24-OCT-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 7.0%; Score 127.5; DB 6; Length 1466;
Best Local Similarity 25.4%; Pred. No. 0.66;
RESULT 1107
ID ABR47418 standard; protein; 1466 AA.
DE Breast cancer associated protein sequence SEQ ID NO:68.
FN WO200304989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 7.0%; Score 127.5; DB 6; Length 1466;
Best Local Similarity 25.4%; Pred. No. 0.66;
RESULT 1108
ID ADP65248 standard; protein; 1466 AA.
DE Human alpha 1 type III collagen preproprotein.
FN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 7.0%; Score 127.5; DB 7; Length 1466;
Best Local Similarity 25.4%; Pred. No. 0.66;
RESULT 1109
ID ADP65210 standard; protein; 1466 AA.
DE Human alpha 1 type III collagen preproprotein.
FN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 7.0%; Score 127.5; DB 7; Length 1466;
Best Local Similarity 25.4%; Pred. No. 0.66;
RESULT 1110
ID ADQ26091 standard; protein; 1466 AA.
DE Type III, alpha 1 collagen.
FN WO2004056386-A2.
PD 08-JUL-2004.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 7.0%; Score 127.5; DB 8; Length 1466;
Best Local Similarity 25.4%; Pred. No. 0.66;
RESULT 1111
ID ADQ29677 standard; protein; 1466 AA.
DE Human colorectal cancer-associated protein #32.
FN EPI439393-A2.
PD 21-JUL-2004.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 7.0%; Score 127.5; DB 8; Length 1466;
Best Local Similarity 25.4%; Pred. No. 0.66;
RESULT 1112
ID ADR16802 standard; protein; 1466 AA.
DE Human collagen III alpha2 (III) fragment protein.
FN US2004151731-A1.
PD 05-AUG-2004.
PA (JICH/) JICHA D L.
Query Match 7.0%; Score 127.5; DB 8; Length 1466;
Best Local Similarity 25.4%; Pred. No. 0.66;
RESULT 1113
ID ADR16427 standard; protein; 1466 AA.

DE Human collagen I alpha2 (III) fragment protein.
FN US2004151732-A1.
PD 05-AUG-2004.
PA (JICH/) JICHA D L.
PA (PELU/) PELUSE S.
Query Match 7.0%; Score 127.5; DB 8; Length 1466;
Best Local Similarity 25.4%; Pred. No. 0.66;
RESULT 1114
ID ABM80366 standard; protein; 1466 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO2665, SEQ:922.
FN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 127.5; DB 8; Length 1466;
Best Local Similarity 25.4%; Pred. No. 0.66;
RESULT 1115
ID ADR67267 standard; protein; 1466 AA.
DE Human bladder cancer associated amino acid sequence.
FN WO2004078613-A2.
PD 10-SEP-2004.
PA (HERR/) HERR A.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (STAU/) STAUB E.
PA (PILA/) PILARSKY C.
PA (SPEC/) SPECHT T.
Query Match 7.0%; Score 127.5; DB 8; Length 1466;
Best Local Similarity 25.4%; Pred. No. 0.66;
RESULT 1116
ID ADV70235 standard; protein; 1466 AA.
DE Tumour-associated antigenic target polypeptide TAT474.
FN WO2004112829-A2.
PD 29-DEC-2004.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 127.5; DB 9; Length 1466;
Best Local Similarity 25.4%; Pred. No. 0.66;
RESULT 1117
ID ADZ09873 standard; protein; 1466 AA.
DE Human breast cancer marker COL3A1 protein.
FN EPI522594-A2.
PD 13-APR-2005.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 7.0%; Score 127.5; DB 9; Length 1466;
Best Local Similarity 25.4%; Pred. No. 0.66;
RESULT 1118
ID AEA04495 standard; protein; 1466 AA.
DE Human protein from gene overexpressed in cancer, COL3A1.
FN WO2005044990-A2.
PD 19-MAY-2005.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 7.0%; Score 127.5; DB 9; Length 1466;
Best Local Similarity 25.4%; Pred. No. 0.66;
RESULT 1119
ID AEF69866 standard; protein; 1466 AA.
DE Microsatellite instability colorectal tumor marker protein SEQ ID NO:44.
FN WO2006015047-A2.
PD 09-FEB-2006.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 7.0%; Score 127.5; DB 10; Length 1466;
Best Local Similarity 25.4%; Pred. No. 0.66;
RESULT 1120
ID AEF69989 standard; protein; 1466 AA.
DE Colorectal cancer-associated marker protein SEQ ID NO:167.
FN WO2006015047-A2.
PD 09-FEB-2006.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 7.0%; Score 127.5; DB 10; Length 1466;
Best Local Similarity 25.4%; Pred. No. 0.66;
RESULT 1121
ID AEH24255 standard; protein; 1466 AA.

DE Human type III collagen protein - SEQ ID 1.
PN US2006100138-A1.
PD 11-MAY-2006.
PA (OLSE/) OLSEN D R.
PA (POLA/) POLAREK J W.
PA (YANG/) YANG C.
Query Match 7.0%; Score 127.5; DB 10; Length 1466;
Best Local Similarity 25.4%; Pred. No. 0.66;
RESULT 1122
ID ABG15191 standard; protein; 1469 AA.
DE Novel human diagnostic protein #15182.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 127.5; DB 4; Length 1469;
Best Local Similarity 25.4%; Pred. No. 0.66;
RESULT 1123
ID AAB40755 standard; protein; 1485 AA.
DE Human ORFX ORF519 polypeptide sequence SEQ ID NO:1038.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 7.0%; Score 127.5; DB 3; Length 1485;
Best Local Similarity 21.5%; Pred. No. 0.67;
RESULT 1124
ID ABG03458 standard; protein; 1485 AA.
DE Novel human diagnostic protein #3449.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 127.5; DB 4; Length 1485;
Best Local Similarity 21.5%; Pred. No. 0.67;
RESULT 1125
ID ABR64194 standard; protein; 1485 AA.
DE Angiogenesis protein BNO70.
PN WO2003027285-A1.
PD 03-APR-2003.
PA (BION-) BIONOMICS LTD.
Query Match 7.0%; Score 127.5; DB 6; Length 1485;
Best Local Similarity 21.5%; Pred. No. 0.67;
RESULT 1126
ID ADQ97166 standard; protein; 1539 AA.
DE Human cancer associated sequence HP1-08-009, SEQ ID 142.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 7.0%; Score 127.5; DB 8; Length 1539;
Best Local Similarity 21.5%; Pred. No. 0.7;
RESULT 1127
ID ADU04510 standard; protein; 1572 AA.
DE SLPI-Collagen III amino acid sequence, seq id 27.
PN GB2400852-A.
PD 27-OCT-2004.
PA (UYMA-) UNIV VICTORIA MANCHESTER.
Query Match 7.0%; Score 127.5; DB 8; Length 1572;
Best Local Similarity 25.4%; Pred. No. 0.72;
RESULT 1128
ID ADU04497 standard; protein; 1604 AA.
DE Modified pro-alpha chain amino acid, seq id 14.
PN GB2400852-A.
PD 27-OCT-2004.
PA (UYMA-) UNIV VICTORIA MANCHESTER.
Query Match 7.0%; Score 127; DB 9; Length 1014;
Best Local Similarity 26.7%; Pred. No. 0.46;
RESULT 1129
ID ABM84483 standard; protein; 1611 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4732.
PN WO200403973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.0%; Score 127.5; DB 8; Length 1611;
Best Local Similarity 26.6%; Pred. No. 0.74;
RESULT 1130
ID AEA64562 standard; protein; 1642 AA.
DE Human lupus-related protein #10.
PN WO2004076639-A2.
PD 10-SEP-2004.
PA (AMHP) WYETH.
PA (OTOO/) O'TOOLE M M.
PA (WEIL/) WEI L.
Query Match 7.0%; Score 127.5; DB 8; Length 1642;
Best Local Similarity 26.6%; Pred. No. 0.75;
RESULT 1131
ID ADD47063 standard; protein; 1670 AA.
DE Human Protein NP_000082, SEQ ID NO 12751.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.0%; Score 127.5; DB 7; Length 1670;
Best Local Similarity 26.8%; Pred. No. 0.77;
RESULT 1132
ID AEA64561 standard; protein; 1670 AA.
DE Human lupus-related protein #9.
PN WO2004076639-A2.
PD 10-SEP-2004.
PA (AMHP) WYETH.
PA (OTOO/) O'TOOLE M M.
PA (WEIL/) WEI L.
Query Match 7.0%; Score 127.5; DB 8; Length 1670;
Best Local Similarity 26.6%; Pred. No. 0.77;
RESULT 1133
ID ABR42661 standard; protein; 1726 AA.
DE Decorin-modified pro-alpha chain.
PN WO2003035692-A2.
PD 01-MAY-2003.
PA (UYMA-) UNIV VICTORIA MANCHESTER.
Query Match 7.0%; Score 127.5; DB 6; Length 1726;
Best Local Similarity 25.4%; Pred. No. 0.8;
RESULT 1134
ID ADU04493 standard; protein; 1950 AA.
DE Modified pro-alpha chain amino acid sequence, seq id 10.
PN GB2400852-A.
PD 27-OCT-2004.
PA (UYMA-) UNIV VICTORIA MANCHESTER.
Query Match 7.0%; Score 127.5; DB 8; Length 1950;
Best Local Similarity 25.4%; Pred. No. 0.93;
RESULT 1135
ID ABO58767 standard; protein; 430 AA.
DE Human genome derived single exon protein #5001.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 7.0%; Score 127; DB 8; Length 430;
Best Local Similarity 24.7%; Pred. No. 0.17;
RESULT 1136
ID ADM99578 standard; protein; 1014 AA.
DE Human gelatin protein - SEQ ID 11.
PN WO2005012356-A2.
PD 10-FEB-2005.
PA (FIBR-) FIBROGEN INC.
Query Match 7.0%; Score 127; DB 9; Length 1014;
Best Local Similarity 26.7%; Pred. No. 0.46;
RESULT 1137
ID AAE06644 standard; protein; 1106 AA.
DE Human Cubitus interruptus (Ci) homologue protein, GLI-1.
PN WO200156376-A1.
PD 09-AUG-2001.
PA (KARO-) KAROLINSKA INNOVATIONS AB.
Query Match 7.0%; Score 127; DB 4; Length 1106;
Best Local Similarity 22.2%; Pred. No. 0.51;
RESULT 1138
ID AAB70611 standard; protein; 1106 AA.
DE Human GLI-1 amino acid sequence SEQ ID NO:5.
DE

PN W0200112655-A1.
PD 22-FEB-2001.
PA (KARO-) KAROLINSKA INNOVATIONS AB.
Query Match 7.0%; Score 127; DB 4; Length 1106;
Best Local Similarity 22.2%; Pred. No. 0.51;
RESULT 1139
ID AAU12085 standard; protein; 1106 AA.
DE Human glioma-associated oncogene-1 protein.
PN US6329203-B1.
PD 11-DEC-2001.
PA (ISIS-) ISIS PHARM INC.
Query Match 7.0%; Score 127; DB 5; Length 1106;
Best Local Similarity 22.2%; Pred. No. 0.51;
RESULT 1140
ID AAO17111 standard; protein; 1106 AA.
DE Human Gli1 protein SEQ ID NO: 15.
PN W0200211752-A1.
PD 14-FEB-2002.
PA (TAKA) TAKEDA CHEM IND LTD.
Query Match 7.0%; Score 127; DB 5; Length 1106;
Best Local Similarity 22.2%; Pred. No. 0.51;
RESULT 1141
ID AAO17109 standard; protein; 1106 AA.
DE Human Gli1 protein SEQ ID NO: 11.
PN W0200211752-A1.
PD 14-FEB-2002.
PA (TAKA) TAKEDA CHEM IND LTD.
Query Match 7.0%; Score 127; DB 5; Length 1106;
Best Local Similarity 22.2%; Pred. No. 0.51;
RESULT 1142
ID AAO17110 standard; protein; 1106 AA.
DE Human Gli1 protein SEQ ID NO: 13.
PN W0200211752-A1.
PD 14-FEB-2002.
PA (TAKA) TAKEDA CHEM IND LTD.
Query Match 7.0%; Score 127; DB 5; Length 1106;
Best Local Similarity 22.2%; Pred. No. 0.51;
RESULT 1143
ID ADA83748 standard; protein; 1106 AA.
DE Human GLI protein.
PN W02002103028-A2.
PD 27-DEC-2002.
PA (BIOM-) BIOMEDICAL CENT.
Query Match 7.0%; Score 127; DB 6; Length 1106;
Best Local Similarity 22.2%; Pred. No. 0.51;
RESULT 1144
ID ADD19024 standard; protein; 1106 AA.
DE Human disease related protein SeqID513.
PN W02003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 7.0%; Score 127; DB 7; Length 1106;
Best Local Similarity 22.2%; Pred. No. 0.51;
RESULT 1145
ID ABM81418 standard; protein; 1106 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO9112, SEQ:3668.
PN W02004030615-A2.
PD 15-APR-2004.
PA (GETH) GEMENTECH INC.
Query Match 7.0%; Score 127; DB 8; Length 1106;
Best Local Similarity 22.2%; Pred. No. 0.51;
RESULT 1146
ID ADX06067 standard; protein; 1106 AA.
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 632.
PN W02005012875-A2.
PD 10-FEB-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 7.0%; Score 127; DB 9; Length 1106;
Best Local Similarity 22.2%; Pred. No. 0.51;
RESULT 1147
ID AEA27506 standard; protein; 1106 AA.
DE Human zinc finger protein transcription factor.GLI1, SEQ ID NO: 16.
PN US2005112707-A1.

PD 26-MAY-2005.
PA (ALTA/) ALTABA A R I.
PA (SANC/) SANCHEZ P.
PA (ROMW/) ROM W.
PA (WONG/) WONG K T.
Query Match 7.0%; Score 127; DB 9; Length 1106;
Best Local Similarity 22.2%; Pred. No. 0.51;
RESULT 1148
ID AEA30109 standard; protein; 1106 AA.
DE Glioblastoma-related zinc finger protein #8.
PN US2005110922-A1.
PD 16-JUN-2005.
PA (ALTA/) ALTABA A R I.
PA (DATT/) DATTA S.
PA (DATT/) DATTA M.
Query Match 7.0%; Score 127; DB 9; Length 1106;
Best Local Similarity 22.2%; Pred. No. 0.51;
RESULT 1149
ID AAB70617 standard; protein; 1118 AA.
DE Human haematoglutinin-tagged GLI-1 amino acid sequence SEQ ID NO:11.
PN W0200112655-A1.
PD 22-FEB-2001.
PA (KARO-) KAROLINSKA INNOVATIONS AB.
Query Match 7.0%; Score 127; DB 4; Length 1118;
Best Local Similarity 22.2%; Pred. No. 0.52;
RESULT 1150
ID ABB98398 standard; protein; 19938 AA.
DE Streptomyces viridochromogenes Avi gene cluster polypeptide frame 1.
PN W0200268436-A1.
PD 06-SEP-2002.
PA (COMB-) COMBINATURE BIOPHARM AG.
Query Match 7.0%; Score 127; DB 6; Length 19938;
Best Local Similarity 22.2%; Pred. No. 16;
RESULT 1151
ID ADM87821 standard; protein; 342 AA.
DE Human EST Derived amino acid sequence SEQ ID NO:914.
PN W02004009834-A2.
PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 6.9%; Score 126.5; DB 8; Length 342;
Best Local Similarity 23.5%; Pred. No. 0.14;
RESULT 1152
ID ABO81861 standard; protein; 442 AA.
DE Pseudomonas aeruginosa polypeptide #14036.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.9%; Score 126.5; DB 7; Length 442;
Best Local Similarity 23.3%; Pred. No. 0.19;
RESULT 1153
ID AAB56866 standard; protein; 531 AA.
DE Human prostate cancer antigen protein sequence SEQ ID NO:1444.
PN W0200055174-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 6.9%; Score 126.5; DB 3; Length 531;
Best Local Similarity 27.6%; Pred. No. 0.23;
RESULT 1154
ID AAR12229 standard; protein; 576 AA.
DE Type/androgen receptor N-terminal domain fusion protein.
PN W09107423-A.
PD 30-MAY-1991.
PA (ARCH-) ARCH DEV CORP.
Query Match 6.9%; Score 126.5; DB 2; Length 576;
Best Local Similarity 26.4%; Pred. No. 0.26;
RESULT 1155
ID ABG69471 standard; protein; 638 AA.
DE Human bait protein splicing factor 1.
PN W0200253726-A2.
PD 11-JUL-2002.
PA (HYBR-) HYBRIGENICS.
PA (CNRS) CENT NAT RECH SCI.

Query Match 6.9%; Score 126.5; DB 5; Length 638;
 Best Local Similarity 27.6%; Pred. No. 0.29;
 RESULT 1156
 ID ABO53021 standard; protein; 639 AA.
 DE Human splinosome associated protein (SAP) #81.
 PN US2003068803-A1.
 PD 10-APR-2003.
 PA (REED/) REED R.
 PA (ZHOU/) ZHOU Z.
 Query Match 6.9%; Score 126.5; DB 6; Length 639;
 Best Local Similarity 27.6%; Pred. No. 0.29;
 RESULT 1157
 ID AAU10545 standard; protein; 668 AA.
 DE Rat synapsin IB (YSG8) polypeptide.
 PN WO200175440-A2.
 PD 11-OCT-2001.
 PA (WELF-) WELFIDE CORP.
 Query Match 6.9%; Score 126.5; DB 5; Length 668;
 Best Local Similarity 22.8%; Pred. No. 0.31;
 RESULT 1158
 ID AAE36862 standard; protein; 714 AA.
 DE Human collagen type II protein.
 PN WO2003021226-A2.
 PD 13-MAR-2003.
 PA (PHAA) PHARMACIA CORP.
 Query Match 6.9%; Score 126.5; DB 6; Length 714;
 Best Local Similarity 23.4%; Pred. No. 0.33;
 RESULT 1159
 ID ADI33185 standard; protein; 714 AA.
 DE Human collagen type II-related protein.
 PN US2003219843-A1.
 PD 27-NOV-2003.
 PA (WELS/) WELSCH D J.
 PA (DUFF/) DUFFIN K L.
 PA (NEMI/) NEMROWSKIY O V.
 PA (DUFF/) DUFFIELD D R.
 PA (SUNY/) SUNYER T.
 PA (HOWA/) HOWARD C P.
 PA (ABRA/) ABRAMS M.
 Query Match 6.9%; Score 126.5; DB 8; Length 714;
 Best Local Similarity 23.4%; Pred. No. 0.33;
 RESULT 1160
 ID RAM40492 standard; protein; 759 AA.
 DE Human polypeptide SEQ ID NO 5423.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 6.9%; Score 126.5; DB 4; Length 759;
 Best Local Similarity 23.3%; Pred. No. 0.36;
 RESULT 1161
 ID RAM40493 standard; protein; 759 AA.
 DE Human polypeptide SEQ ID NO 5424.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 6.9%; Score 126.5; DB 4; Length 759;
 Best Local Similarity 23.3%; Pred. No. 0.36;
 RESULT 1162
 ID AEJ43411 standard; protein; 1017 AA.
 DE Human unidentified protein II alpha 1.
 PN WO9316724-A1.
 PD 02-SEP-1993.
 PA (AUTO-) AUTOIMMUNE INC.
 Query Match 6.9%; Score 126.5; DB 2; Length 1017;
 Best Local Similarity 23.4%; Pred. No. 0.51;
 RESULT 1163
 ID ABB59410 standard; protein; 1612 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 5022.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 6.9%; Score 126.5; DB 4; Length 1612;
 Best Local Similarity 22.3%; Pred. No. 0.89;

RESULT 1164
 ID ADL25642 standard; protein; 4952 AA.
 DE Human diagnostic protein, NOV18.
 PN US2004005557-A1.
 PD 08-JAN-2004.
 PA (PADI/) PADIGARU M.
 PA (ALSO/) ALSOBROOK J P.
 PA (COLM/) COLMAN S D.
 PA (SPYT/) SPYTEK K A.
 PA (BOLD/) BOLDOG F L.
 PA (VERN/) VERNET C A M.
 PA (LILL/) LI L.
 PA (SHEN/) SHENOY S G.
 PA (CASM/) CASMAN S J.
 PA (GUOX/) GUO X.
 PA (EDIN/) EDINGER S R.
 PA (MACD/) MACDOUGALL J R.
 PA (MALY/) MALYANKAR U M.
 PA (PATT/) PATTURAJAN M.
 PA (SHIM/) SHIMKETS R A.
 PA (PENA/) PENNA C E A.
 PA (TCHE/) TCHERNEV V T.
 PA (ZERH/) ZERHUSEN B D.
 PA (MILL/) MILLET I.
 PA (LEPL/) MILLER C E.
 PA (SMIT/) SMITHSON G.
 PA (BAUM/) BAUMGARTNER J C.
 PA (HERR/) HERRMANN J L.
 PA (PEYM/) PEYMAN J A.
 PA (GORM/) GORMAN L.
 PA (MEZE/) MEZES P D.
 PA (KEKU/) KEKUDA R.
 PA (TAUP/) TAUPIER R J.
 PA (GERL/) GERLACH V.
 PA (GROS/) GROSSE W M.
 PA (LIUX/) LIU X.
 PA (ELLE/) ELLERMAN K.
 PA (ROTH/) ROTHENBERG M.
 PA (STOW/) STONE D J.
 PA (BURG/) BURGESS C E.
 Query Match 6.9%; Score 126.5; DB 8; Length 4952;
 Best Local Similarity 24.2%; Pred. No. 3.4;
 RESULT 1165
 ID ASG10927 standard; protein; 325 AA.
 DE Novel human diagnostic protein #10918.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 6.9%; Score 126; DB 4; Length 325;
 Best Local Similarity 30.3%; Pred. No. 0.14;
 RESULT 1166
 ID ABM5384 standard; protein; 391 AA.
 DE Mouse protein sequence MCP22413.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 6.9%; Score 126; DB 7; Length 391;
 Best Local Similarity 25.7%; Pred. No. 0.18;
 RESULT 1167
 ID AAB68065 standard; protein; 416 AA.
 DE Amino acid sequence of a recombinant human gelatin.
 PN WO200134801-A2.
 PD 17-MAY-2001.
 PA (FIBR-) FIBROGEN INC.
 Query Match 6.9%; Score 126; DB 4; Length 416;
 Best Local Similarity 25.9%; Pred. No. 0.19;
 RESULT 1168
 ID AAE02711 standard; protein; 416 AA.
 DE Human alaphal (I) type I collagen helical domain (residues 615-1030).
 PN WO200134646-A2.
 PD 17-MAY-2001.
 PA (FIBR-) FIBROGEN INC.

Query Match
Best Local Similarity 6.9%; Score 126; DB 4; Length 416;
RESULT 1169
ID ADK341103 standard; protein; 416 AA.
DE Novel human polypeptide SeqID6185.
PN WO200216439-A2.
PD 28-FEB-2002.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 6.9%; Score 126; DB 5; Length 416;
RESULT 1170
ID ADB84298 standard; protein; 416 AA.
DE Recombinant gelatin #11.
PN US2003064074-A1.
PD 03-APR-2003.
PA (CHAN/) CHANG R C.
PA (KIVI/) KIVIRIKKO K I.
PA (NEFF/) NEFF T B.
PA (OLSE/) OLSEN D R.
PA (POLA/) POLAREK J W.
Query Match
Best Local Similarity 6.9%; Score 126; DB 7; Length 416;
RESULT 1171
ID AED81096 standard; protein; 483 AA.
DE Human IRX5 protein, SEQ ID No:4.
PN WO2005110464-A2.
PD 24-NOV-2005.
PA (UYOR-) UNIV OREGON HEALTH SCI.
Query Match
Best Local Similarity 6.9%; Score 126; DB 9; Length 483;
RESULT 1172
ID AEI17445 standard; protein; 483 AA.
DE Human cancer treatment biomarker amino acid sequence - SEQ ID 332.
PN US2006121511-A1.
PD 08-JUN-2006.
PA (LEE/) LEE H.
PA (SHAW/) SHAW P.
PA (CLAR/) CLARK E A.
Query Match
Best Local Similarity 6.9%; Score 126; DB 10; Length 483;
RESULT 1173
ID ADM99569 standard; protein; 498 AA.
DE Human gelatin protein - SEQ ID 2.
PN WO2005012356-A2.
PD 10-FEB-2005.
PA (FIBR-) FIBROGEN INC.
Query Match
Best Local Similarity 6.9%; Score 126; DB 9; Length 498;
RESULT 1174
ID ADM99568 standard; protein; 498 AA.
DE Human gelatin protein - SEQ ID 1.
PN WO2005012356-A2.
PD 10-FEB-2005.
PA (FIBR-) FIBROGEN INC.
Query Match
Best Local Similarity 6.9%; Score 126; DB 9; Length 498;
RESULT 1175
ID AAB68062 standard; protein; 500 AA.
DE Amino acid sequence of a recombinant human gelatin.
PN WO200134801-A2.
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match
Best Local Similarity 6.9%; Score 126; DB 4; Length 500;
RESULT 1176
ID AAE02708 standard; protein; 500 AA.
DE Human alpha1 (I) type I collagen helical domain (residues 531-1030).
PN WO200134646-A2.
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match
Best Local Similarity 6.9%; Score 126; DB 4; Length 500;
RESULT 1177
ID AAE02718 standard; protein; 662 AA.
DE Amino acid sequence of a recombinant human gelatin.
PN WO200134801-A2.
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match
Best Local Similarity 6.9%; Score 126; DB 4; Length 510;
RESULT 1178
ID AAB68066 standard; protein; 510 AA.
DE Amino acid sequence of a recombinant human gelatin.
PN WO200134801-A2.
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match
Best Local Similarity 6.9%; Score 126; DB 4; Length 510;
RESULT 1179
ID AAE02712 standard; protein; 510 AA.
DE Recombinant human gelatin #1.
PN WO200134646-A2.
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match
Best Local Similarity 6.9%; Score 126; DB 4; Length 510;
RESULT 1180
ID ADB84299 standard; protein; 510 AA.
DE Recombinant gelatin #12.
PN US2003064074-A1.
PD 03-APR-2003.
PA (CHAN/) CHANG R C.
PA (KIVI/) KIVIRIKKO K I.
PA (NEFF/) NEFF T B.
PA (OLSE/) OLSEN D R.
PA (POLA/) POLAREK J W.
Query Match
Best Local Similarity 6.9%; Score 126; DB 7; Length 510;
RESULT 1181
ID ADE87046 standard; protein; 516 AA.
DE Human pancreatic cell protein sequence SeqID506.
PN WO2003060145-A2.
PD 24-JUL-2003.
PA (DIAD-) DIADEXUS INC.
Query Match
Best Local Similarity 6.9%; Score 126; DB 7; Length 516;
RESULT 1182
ID ADM99570 standard; protein; 660 AA.
DE Human gelatin protein - SEQ ID 3.
PN WO2005012356-A2.
PD 10-FEB-2005.
PA (FIBR-) FIBROGEN INC.
Query Match
Best Local Similarity 6.9%; Score 126; DB 9; Length 660;
RESULT 1183
ID ADM99571 standard; protein; 660 AA.
DE Human gelatin protein - SEQ ID 4.
PN WO2005012356-A2.
PD 10-FEB-2005.
PA (FIBR-) FIBROGEN INC.
Query Match
Best Local Similarity 6.9%; Score 126; DB 9; Length 660;
RESULT 1184
ID AAB68072 standard; protein; 662 AA.
DE Amino acid sequence of a recombinant human gelatin.
PN WO200134801-A2.
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match
Best Local Similarity 6.9%; Score 126; DB 4; Length 662;
RESULT 1185
ID AAE02718 standard; protein; 662 AA.

DE Human alpha1 (I) type I collagen helical domain (residues 531-1192).
PN WO200134646-A2.
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match 6.9%; Score 126; DB 4; Length 662;
Best Local Similarity 25.9%; Pred. No. 0.33;
RESULT 1186
ID ADB84306 standard; protein; 662 AA.
DE Recombinant gelatin #18.
PN US2003064074-A1.
PD 03-APR-2003.
PA (CHAN/) CHANG R C.
PA (KIVI/) KIVIRIKKO K I.
PA (NEFF/) NEFF T B.
PA (OLSE/) OLSEN D R.
PA (POLA/) POLAREK J W.
Query Match 6.9%; Score 126; DB 7; Length 662;
Best Local Similarity 25.9%; Pred. No. 0.33;
RESULT 1187
ID ADE28201 standard; protein; 685 AA.
DE Human MDDT protein - SEQ ID 51.
PN WO2003046152-A2.
PD 05-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.9%; Score 126; DB 7; Length 685;
Best Local Similarity 23.3%; Pred. No. 0.35;
RESULT 1188
ID ABP70830 standard; protein; 743 AA.
DE Marine CQSP9.
PN WO2003022992-A2.
PD 20-MAR-2003.
PA (SCHE) SCHERING CORP.
Query Match 6.9%; Score 126; DB 6; Length 743;
Best Local Similarity 24.5%; Pred. No. 0.38;
RESULT 1189
ID ADN95128 standard; protein; 760 AA.
DE Human LEC protein sequence SeqID50.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 6.9%; Score 126; DB 7; Length 760;
Best Local Similarity 23.3%; Pred. No. 0.39;
RESULT 1190
ID ADE87052 standard; protein; 886 AA.
DE Human pancreatic cell protein sequence SeqID512.
PN WO2003060145-A2.
PD 24-JUL-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 6.9%; Score 126; DB 7; Length 886;
Best Local Similarity 25.9%; Pred. No. 0.47;
RESULT 1191
ID ABU96717 standard; protein; 986 AA.
DE Human nucleic acid-associated protein (NAAAP) #46.
PN WO2003023003-A2.
PD 20-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.9%; Score 126; DB 6; Length 986;
Best Local Similarity 26.8%; Pred. No. 0.54;
RESULT 1192
ID ADW99574 standard; protein; 1014 AA.
DE Human gelatin protein - SEQ ID 7.
PN WO2005012356-A2.
PD 10-FEB-2005.
PA (FIBR-) FIBROGEN INC.
Query Match 6.9%; Score 126; DB 9; Length 1014;
Best Local Similarity 25.9%; Pred. No. 0.56;
RESULT 1193
ID ADW99573 standard; protein; 1014 AA.
DE Human gelatin protein - SEQ ID 6.
PN WO2005012356-A2.
PD 10-FEB-2005.
PA (FIBR-) FIBROGEN INC.

Query Match 6.9%; Score 126; DB 9; Length 1014;
Best Local Similarity 25.9%; Pred. No. 0.56;
RESULT 1194
ID ADW99572 standard; protein; 1014 AA.
DE Human gelatin protein - SEQ ID 5.
PN WO2005012356-A2.
PD 10-FEB-2005.
PA (FIBR-) FIBROGEN INC.
Query Match 6.9%; Score 126; DB 9; Length 1014;
Best Local Similarity 25.9%; Pred. No. 0.56;
RESULT 1195
ID ADW99580 standard; protein; 1014 AA.
DE Human gelatin protein - SEQ ID 13.
PN WO2005012356-A2.
PD 10-FEB-2005.
PA (FIBR-) FIBROGEN INC.
Query Match 6.9%; Score 126; DB 9; Length 1014;
Best Local Similarity 25.9%; Pred. No. 0.56;
RESULT 1196
ID ADZ70363 standard; protein; 1040 AA.
DE Human protein from lung cancer marker gene COL1A1.
PN WO2005032495-A2.
PD 14-APR-2005.
PA (FARB) BAYER PHARM CORP.
Query Match 6.9%; Score 126; DB 9; Length 1040;
Best Local Similarity 25.9%; Pred. No. 0.57;
RESULT 1197
ID AAY84541 standard; protein; 1057 AA.
DE Amino acid sequence of a human collagen 1 (alpha1) protein.
PN EP92586-A2.
PD 12-APR-2000.
PA (USSU) US SURGICAL CORP.
Query Match 6.9%; Score 126; DB 3; Length 1057;
Best Local Similarity 25.9%; Pred. No. 0.59;
RESULT 1198
ID AAY84544 standard; protein; 1057 AA.
DE A human collagen 1 (alpha1) protein helical region.
PN EP92586-A2.
PD 12-APR-2000.
PA (USSU) US SURGICAL CORP.
Query Match 6.9%; Score 126; DB 3; Length 1057;
Best Local Similarity 25.9%; Pred. No. 0.59;
RESULT 1199
ID AAY84403 standard; protein; 1058 AA.
DE Amino acid sequence of human type 1 (alpha1) collagen polypeptide.
PN WO200014201-A1.
PD 16-MAR-2000.
PA (USSU) US SURGICAL CORP.
PA (PAOL/) PAOLELLA D N.
PA (GRUS/) GRUSKIN E A.
PA (BUEC/) BUECHTER D D.
Query Match 6.9%; Score 126; DB 3; Length 1058;
Best Local Similarity 25.9%; Pred. No. 0.59;
RESULT 1200
ID AAR89472 standard; protein; 1107 AA.
DE Collagen/decorin(aa46-93) fusion protein.
PN CA2151547-A.
PD 11-DEC-1995.
PA (USSU) US SURGICAL CORP.
Query Match 6.9%; Score 126; DB 2; Length 1107;
Best Local Similarity 25.9%; Pred. No. 0.62;
RESULT 1201
ID AAY84540 standard; protein; 1107 AA.
DE Amino acid sequence of a chimeric collagen 1 (alpha1)/decorin protein.
PN EP92586-A2.
PD 12-APR-2000.
PA (USSU) US SURGICAL CORP.
Query Match 6.9%; Score 126; DB 3; Length 1107;
Best Local Similarity 25.9%; Pred. No. 0.62;
RESULT 1202
ID ADE87050 standard; protein; 1161 AA.
DE Human pancreatic cell protein sequence SeqID510.
PN WO2003060145-A2.

PD 24-JUL-2003.
 PA (DIAD-) DIADEXUS INC.
 Query Match 6.9%; Score 126; DB 7; Length 1161;
 Best Local Similarity 25.9%; Pred. No. 0.66;
 RESULT 1203
 ID AAR89469 standard; protein; 1169 AA.
 DE Collagen/BMP-2B fusion protein.
 PN CA2151547-A.
 PD 11-DEC-1995.
 PA (USSU) US SURGICAL CORP.
 Query Match 6.9%; Score 126; DB 2; Length 1169;
 Best Local Similarity 25.9%; Pred. No. 0.66;
 RESULT 1204
 ID AAY84537 standard; protein; 1169 AA.
 DE Amino acid sequence of a chimeric collagen 1 (alpha1)/BMP-2B protein.
 PN EP92586-A2.
 PD 12-APR-2000.
 PA (USSU) US SURGICAL CORP.
 Query Match 6.9%; Score 126; DB 3; Length 1169;
 Best Local Similarity 25.9%; Pred. No. 0.66;
 RESULT 1205
 ID AAR89470 standard; protein; 1171 AA.
 DE Collagen/TGF-beta-1 fusion protein.
 PN CA2151547-A.
 PD 11-DEC-1995.
 PA (USSU) US SURGICAL CORP.
 Query Match 6.9%; Score 126; DB 2; Length 1171;
 Best Local Similarity 25.9%; Pred. No. 0.66;
 RESULT 1206
 ID AAY84538 standard; protein; 1171 AA.
 DE A chimeric collagen 1 (alpha1)/TGF-beta1 protein.
 PN EP92586-A2.
 PD 12-APR-2000.
 PA (USSU) US SURGICAL CORP.
 Query Match 6.9%; Score 126; DB 3; Length 1171;
 Best Local Similarity 25.9%; Pred. No. 0.66;
 RESULT 1207
 ID ADE87057 standard; protein; 1211 AA.
 DE Human pancreatic cell protein sequence SeqID517.
 PN WO2003060145-A2.
 PD 24-JUL-2003.
 PA (DIAD-) DIADEXUS INC.
 Query Match 6.9%; Score 126; DB 7; Length 1211;
 Best Local Similarity 25.9%; Pred. No. 0.69;
 RESULT 1208
 ID ADE87062 standard; protein; 1226 AA.
 DE Human pancreatic cell protein sequence SeqID522.
 PN WO2003060145-A2.
 PD 24-JUL-2003.
 PA (DIAD-) DIADEXUS INC.
 Query Match 6.9%; Score 126; DB 7; Length 1226;
 Best Local Similarity 25.9%; Pred. No. 0.7;
 RESULT 1209
 ID ADS98184 standard; protein; 1284 AA.
 DE Protein factor discovery related isolated human polypeptide, SEQ ID 448.
 PN WO2004087874-A2.
 PD 14-OCT-2004.
 PA (NUVE-) NUVELO INC.
 PA (DRMA/) DRMANAC R T.
 Query Match 6.9%; Score 126; DB 8; Length 1284;
 Best Local Similarity 25.9%; Pred. No. 0.74;
 RESULT 1210
 ID AAR71701 standard; protein; 1341 AA.
 DE Collagen alpha 1 (I) chain precursor.
 PN WO9508115-A1.
 PD 23-MAR-1995.
 PA (OSTE-) OSTEOMETER AS.
 Query Match 6.9%; Score 126; DB 2; Length 1341;
 Best Local Similarity 25.9%; Pred. No. 0.78;
 RESULT 1211
 ID AAY96122 standard; peptide; 1341 AA.
 DE Collagen type I alpha-1.
 PN US6110689-A.

PD 29-AUG-2000.
 PA (OSTE-) OSTEOMETER AS.
 Query Match 6.9%; Score 126; DB 3; Length 1341;
 Best Local Similarity 25.9%; Pred. No. 0.78;
 RESULT 1212
 ID AAE16475 standard; protein; 1341 AA.
 DE Human collagen alpha (I) protein.
 PN US6323314-B1.
 PD 27-NOV-2001.
 PA (OSTE-) OSTEOMETER AS.
 Query Match 6.9%; Score 126; DB 5; Length 1341;
 Best Local Similarity 25.9%; Pred. No. 0.78;
 RESULT 1213
 ID ABB80733 standard; protein; 1341 AA.
 DE Collagen type I-alpha protein.
 PN US6355442-B1.
 PD 12-MAR-2002.
 PA (OSTE-) OSTEOMETER BIOTECH AS.
 Query Match 6.9%; Score 126; DB 5; Length 1341;
 Best Local Similarity 25.9%; Pred. No. 0.78;
 RESULT 1214
 ID ABB09625 standard; peptide; 1341 AA.
 DE Amino acid sequence of human collagen type I alpha1.
 PN US6342361-B1.
 PD 29-JAN-2002.
 PA (OSTE-) OSTEOMETER BIOTECH AS.
 Query Match 6.9%; Score 126; DB 5; Length 1341;
 Best Local Similarity 25.9%; Pred. No. 0.78;
 RESULT 1215
 ID ADF13075 standard; protein; 1341 AA.
 DE Human collagen alpha(I) chain precursor.
 PN US2003119058-A1.
 PD 26-JUN-2003.
 PA (OSTE-) OSTEOMETER AS.
 Query Match 6.9%; Score 126; DB 7; Length 1341;
 Best Local Similarity 25.9%; Pred. No. 0.78;
 RESULT 1216
 ID AAR89471 standard; protein; 1388 AA.
 DE Collagen/decorin fusion protein.
 PN CA2151547-A.
 PD 11-DEC-1995.
 PA (USSU) US SURGICAL CORP.
 Query Match 6.9%; Score 126; DB 2; Length 1388;
 Best Local Similarity 25.9%; Pred. No. 0.81;
 RESULT 1217
 ID AAY84539 standard; protein; 1388 AA.
 DE Amino acid sequence of a chimeric collagen 1 (alpha1)/decorin protein.
 PN EP92586-A2.
 PD 12-APR-2000.
 PA (USSU) US SURGICAL CORP.
 Query Match 6.9%; Score 126; DB 3; Length 1388;
 Best Local Similarity 25.9%; Pred. No. 0.81;
 RESULT 1218
 ID AAY56800 standard; protein; 1411 AA.
 DE Human preproalpha 1 (I) collagen.
 PN EP967226-A2.
 PD 29-DEC-1999.
 PA (COHE-) COHESION TECHNOLOGIES INC.
 Query Match 6.9%; Score 126; DB 3; Length 1411;
 Best Local Similarity 25.9%; Pred. No. 0.83;
 RESULT 1219
 ID ABG93947 standard; protein; 1461 AA.
 DE Human polypeptide orthologous to DACC-11.
 PN WO200264625-A1.
 PD 22-AUG-2002.
 PA (ADPP-) ADP PHARM PTY LTD.
 PA (UNSY) UNIV SYDNEY.
 Query Match 6.9%; Score 126; DB 5; Length 1461;
 Best Local Similarity 25.9%; Pred. No. 0.86;
 RESULT 1220
 ID AAW68485 standard; protein; 1464 AA.
 DE Human recombinant collagen protein.
 PN WO9827202-A1.

PD 25-JUN-1998.
PA (BIOC-) BIOCEM SA.
Query Match 6.9%; Score 126; DB 2; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1221
ID AAB82454 standard; protein; 1464 AA.
DE Human pro-alpha-1 chain of type I procollagen.
PN WO200144455-A2.
PD 21-JUN-2001.
PA (ASTR-) ASTRAZENECA AB.
PA (ASTR-) ASTRAZENECA UK LTD.
Query Match 6.9%; Score 126; DB 4; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1222
ID AAU14136 standard; protein; 1464 AA.
DE Human novel protein #7.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 126; DB 4; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1223
ID ABB90764 standard; protein; 1464 AA.
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 261.
PN WO200210217-A2.
PD 07-FEB-2002.
PA (UYJO-) UNIV JOHNS HOPKINS.
Query Match 6.9%; Score 126; DB 5; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1224
ID ABP68610 standard; protein; 1464 AA.
DE Human pancreatic cancer expressed protein SEQ ID NO 159.
PN WO200260317-A2.
PD 08-AUG-2002.
PA (CORI-) CORIXA CORP.
Query Match 6.9%; Score 126; DB 5; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1225
ID ABUS4471 standard; protein; 1464 AA.
DE Human tumour endothelial marker TEM 38.
PN WO200283874-A2.
PD 24-OCT-2002.
PA (UYJO-) UNIV JOHNS HOPKINS.
Query Match 6.9%; Score 126; DB 6; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1226
ID ABR47417 standard; protein; 1464 AA.
DE Breast cancer associated protein sequence SEQ ID NO:65.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 6.9%; Score 126; DB 6; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1227
ID ABR92064 standard; protein; 1464 AA.
DE Human cervical cancer cell marker protein SEQ ID NO:36.
PN WO2002101075-A2.
PD 19-DEC-2002.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 6.9%; Score 126; DB 6; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1228
ID ADD14142 standard; protein; 1464 AA.
DE Human src biomarker polypeptide SEQ ID NO:331.
PN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match 6.9%; Score 126; DB 7; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1229
ID ADD45059 standard; protein; 1464 AA.
DE Human Protein P02452, SEQ ID NO 10491.
PN WO2003016475-A2.

PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match 6.9%; Score 126; DB 7; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1230
ID ADD45055 standard; protein; 1464 AA.
DE Human Protein P02452, SEQ ID NO 10487.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match 6.9%; Score 126; DB 7; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1231
ID ADD45051 standard; protein; 1464 AA.
DE Human Protein P02452, SEQ ID NO 10483.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match 6.9%; Score 126; DB 7; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1232
ID ADP65246 standard; protein; 1464 AA.
DE Human alpha 1 type I collagen preproprotein, Collagen I, alpha-1.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 6.9%; Score 126; DB 7; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1233
ID ADQ19470 standard; protein; 1464 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2289.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 6.9%; Score 126; DB 8; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1234
ID ADQ29653 standard; protein; 1464 AA.
DE Human colorectal cancer-associated protein #8.
PN EP1439393-A2.
PD 21-JUL-2004.
PA (FARB-) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 6.9%; Score 126; DB 8; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1235
ID ADR16800 standard; protein; 1464 AA.
DE Human collagen I alpha1 (I) chain protein.
PN US2004151731-A1.
PD 05-AUG-2004.
PA (JICH/) JICHA D L.
PA (JICH/) JICHA D L.
Query Match 6.9%; Score 126; DB 8; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1236
ID ADR16425 standard; protein; 1464 AA.
DE Human collagen I alpha1 (I) chain protein.
PN US2004151732-A1.
PD 05-AUG-2004.
PA (JICH/) JICHA D L.
PA (PELU/) PELUSE S.
Query Match 6.9%; Score 126; DB 8; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1237
ID ADR99144 standard; protein; 1464 AA.
DE Collagen, type 1, alpha 1, COL1A1, SEQ ID 150.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB-) BAYER PHARM CORP.
Query Match 6.9%; Score 126; DB 8; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;

RESULT 1238
ID ADV87000 standard; protein; 1464 AA.
DE Collagen type I precursor chain COL1A1.
PN W02004110470-A2.
PD 23-DEC-2004.
PA (UYBR-) UNIV BRISTOL.
Query Match 6.9%; Score 126; DB 9; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1239
ID ADV70233 standard; protein; 1464 AA.
DE Tumor-associated antigenic target polypeptide TAT472.
PN W02004112829-A2.
PD 23-DEC-2004.
PA (GETH) GENENTECH INC.
Query Match 6.9%; Score 126; DB 9; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1240
ID ADX58061 standard; protein; 1464 AA.
DE Amino acid sequence of a human collagen-like peptide.
PN W02005011740-A1.
PD 10-FEB-2005.
PA (FUJF) FUJII PHOTO FILM BV.
Query Match 6.9%; Score 126; DB 9; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1241
ID ADZ26573 standard; protein; 1464 AA.
DE Human type I collagen.
PN W02005030999-A1.
PD 07-APR-2005.
PA (DAND) DANA FARBBER CANCER INST INC.
Query Match 6.9%; Score 126; DB 9; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1242
ID ADZ09874 standard; protein; 1464 AA.
DE Human breast cancer marker COL1A1 protein.
PN EP1522594-A2.
PD 13-APR-2005.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 6.9%; Score 126; DB 9; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1243
ID AEA04480 standard; protein; 1464 AA.
DE Human protein from gene overexpressed in cancer, COL1A1.
PN W02005044990-A2.
PD 19-MAY-2005.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 6.9%; Score 126; DB 9; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1244
ID AEE23574 standard; protein; 1464 AA.
DE Novel human protein amino acid sequence - SEQ ID 243.
PN US2005266423-A1.
PD 01-DEC-2005.
PA (NUVE-) NUVELO INC.
Query Match 6.9%; Score 126; DB 10; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1245
ID AEF69965 standard; protein; 1464 AA.
DE Colorectal cancer-associated marker protein SEQ ID NO:143.
PN W02006015047-A2.
PD 09-FEB-2006.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 6.9%; Score 126; DB 10; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1246
ID AEH24256 standard; protein; 1464 AA.
DE Human type I collagen protein - SEQ ID 2.
PN US2006100138-A1.
PD 11-MAY-2006.
PA (OLSE/) OLSEN D R.
PA (POLA/) POLAREK J W.

PA (YANG/) YANG C.
Query Match 6.9%; Score 126; DB 10; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1247
ID AEI67938 standard; protein; 1464 AA.
DE Human prepro-alpha1(I) collagen polypeptide.
PN W02006089329-A2.
PD 29-JUN-2006.
PA (NATH/) NATH R K.
Query Match 6.9%; Score 126; DB 10; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1248
ID AEK09685 standard; protein; 1464 AA.
DE Human collagen protein, COL1A1.
PN W02006091099-A2.
PD 31-AUG-2006.
PA (FUJF) FUJII PHOTO FILM BV.
Query Match 6.9%; Score 126; DB 10; Length 1464;
Best Local Similarity 25.9%; Pred. No. 0.86;
RESULT 1249
ID AED74268 standard; protein; 1467 AA.
DE Human placental protein SEQ ID NO:1096.
PN US2005255114-A1.
PD 17-NOV-2005.
PA (NUVE-) NUVELO INC.
Query Match 6.9%; Score 126; DB 9; Length 1467;
Best Local Similarity 25.9%; Pred. No. 0.87;
RESULT 1250
ID AEG73574 standard; protein; 1489 AA.
DE Thiol protease aleurain signal sequence/collagen alpha 1 fusion protein.
PN W02006035442-A2.
PD 06-APR-2006.
PA (COLL-) COLPLANT LTD.
Query Match 6.9%; Score 126; DB 10; Length 1489;
Best Local Similarity 25.9%; Pred. No. 0.88;
RESULT 1251
ID AEG22679 standard; protein; 1518 AA.
DE Novel human diagnostic protein #22670.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 126; DB 4; Length 1518;
Best Local Similarity 25.9%; Pred. No. 0.9;
RESULT 1252
ID ADS98730 standard; protein; 1518 AA.
DE Protein factor discovery related human contig polypeptide, SEQ ID 994.
PN W02004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
PA (DRMA/) DRMANAC R T.
Query Match 6.9%; Score 126; DB 8; Length 1518;
Best Local Similarity 25.9%; Pred. No. 0.9;
RESULT 1253
ID ABB66232 standard; protein; 2309 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 25488.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.9%; Score 126; DB 4; Length 2309;
Best Local Similarity 24.4%; Pred. No. 1.5;
RESULT 1254
ID ADF94862 standard; protein; 605 AA.
DE Human gene 16-encoded ACRP30-like protein, SEQ ID NO:65.
PN W02003031586-A2.
PD 17-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (BLON/) BLONDEL O.
PA (RUBE/) RUBEN S M.
Query Match 6.9%; Score 125.5; DB 7; Length 605;
Best Local Similarity 25.5%; Pred. No. 0.33;
RESULT 1255
ID ADN95570 standard; protein; 744 AA.
DE Human BEC/LEC-related protein sequence SeqID493.

PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN-) LICENTIA LTD.
Query Match 6.9%; Score 125.5; DB 7; Length 744;
Best Local Similarity 25.5%; Pred. No. 0.42;
RESULT 1256
ID ADV86398 standard; protein; 744 AA.
DE Novel C1q domain-containing protein #19.
PN US2004248156-A1.
PD 09-DEC-2004.
PA (HUT7/) HU T.
PA (TANG/) TANG Y T.
PA (GHOS/) GHOSH M J.
PA (WANG/) WANG J.
PA (WANG/) WANG Z.
PA (ZHAO/) ZHAO Q.
PA (XUCC/) XU C.
PA (MULE/) MULERO J.
Query Match 6.9%; Score 125.5; DB 9; Length 744;
Best Local Similarity 25.5%; Pred. No. 0.42;
RESULT 1257
ID AAW82646 standard; protein; 752 AA.
DE Ehrlichia sp. extended HGE-14 reverse complementaryt protein #2.
PN WO9842740-A2.
PD 01-OCT-1998.
PA (CORI-) CORIXA CORP.
Query Match 6.9%; Score 125.5; DB 2; Length 752;
Best Local Similarity 25.0%; Pred. No. 0.43;
RESULT 1258
ID RAY78540 standard; protein; 752 AA.
DE Ehrlichia antigen 14 (HGE-14) protein sequence #4.
PN WO200000615-A2.
PD 06-JAN-2000.
PA (CORI-) CORIXA CORP.
Query Match 6.9%; Score 125.5; DB 3; Length 752;
Best Local Similarity 25.0%; Pred. No. 0.43;
RESULT 1259
ID ABG93434 standard; protein; 752 AA.
DE Ehrlichia corrected sequence of antigen HGE-14.
PN US2002086984-A1.
PD 04-JUL-2002.
PA (CORI-) CORIXA CORP.
Query Match 6.9%; Score 125.5; DB 5; Length 752;
Best Local Similarity 25.0%; Pred. No. 0.43;
RESULT 1260
ID ABG93419 standard; protein; 752 AA.
DE Ehrlichia antigen HGE-14 from reverse complement sequence #3.
PN US2002086984-A1.
PD 04-JUL-2002.
PA (CORI-) CORIXA CORP.
Query Match 6.9%; Score 125.5; DB 5; Length 752;
Best Local Similarity 25.0%; Pred. No. 0.43;
RESULT 1261
ID AAU73231 standard; protein; 752 AA.
DE Human granulocytic ehrlichiosis, (HGE) antigen #47.
PN WO200185949-A2.
PD 15-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 6.9%; Score 125.5; DB 5; Length 752;
Best Local Similarity 25.0%; Pred. No. 0.43;
RESULT 1262
ID AAU73216 standard; protein; 752 AA.
DE Human granulocytic ehrlichiosis, (HGE) antigen #32.
PN WO200185949-A2.
PD 15-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 6.9%; Score 125.5; DB 5; Length 752;
Best Local Similarity 25.0%; Pred. No. 0.43;
RESULT 1263
ID ABB64403 standard; protein; 993 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 20001.
PN WO200171042-A2.

PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 6.9%; Score 125.5; DB 4; Length 993;
Best Local Similarity 20.4%; Pred. No. 0.6;
RESULT 1264
ID AAE02532 standard; protein; 1463 AA.
DE Bovine alpai(1) collagen.
PN WO200134647-A2.
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match 6.9%; Score 125.5; DB 4; Length 1463;
Best Local Similarity 25.6%; Pred. No. 0.95;
RESULT 1265
ID AEG49841 standard; protein; 1487 AA.
DE Human variant type II collagen (COL2A1) amino acid sequence - SEQ ID 7.
PN US2006051794-A1.
PD 09-MAR-2006.
PA (TSAL/) TSAI S.
PA (LIUY/) LIU Y.
PA (CHEN/) CHEN W.
Query Match 6.9%; Score 125.5; DB 10; Length 1487;
Best Local Similarity 23.7%; Pred. No. 0.97;
RESULT 1266
ID AAU78460 standard; protein; 1494 AA.
DE Mouse beta-catenin nuclear localised protein.
PN WO200224738-A1.
PD 28-MAR-2002.
PA (KYOW-) KYOWA HAKKO KOGYO KK.
Query Match 6.9%; Score 125.5; DB 5; Length 1494;
Best Local Similarity 23.8%; Pred. No. 0.97;
RESULT 1267
ID AAW40115 standard; protein; 546 AA.
DE Human alpha-5(IV) collagen protein.
PN US5731192-A.
PD 24-MAR-1998.
PA (UYIA-) UNIV YALE.
Query Match 6.9%; Score 125; DB 2; Length 546;
Best Local Similarity 22.4%; Pred. No. 0.32;
RESULT 1268
ID ADV42112 standard; protein; 585 AA.
DE Mosquito resilin homolog.
PN WO2004104043-A1.
PD 02-DEC-2004.
PA (CSIR-) COMMONWEALTH SCI & IND RES ORG.
Query Match 6.9%; Score 125; DB 9; Length 585;
Best Local Similarity 25.4%; Pred. No. 0.35;
RESULT 1269
ID ADV44209 standard; protein; 585 AA.
DE African malaria mosquito resilin polypeptide #1.
PN WO2004104042-A1.
PD 02-DEC-2004.
PA (CSIR-) COMMONWEALTH SCI & IND RES ORG.
Query Match 6.9%; Score 125; DB 9; Length 585;
Best Local Similarity 25.4%; Pred. No. 0.35;
RESULT 1270
ID ABP43633 standard; protein; 632 AA.
DE IV collagen alpha 5 chain COL4A5 gene.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 125; DB 5; Length 632;
Best Local Similarity 22.4%; Pred. No. 0.38;
RESULT 1271
ID AEC12082 standard; protein; 636 AA.
DE Rat surrogate marker of neuropathic pain protein SEQ ID NO 428.
PN WO2005083125-A2.
PD 09-SEP-2005.
PA (BIOJ-) BIOGEN IDEC MA INC.
Query Match 6.9%; Score 125; DB 9; Length 636;
Best Local Similarity 25.1%; Pred. No. 0.38;
RESULT 1272
ID ADN19622 standard; protein; 639 AA.
DE Bacterial polypeptide #2275.

PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.9%; Score 125; DB 8; Length 639;
Best Local Similarity 24.3%; Pred. No. 0.39;
RESULT 1273
ID AAE32996 standard; protein; 895 AA.
DE Macaca mulatta androgen receptor (rhAR) allelic variant protein.
PN WO200290529-A1.
PD 14-NOV-2002.
PA (MERI) MERCK & CO INC.
Query Match 6.9%; Score 125; DB 6; Length 895;
Best Local Similarity 24.2%; Pred. No. 0.58;
RESULT 1274
ID AAE32995 standard; protein; 895 AA.
DE Macaca mulatta androgen receptor (rhAR).
PN WO200290529-A1.
PD 14-NOV-2002.
PA (MERI) MERCK & CO INC.
Query Match 6.9%; Score 125; DB 6; Length 895;
Best Local Similarity 24.2%; Pred. No. 0.58;
RESULT 1275
ID ADQ19402 standard; protein; 910 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2221.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 6.9%; Score 125; DB 8; Length 910;
Best Local Similarity 22.4%; Pred. No. 0.59;
RESULT 1276
ID ABO84442 standard; protein; 1268 AA.
DE Human cancer-associated protein HP7-221.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.9%; Score 125; DB 8; Length 1268;
Best Local Similarity 22.4%; Pred. No. 0.87;
RESULT 1277
ID ABO84443 standard; protein; 1283 AA.
DE Human cancer-associated protein HP7-221.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.9%; Score 125; DB 8; Length 1283;
Best Local Similarity 22.4%; Pred. No. 0.89;
RESULT 1278
ID ABG04839 standard; protein; 1685 AA.
DE Novel human diagnostic protein #4830.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 125; DB 4; Length 1685;
Best Local Similarity 22.4%; Pred. No. 1.2;
RESULT 1279
ID ABO84444 standard; protein; 1685 AA.
DE Human cancer-associated protein HP7-221.3.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.9%; Score 125; DB 8; Length 1685;
Best Local Similarity 22.4%; Pred. No. 1.2;
RESULT 1280
ID ABG15619 standard; protein; 1693 AA.
DE Novel human diagnostic protein #15610.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 125; DB 4; Length 1693;
Best Local Similarity 22.4%; Pred. No. 1.2;
RESULT 1281
ID ADN24379 standard; protein; 1759 AA.
DE Bacterial polypeptide #7032.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.9%; Score 125; DB 8; Length 1759;
Best Local Similarity 24.2%; Pred. No. 1.3;
RESULT 1282
ID ADC21544 standard; protein; 1014 AA.
DE Human type II collagen protein sequence.
PN WO2003006603-A2.
PD 23-JAN-2003.
PA (AREX-) AREXIS AB.
Query Match 6.8%; Score 124.5; DB 7; Length 1014;
Best Local Similarity 23.7%; Pred. No. 0.73;
RESULT 1283
ID AED95251 standard; protein; 1014 AA.
DE Mature human collagen type II.
PN WO2005106495-A1.
PD 10-NOV-2005.
PA (PHAA) PHARMACIA & UPJOHN CO LLC.
Query Match 6.8%; Score 124.5; DB 9; Length 1014;
Best Local Similarity 23.7%; Pred. No. 0.73;
RESULT 1284
ID ABM83560 standard; protein; 1417 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3809.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.8%; Score 124.5; DB 8; Length 1417;
Best Local Similarity 23.7%; Pred. No. 1.1;
RESULT 1285
ID AAR59751 standard; protein; 1418 AA.
DE Type II collagen.
PN WO9414070-A1.
PD 23-JUN-1994.
PA (SHRI-) SHRINERS HOSPITALS FOR CRIPPLED CHILDREN.
Query Match 6.8%; Score 124.5; DB 2; Length 1418;
Best Local Similarity 23.7%; Pred. No. 1.1;
RESULT 1286
ID AAR71703 standard; protein; 1418 AA.
DE Collagen alpha 1 (II) chain precursor.
PN WO9508115-A1.
PD 23-MAR-1995.
PA (OSTE-) OSTEOMETER AS.
Query Match 6.8%; Score 124.5; DB 2; Length 1418;
Best Local Similarity 23.7%; Pred. No. 1.1;
RESULT 1287
ID AAY96124 standard; peptide; 1418 AA.
DE Collagen type II alpha-1.
PN US6110689-A.
PD 29-AUG-2000.
PA (OSTE-) OSTEOMETER AS.
Query Match 6.8%; Score 124.5; DB 3; Length 1418;
Best Local Similarity 23.7%; Pred. No. 1.1;
RESULT 1288
ID AAB35624 standard; protein; 1418 AA.
DE Human type II collagen.
PN US6132976-A.
PD 17-OCT-2000.
PA (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.
Query Match 6.8%; Score 124.5; DB 4; Length 1418;
Best Local Similarity 23.7%; Pred. No. 1.1;
RESULT 1289
ID AAE16477 standard; protein; 1418 AA.
DE Human collagen alpha1 (II) protein.
PN US6323314-B1.
PD 27-NOV-2001.

PA (OSTE-) OSTEOMETER AS.
Query Match 6.8%; Score 124.5; DB 5; Length 1418;
Best Local Similarity 23.7%; Pred. No. 1.1;
RESULT 1290
ID ABB80735 standard; protein; 1418 AA.
DE Collagen type II-alpha protein.
PN US6355442-B1.
PD 12-MAR-2002.
PA (OSTE-) OSTEOMETER BIOTECH AS.
Query Match 6.8%; Score 124.5; DB 5; Length 1418;
Best Local Similarity 23.7%; Pred. No. 1.1;
RESULT 1291
ID ABG93927 standard; protein; 1418 AA.
DE Human polypeptide orthologous to DACC-2.
PN WO200264625-A1.
PD 22-AUG-2002.
PA (ADPP-) ADP PHARM PTY LTD.
PA (UNSY) UNIV SYDNEY.
Query Match 6.8%; Score 124.5; DB 5; Length 1418;
Best Local Similarity 23.7%; Pred. No. 1.1;
RESULT 1292
ID ABB09627 standard; peptide; 1418 AA.
DE Amino acid sequence of human collagen type II alpha1.
PN US6342361-B1.
PD 29-JAN-2002.
PA (OSTE-) OSTEOMETER BIOTECH AS.
Query Match 6.8%; Score 124.5; DB 5; Length 1418;
Best Local Similarity 23.7%; Pred. No. 1.1;
RESULT 1293
ID ADF13077 standard; protein; 1418 AA.
DE Human collagen alpha1(II) chain precursor.
PN US2003119058-A1.
PD 26-JUN-2003.
PA (OSTE-) OSTEOMETER AS.
Query Match 6.8%; Score 124.5; DB 7; Length 1418;
Best Local Similarity 23.7%; Pred. No. 1.1;
RESULT 1294
ID AEB25695 standard; protein; 1418 AA.
DE Human collagen related amino acid sequence, seq id 1.
PN FR2865034-A1.
PD 15-JUL-2005.
PA (SYNA-) SYNARC SAS.
Query Match 6.8%; Score 124.5; DB 9; Length 1418;
Best Local Similarity 23.7%; Pred. No. 1.1;
RESULT 1295
ID AED95247 standard; protein; 1418 AA.
DE Immature human collagen type II.
PN WO2005106495-A1.
PD 10-NOV-2005.
PA (PHAA) PHARMACIA & UPJOHN CO LLC.
Query Match 6.8%; Score 124.5; DB 9; Length 1418;
Best Local Similarity 23.7%; Pred. No. 1.1;
RESULT 1296
ID ADJ69192 standard; protein; 1448 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID998.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.8%; Score 124.5; DB 7; Length 1448;
Best Local Similarity 18.5%; Pred. No. 1.1;
RESULT 1297
ID ABG61861 standard; protein; 1487 AA.
DE Prostate cancer-associated protein #62.
PN WO200230268-A2.
PD 18-APR-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.8%; Score 124.5; DB 5; Length 1487;
Best Local Similarity 23.7%; Pred. No. 1.2;
RESULT 1298
ID ABP56769 standard; protein; 1487 AA.
DE Collagen IIA protein.
PN WO2002100426-A1.

PD 19-DEC-2002.
PA (SMIN) SMITH & NEPHEW PLC.
Query Match 6.8%; Score 124.5; DB 6; Length 1487;
Best Local Similarity 23.7%; Pred. No. 1.2;
RESULT 1299
ID ADX15809 standard; protein; 1487 AA.
DE Human Col 2A1.
PN WO2005012512-A1.
PD 10-FEB-2005.
PA (NAKA/) NAKAMURA N.
Query Match 6.8%; Score 124.5; DB 9; Length 1487;
Best Local Similarity 23.7%; Pred. No. 1.2;
RESULT 1300
ID AEG49837 standard; protein; 1487 AA.
DE Human type II collagen (COL2A1) amino acid sequence - SEQ ID 3.
PN US2006051794-A1.
PD 09-MAR-2006.
PA (TSAL/) TSAL S.
PA (LIUY/) LIU Y.
PA (CHEN/) CHEN W.
Query Match 6.8%; Score 124.5; DB 10; Length 1487;
Best Local Similarity 23.7%; Pred. No. 1.2;
RESULT 1301
ID AEG49839 standard; protein; 1487 AA.
DE Human variant type II collagen (COL2A1) amino acid sequence - SEQ ID 5.
PN US2006051794-A1.
PD 09-MAR-2006.
PA (TSAL/) TSAL S.
PA (LIUY/) LIU Y.
PA (CHEN/) CHEN W.
Query Match 6.8%; Score 124.5; DB 10; Length 1487;
Best Local Similarity 23.7%; Pred. No. 1.2;
RESULT 1302
ID AEG12880 standard; protein; 295 AA.
DE Human lung cancer diagnosis related protein Q96CP3 SEQ ID NO:1444.
PN US2006046257-A1.
PD 02-MAR-2006.
PA (POLL/) POLLOCK S.
PA (LEVI/) LEVINE Z.
PA (NOVI/) NOVIK A.
PA (DAHA/) DAHARY D.
PA (SORE/) SOREK R.
PA (TOPO/) TOPORIK A.
PA (SAME/) SAMEAH-GREENWALD S.
PA (SELL/) SELLA-TAVOR O.
PA (DIBE/) DIBER A.
PA (COJO/) COJOCARU G S.
PA (AYAL/) AYALON-SOFFER M.
PA (WALA/) WALACH S.
PA (AKIV/) AKIVA P.
PA (KERE/) KEREN N.
PA (SHEW/) SHEMESH R.
Query Match 6.8%; Score 124; DB 10; Length 295;
Best Local Similarity 27.4%; Pred. No. 0.18;
RESULT 1303
ID ABO68869 standard; protein; 299 AA.
DE Pseudomonas aeruginosa polypeptide #1044.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.8%; Score 124; DB 7; Length 299;
Best Local Similarity 29.0%; Pred. No. 0.19;
RESULT 1304
ID AAG38842 standard; protein; 304 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47977.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.8%; Score 124; DB 3; Length 304;
Best Local Similarity 24.2%; Pred. No. 0.19;
RESULT 1305
ID ABP56228 standard; protein; 439 AA.
DE HisPrPDPcr fusion prion protein dimer SEQ ID NO:2.
PN EP1251138-A1.

PD 23-OCT-2002.
PA (SCHA/) SCHAETZL H.
Query Match 6.8%; Score 124; DB 6; Length 439;
Best Local Similarity 22.0%; Pred. No. 0.3;
RESULT 1306
ID AEJ13420 standard; protein; 630 AA.
DE Cancer-associated protein - SEQ ID 428.
PN US2006154250-A1.
PD 13-JUL-2006.
PA (MORR/) MORRIS D W.
PA (WALA/) MALANDRO M S.
Query Match 6.8%; Score 124; DB 10; Length 630;
Best Local Similarity 25.0%; Pred. No. 0.45;
RESULT 1307
ID AEJ13424 standard; protein; 720 AA.
DE Cancer-associated protein - SEQ ID 432.
PN US2006154250-A1.
PD 13-JUL-2006.
PA (MORR/) MORRIS D W.
PA (WALA/) MALANDRO M S.
Query Match 6.8%; Score 124; DB 10; Length 720;
Best Local Similarity 25.0%; Pred. No. 0.53;
RESULT 1308
ID ABA42952 standard; protein; 863 AA.
DE Human ORF2716 polypeptide sequence SEQ ID NO:5432.
PN W0200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.8%; Score 124; DB 3; Length 863;
Best Local Similarity 27.4%; Pred. No. 0.66;
RESULT 1309
ID AAB90819 standard; protein; 881 AA.
DE Human shear stress-response protein SEQ ID NO: 146.
PN W0200125427-A1.
PD 12-APR-2001.
PA (KIOW/) KIOWA HAKKO KOGYO KK.
PA (NOJI/) NOJIMA H.
Query Match 6.8%; Score 124; DB 4; Length 881;
Best Local Similarity 27.4%; Pred. No. 0.68;
RESULT 1310
ID AAG65820 standard; protein; 881 AA.
DE Human GTPase activating protein-4 (GAP-4).
PN W0200172828-A2.
PD 04-OCT-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.8%; Score 124; DB 4; Length 881;
Best Local Similarity 27.4%; Pred. No. 0.68;
RESULT 1311
ID AEL57497 standard; protein; 898 AA.
DE Human collagen alpha 3(IV) chain precursor, SEQ ID NO: 1960.
PN US2006216722-A1.
PD 28-SEP-2006.
PA (BETS/) BETSHOLTZ C.
PA (TRYG/) TRYGGVASON K.
PA (TAKE/) TAKEMOTO M.
PA (HELL/) HE L.
PA (PATR/) PATRAKKAS J.
Query Match 6.8%; Score 124; DB 10; Length 898;
Best Local Similarity 25.3%; Pred. No. 0.69;
RESULT 1312
ID AAB42926 standard; protein; 903 AA.
DE Human ORF2690 polypeptide sequence SEQ ID NO:5380.
PN W0200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.8%; Score 124; DB 3; Length 903;
Best Local Similarity 27.4%; Pred. No. 0.7;
RESULT 1313
ID ADJ69021 standard; protein; 903 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID827.
PN W02003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.
Query Match 6.8%; Score 124; DB 7; Length 903;
Best Local Similarity 27.4%; Pred. No. 0.7;
RESULT 1314
ID ABO84589 standard; protein; 903 AA.
DE Human cancer-associated protein HP17-008.4.
PN W02004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.8%; Score 124; DB 8; Length 903;
Best Local Similarity 23.0%; Pred. No. 0.7;
RESULT 1315
ID AAU28194 standard; protein; 940 AA.
DE Novel human secretory protein, Seq ID No 363.
PN W0200166689-A2.
PD 13-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 124; DB 4; Length 940;
Best Local Similarity 25.1%; Pred. No. 0.73;
RESULT 1316
ID AEB56505 standard; protein; 940 AA.
DE Radiochemotherapy response detection associated protein SEQ ID NO 80.
PN W02005073411-A1.
PD 11-AUG-2005.
PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.
Query Match 6.8%; Score 124; DB 9; Length 940;
Best Local Similarity 25.1%; Pred. No. 0.73;
RESULT 1317
ID AAU28382 standard; protein; 968 AA.
DE Novel human secretory protein, Seq ID No 739.
PN W0200166689-A2.
PD 13-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 124; DB 4; Length 968;
Best Local Similarity 25.1%; Pred. No. 0.76;
RESULT 1318
ID AEG13169 standard; protein; 1120 AA.
DE Human lung cancer diagnosis related protein T08446_PEA_1_P18 fragment.
PN US2006046257-A1.
PD 02-MAR-2006.
PA (POLL/) POLLOCK S.
PA (LEVI/) LEVINE Z.
PA (NOVI/) NOVIK A.
PA (DAHA/) DAHARY D.
PA (SORE/) SOREK R.
PA (TOPO/) TOPORIK A.
PA (SAME/) SAMEAH-GREENWALD S.
PA (SELL/) SELLA-TAVOR O.
PA (DIBE/) DIBER A.
PA (COJO/) COJOCARU G S.
PA (AVAL/) AVALON-SOFFER M.
PA (WALA/) WALACH S.
PA (AKIV/) AKIVA P.
PA (KERE/) KEREN N.
PA (SHEM/) SHEMESH R.
Query Match 6.8%; Score 124; DB 10; Length 1120;
Best Local Similarity 27.4%; Pred. No. 0.91;
RESULT 1319
ID ADM04980 standard; protein; 1126 AA.
DE Human protein of the invention SEQ ID NO:3665.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.8%; Score 124; DB 7; Length 1126;
Best Local Similarity 27.4%; Pred. No. 0.91;
RESULT 1320
ID AEC87910 standard; protein; 1126 AA.
DE Human cDNA clone protein NT2RP70027380, SEQ ID 3665.
PN EP1580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.8%; Score 124; DB 9; Length 1126;
Best Local Similarity 27.4%; Pred. No. 0.91;

```
RESULT 1321
ID AEG12806 standard; protein; 1305 AA.
DE Human lung cancer diagnosis related protein T08446_PEA_1_P18.
PN US2006046257-A1.
PD 02-NAR-2006.
PA (POLI/) POLLOCK S.
PA (LEVI/) LEVINE Z.
PA (NOVI/) NOVIK A.
PA (DAHA/) DAHARY D.
PA (SORE/) SOREK R.
PA (TOPO/) TOPORIK A.
PA (SAME/) SAMEAH-GREENWALD S.
PA (SELL/) SELLA-TAVOR O.
PA (DIBE/) DIBER A.
PA (COJO/) COJOCARU G S.
PA (AYAL/) AYALON-SOFFER M.
PA (WALA/) WALACH S.
PA (AKIV/) AKIVA P.
PA (KERE/) KEREN N.
PA (SHEM/) SHEMESH R.
Query Match 6.8%; Score 124; DB 10; Length 1305;
Best Local Similarity 27.4%; Pred. No. 1.1;
RESULT 1322
ID AAW76734 standard; protein; 1315 AA.
DE Human mdia Rho targeting protein.
PN JP10262680-A.
PD 06-OCT-1998.
PA (KIRI ) KIRIN BREWERY KK.
Query Match 6.8%; Score 124; DB 2; Length 1315;
Best Local Similarity 26.2%; Pred. No. 1.1;
RESULT 1323
ID ABO84586 standard; protein; 1336 AA.
DE Human cancer-associated protein HPI7-008.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.8%; Score 124; DB 8; Length 1336;
Best Local Similarity 23.0%; Pred. No. 1.1;
RESULT 1324
ID ABO84591 standard; protein; 1336 AA.
DE Human cancer-associated protein HPI7-008.6.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.8%; Score 124; DB 8; Length 1336;
Best Local Similarity 23.0%; Pred. No. 1.1;
RESULT 1325
ID ABO84592 standard; protein; 1516 AA.
DE Human cancer-associated protein HPI7-008.7.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.8%; Score 124; DB 8; Length 1516;
Best Local Similarity 23.0%; Pred. No. 1.3;
RESULT 1326
ID ABO84588 standard; protein; 1516 AA.
DE Human cancer-associated protein HPI7-008.3.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.8%; Score 124; DB 8; Length 1516;
Best Local Similarity 23.0%; Pred. No. 1.3;
RESULT 1327
ID AAU71956 standard; protein; 1532 AA.
DE Human bone marrow tissue polypeptide #34.
PN WO200179447-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 124; DB 4; Length 1532;
Best Local Similarity 19.3%; Pred. No. 1.3;
RESULT 1328
ID AEA20119 standard; protein; 1709 AA.
DE Novel human polypeptide SEQ ID NO 813.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 6.8%; Score 124; DB 9; Length 1709;
Best Local Similarity 19.3%; Pred. No. 1.5;
RESULT 1329
ID AEF41876 standard; protein; 1709 AA.
DE Human modifier of IGF (MIGF) trinucleotide repeat containing 6.
PN WO2006009947-A2.
PD 26-JAN-2006.
PA (EXEL-) EXELIXIS INC.
Query Match 6.8%; Score 124; DB 10; Length 1709;
Best Local Similarity 19.3%; Pred. No. 1.5;
RESULT 1330
ID AAG77792 standard; protein; 1739 AA.
DE Murine pro-alpha-3(V) fibrillar procollagen polypeptide.
PN WO200164871-A2.
PD 07-SEP-2001.
PA (WISC ) WISCONSIN ALUMNI RES FOUND.
Query Match 6.8%; Score 124; DB 4; Length 1739;
Best Local Similarity 25.8%; Pred. No. 1.5;
RESULT 1331
ID RAO30408 standard; protein; 267 AA.
DE Human secreted protein (SECP)-11.
PN WO2003046196-A1.
PD 05-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.8%; Score 123.5; DB 7; Length 267;
Best Local Similarity 25.3%; Pred. No. 0.18;
RESULT 1332
ID ABG09363 standard; protein; 394 AA.
DE Novel human diagnostic protein #9354.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 123.5; DB 4; Length 394;
Best Local Similarity 27.6%; Pred. No. 0.28;
RESULT 1333
ID ADF60535 standard; protein; 394 AA.
DE Human contig polypeptide sequence SEQ ID NO:2902.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 123.5; DB 7; Length 394;
Best Local Similarity 27.6%; Pred. No. 0.28;
RESULT 1334
ID AAB06023 standard; protein; 401 AA.
DE Polar gelatin P tetramer, P4.
PN EP1014176-A2.
PD 28-JUN-2000.
PA (FUJF ) FUJI PHOTO FILM BV.
Query Match 6.8%; Score 123.5; DB 3; Length 401;
Best Local Similarity 28.6%; Pred. No. 0.29;
RESULT 1335
ID ABB65306 standard; protein; 453 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 22710.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 6.8%; Score 123.5; DB 4; Length 453;
Best Local Similarity 29.3%; Pred. No. 0.34;
RESULT 1336
ID ADV95808 standard; protein; 503 AA.
DE Chicken type IX collagen alpha 1 precursor.
PN WO2004110475-A1.
PD 23-DEC-2004.
PA (NUTR-) INST NUTRACEUTICAL RES PTY LTD.
Query Match 6.8%; Score 123.5; DB 9; Length 503;
Best Local Similarity 26.9%; Pred. No. 0.38;
RESULT 1337
ID RAY72375 standard; protein; 599 AA.
DE Amphiphilic recombinant collagen-like polymer, NIN2P4.
PN EP1063565-A1.
```


PD 27-DEC-2000.
 PA (FUJIF) FUJII PHOTO FILM BV.
 Query Match 6.8%; Score 123.5; DB 4; Length 599;
 Best Local Similarity 28.6%; Pred. No. 0.47;
 RESULT 1338
 ID AAY72374 standard; protein; 599 AA.
 DE Amphiphilic recombinant collagen-like polymer, NIN1P4.
 PN EP1063565-A1.
 PD 27-DEC-2000.
 PA (FUJIF) FUJII PHOTO FILM BV.
 Query Match 6.8%; Score 123.5; DB 4; Length 599;
 Best Local Similarity 28.6%; Pred. No. 0.47;
 RESULT 1339
 ID AAW29150 standard; protein; 663 AA.
 DE Dual-specific murine threonine-tyrosine phosphatase M3/6.
 PN WO9706245-A1.
 PD 20-FEB-1997.
 PA (MEDI-) MEDICAL RES COUNCIL.
 Query Match 6.8%; Score 123.5; DB 2; Length 663;
 Best Local Similarity 26.0%; Pred. No. 0.53;
 RESULT 1340
 ID ABR52351 standard; protein; 663 AA.
 DE Protein relating to the invention SEQ ID NO: 40.
 PN WO200257460-A2.
 PD 25-JUL-2002.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match 6.8%; Score 123.5; DB 5; Length 663;
 Best Local Similarity 26.0%; Pred. No. 0.53;
 RESULT 1341
 ID ADI17164 standard; protein; 663 AA.
 DE Murine NOVX protein homologue SeqID 700.
 PN WO200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 6.8%; Score 123.5; DB 5; Length 663;
 Best Local Similarity 26.0%; Pred. No. 0.53;
 RESULT 1342
 ID AAM40012 standard; protein; 1078 AA.
 DE Human polypeptide SEQ ID NO 3157.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 6.8%; Score 123.5; DB 4; Length 1078;
 Best Local Similarity 22.6%; Pred. No. 0.95;
 RESULT 1343
 ID AAW22296 standard; peptide; 1301 AA.
 DE Human alpha-1 (XVIII) collagen chain common sequence HU18(common)36.
 PN WO9856399-A1.
 PD 17-DEC-1998.
 PA (FIBR-) FIBROGEN INC.
 PA (FIFT-) ACAD FINLAND.
 PA (INRM) INST NAT SANTE & RECH MEDICALE.
 Query Match 6.8%; Score 123.5; DB 2; Length 1301;
 Best Local Similarity 24.1%; Pred. No. 1.2;
 RESULT 1344
 ID AAY08694 standard; protein; 1336 AA.
 DE Human collagen 18 protein.
 PN WO926480-A1.
 PD 03-JUN-1999.
 PA (GENE-) GENETIX PHARM INC.
 PA (NASI) MASSACHUSETTS INST TECHNOLOGY.
 Query Match 6.8%; Score 123.5; DB 2; Length 1336;
 Best Local Similarity 24.1%; Pred. No. 1.2;
 RESULT 1345
 ID ABP96308 standard; protein; 1336 AA.
 DE Human endostatin protein.
 PN WO2003016540-A2.
 PD 27-FEB-2003.
 PA (UYVO-) UNIV YORK.
 Query Match 6.8%; Score 123.5; DB 6; Length 1336;
 Best Local Similarity 24.1%; Pred. No. 1.2;
 RESULT 1346
 ID ABO84590 standard; protein; 1472 AA.

DE Human cancer-associated protein HP17-008.5.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 6.8%; Score 123.5; DB 8; Length 1472;
 Best Local Similarity 24.1%; Pred. No. 1.4;
 RESULT 1347
 ID ABO84587 standard; protein; 1475 AA.
 DE Human cancer-associated protein HP17-008.2.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 6.8%; Score 123.5; DB 8; Length 1475;
 Best Local Similarity 24.1%; Pred. No. 1.4;
 RESULT 1348
 ID AAW61562 standard; protein; 1487 AA.
 DE Human type II collagen alpha-chain protein.
 PN WO9835235-A1.
 PD 13-AUG-1998.
 PA (UYSH-) UNIV SHEFFIELD.
 Query Match 6.8%; Score 123.5; DB 2; Length 1487;
 Best Local Similarity 23.7%; Pred. No. 1.4;
 RESULT 1349
 ID ABB83471 standard; protein; 1516 AA.
 DE Human collagen XVIII.
 PN WO200253191-A1.
 PD 11-JUL-2002.
 PA (VIRO-) VIROMED LTD.
 Query Match 6.8%; Score 123.5; DB 5; Length 1516;
 Best Local Similarity 24.1%; Pred. No. 1.4;
 RESULT 1350
 ID ABP68617 standard; protein; 1516 AA.
 DE Human pancreatic cancer expressed protein SEQ ID NO 166.
 PN WO200260317-A2.
 PD 08-AUG-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 6.8%; Score 123.5; DB 5; Length 1516;
 Best Local Similarity 24.1%; Pred. No. 1.4;
 RESULT 1351
 ID ADI58822 standard; protein; 1516 AA.
 DE Angiogenesis inhibitor endostatin.
 PN US2004009920-A1.
 PD 15-JAN-2004.
 PA (RUOS/) RUOSLAHTI E.
 Query Match 6.8%; Score 123.5; DB 8; Length 1516;
 Best Local Similarity 24.1%; Pred. No. 1.4;
 RESULT 1352
 ID ADZ21674 standard; protein; 1516 AA.
 DE Collagen XVIII, marker for rheumatoid arthritis.
 PN WO2005032328-A2.
 PD 14-APR-2005.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 6.8%; Score 123.5; DB 9; Length 1516;
 Best Local Similarity 24.1%; Pred. No. 1.4;
 RESULT 1353
 ID AEB29773 standard; protein; 1516 AA.
 DE Human collagen XVIII alpha 1.
 PN WO2005087667-A2.
 PD 28-JUL-2005.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match 6.8%; Score 123.5; DB 9; Length 1516;
 Best Local Similarity 24.1%; Pred. No. 1.4;
 RESULT 1354
 ID ADS10473 standard; protein; 1712 AA.
 DE Human therapeutic protein - SEQ ID 710.
 PN WO2004080148-A2.
 PD 23-SEP-2004.
 PA (NUVE-) NUVELO INC.
 Query Match 6.8%; Score 123.5; DB 8; Length 1712;
 Best Local Similarity 22.8%; Pred. No. 1.6;
 RESULT 1355
 ID ADU06526 standard; protein; 1712 AA.
 DE Novel bronchial cancer-associated human protein SeqID750.

PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ//) HINZMANN B.
PA (HERM//) HERMANN K.
PA (CAST//) HEIDEN CASTANOS-VELEZ E.
Query Match 6.8%; Score 123.5; DB 8; Length 1712;
Best Local Similarity 22.6%; Pred. No. 1.6;
RESULT 1356
ID ADY5985 standard; protein; 1712 AA.
DE Human collagen IV alpha2 chain.
PN US2005048063-A1.
PD 03-MAR-2005.
PA (RUOS//) RUOSLAHTI E.
PA (ESSL//) ESSLER M.
PA (BROW//) BROWN D M.
Query Match 6.8%; Score 123.5; DB 9; Length 1712;
Best Local Similarity 22.6%; Pred. No. 1.6;
RESULT 1357
ID ABP70829 standard; protein; 744 AA.
DE Human C10SF9.
PN WO2003022992-A2.
PD 20-MAR-2003.
PA (SCHE) SCHERING CORP.
Query Match 6.7%; Score 123; DB 6; Length 744;
Best Local Similarity 25.8%; Pred. No. 0.67;
RESULT 1358
ID ABR92066 standard; protein; 744 AA.
DE Human cervical cancer cell marker protein SEQ ID NO:40.
PN WO2002101075-A2.
PD 19-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.7%; Score 123; DB 6; Length 744;
Best Local Similarity 25.8%; Pred. No. 0.67;
RESULT 1359
ID ABB70046 standard; protein; 759 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 36930.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.7%; Score 123; DB 4; Length 759;
Best Local Similarity 19.9%; Pred. No. 0.68;
RESULT 1360
ID ADL34488 standard; protein; 918 AA.
DE Variant human androgen receptor protein, SEQ ID 6.
PN JP2004008141-A.
PD 15-JAN-2004.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 6.7%; Score 123; DB 8; Length 918;
Best Local Similarity 25.8%; Pred. No. 0.86;
RESULT 1361
ID ADC31094 standard; protein; 963 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1176.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 123; DB 7; Length 963;
Best Local Similarity 22.8%; Pred. No. 0.91;
RESULT 1362
ID AEA20274 standard; protein; 999 AA.
DE Novel human polypeptide SEQ ID NO 968.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 6.7%; Score 123; DB 9; Length 999;
Best Local Similarity 22.8%; Pred. No. 0.95;
RESULT 1363
ID ADW95575 standard; protein; 1014 AA.
DE Human gelatin protein - SEQ ID 8.
PN WO2005012356-A2.
PD 10-FEB-2005.
PA (FIBR-) FIBROGEN INC.
Query Match 6.7%; Score 123; DB 9; Length 1014;
Best Local Similarity 26.7%; Pred. No. 0.96;

RESULT 1364
ID ADM99576 standard; protein; 1014 AA.
DE Human gelatin protein - SEQ ID 9.
PN WO2005012356-A2.
PD 10-FEB-2005.
PA (FIBR-) FIBROGEN INC.
Query Match 6.7%; Score 123; DB 9; Length 1014;
Best Local Similarity 26.7%; Pred. No. 0.96;
RESULT 1365
ID ABB62449 standard; protein; 1039 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 14139.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.7%; Score 123; DB 4; Length 1039;
Best Local Similarity 26.1%; Pred. No. 0.99;
RESULT 1366
ID AAB95146 standard; protein; 1197 AA.
DE Human protein sequence SEQ ID NO:17169.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.7%; Score 123; DB 4; Length 1197;
Best Local Similarity 25.7%; Pred. No. 1.2;
RESULT 1367
ID AAU98889 standard; protein; 1251 AA.
DE Human protease PR7S7.
PN WO200238744-A2.
PD 16-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.7%; Score 123; DB 5; Length 1251;
Best Local Similarity 25.7%; Pred. No. 1.2;
RESULT 1368
ID ABP69291 standard; protein; 1270 AA.
DE Human polypeptide SEQ ID NO 1338.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 123; DB 5; Length 1270;
Best Local Similarity 25.7%; Pred. No. 1.3;
RESULT 1369
ID ADN35279 standard; protein; 1313 AA.
DE Synthetic collagen used as sealant tissue protein.
PN WO2004028404-A2.
PD 08-APR-2004.
PA (FIBR-) FIBROGEN INC.
Query Match 6.7%; Score 123; DB 8; Length 1313;
Best Local Similarity 23.8%; Pred. No. 1.3;
RESULT 1370
ID ADP28764 standard; protein; 1316 AA.
DE Human deubiquitinating protease (DUB7) polypeptide.
PN WO2003083050-A2.
PD 09-OCT-2003.
PA (AVET) AVENTIS PHARM INC.
Query Match 6.7%; Score 123; DB 7; Length 1316;
Best Local Similarity 25.7%; Pred. No. 1.3;
RESULT 1371
ID ADJ76366 standard; protein; 3067 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1618.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 6.7%; Score 123; DB 8; Length 3067;
Best Local Similarity 24.5%; Pred. No. 3.6;
RESULT 1372
ID ABR42792 standard; protein; 254 AA.
DE Mouse prion protein.
PN WO2003045128-A2.
PD 05-JUN-2003.
PA (UINY) UNIV NEW YORK STATE.
Query Match 6.7%; Score 122.5; DB 6; Length 254;
Best Local Similarity 34.6%; Pred. No. 0.2;
RESULT 1373

ID ADC59531 standard; protein; 254 AA.
 DE Mouse prion protein Mo3F4, SEQ ID NO:3.
 PN JP2003149237-A.
 PD 21-MAY-2003.
 PA (RIKA) RIKAGAKU KENKYUSHO.
 Query Match 6.7%; Score 122.5; DB 7; Length 254;
 Best Local Similarity 34.6%; Pred. No. 0.2;
 RESULT 1374
 ID ADC52088 standard; protein; 254 AA.
 DE Mouse prion SEQ ID NO 3.
 PN JP2003155239-A.
 PD 27-MAY-2003.
 PA (RIKA) RIKAGAKU KENKYUSHO.
 Query Match 6.7%; Score 122.5; DB 7; Length 254;
 Best Local Similarity 34.6%; Pred. No. 0.2;
 RESULT 1375
 ID ADY50409 standard; protein; 254 AA.
 DE Mouse prion protein.
 PN WO2005019412-A2.
 PD 03-MAR-2005.
 PA (UYN) UNIV NEW YORK STATE.
 PA (WISN/) WISNIEWSKI T.
 Query Match 6.7%; Score 122.5; DB 9; Length 254;
 Best Local Similarity 34.6%; Pred. No. 0.2;
 RESULT 1376
 ID AAY10856 standard; protein; 272 AA.
 DE Amino acid sequence of a human secreted protein.
 PN WO9907891-A1.
 PD 18-FEB-1999.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 6.7%; Score 122.5; DB 2; Length 272;
 Best Local Similarity 29.9%; Pred. No. 0.22;
 RESULT 1377
 ID ADB47837 standard; protein; 272 AA.
 DE Novel human secreted protein #13.
 PN US2003054443-A1.
 PD 20-MAR-2003.
 PA (RUBE/) RUBEN S M.
 PA (SOPP/) SOPPET D R.
 PA (EBNE/) EBNER R.
 PA (OLSE/) OLSEN H S.
 PA (YOUN/) YOUNG P E.
 PA (FERR/) FERRIE A M.
 PA (YUGG/) YU G.
 PA (NIJJ/) NI J.
 PA (ROSE/) ROSEN C A.
 PA (BREW/) BREWER L A.
 PA (JANA/) JANAT F.
 PA (BIRS/) BIRSE C E.
 Query Match 6.7%; Score 122.5; DB 7; Length 272;
 Best Local Similarity 29.9%; Pred. No. 0.22;
 RESULT 1378
 ID ADJ5392 standard; protein; 272 AA.
 DE Novel human secreted protein #13.
 PN US2004023283-A1.
 PD 05-FEB-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 6.7%; Score 122.5; DB 8; Length 272;
 Best Local Similarity 29.9%; Pred. No. 0.22;
 RESULT 1379
 ID AED67375 standard; protein; 272 AA.
 DE Human immunogenic epitope SEQ ID NO:120.
 PN US2005244845-A1.
 PD 03-NOV-2005.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 6.7%; Score 122.5; DB 9; Length 272;
 Best Local Similarity 29.9%; Pred. No. 0.22;
 RESULT 1380
 ID AEJ16330 standard; protein; 272 AA.
 DE Human cDNA clone HNGIN84 polypeptide product SEQ ID NO: 120.
 PN US2006160126-A1.
 PD 20-JUL-2006.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 6.7%; Score 122.5; DB 10; Length 272;
 Best Local Similarity 29.9%; Pred. No. 0.22;
 RESULT 1381
 ID AAY29515 standard; protein; 527 AA.
 DE Human lung tumour protein SAL-50 2nd predicted amino acid sequence.
 PN WO9938973-A2.
 PD 05-AUG-1999.
 PA (CORI-) CORIXA CORP.
 Query Match 6.7%; Score 122.5; DB 2; Length 527;
 Best Local Similarity 22.3%; Pred. No. 0.48;
 RESULT 1382
 ID AAB44492 standard; protein; 527 AA.
 DE Human lung tumour-specific antigen encoded by cDNA #100.
 PN WO200060077-A2.
 PD 12-OCT-2000.
 PA (CORI-) CORIXA CORP.
 Query Match 6.7%; Score 122.5; DB 3; Length 527;
 Best Local Similarity 22.3%; Pred. No. 0.48;
 RESULT 1383
 ID AAE13805 standard; protein; 527 AA.
 DE Human lung tumour-specific protein SAL-50 #2.
 PN WO200172295-A2.
 PD 04-OCT-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 6.7%; Score 122.5; DB 4; Length 527;
 Best Local Similarity 22.3%; Pred. No. 0.48;
 RESULT 1384
 ID ADD66524 standard; protein; 527 AA.
 DE Human lung tumour-specific related protein, SEQ ID NO 216.
 PN WO200292001-A2.
 PD 21-NOV-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 6.7%; Score 122.5; DB 7; Length 527;
 Best Local Similarity 22.3%; Pred. No. 0.48;
 RESULT 1385
 ID ADE87778 standard; protein; 527 AA.
 DE Human lung tumour antigen polypeptide #86.
 PN US2003118599-A1.
 PD 26-JUN-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 6.7%; Score 122.5; DB 7; Length 527;
 Best Local Similarity 22.3%; Pred. No. 0.48;
 RESULT 1386
 ID ABO80090 standard; protein; 589 AA.
 DE Pseudomonas aeruginosa polypeptide #12265.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 6.7%; Score 122.5; DB 7; Length 589;
 Best Local Similarity 23.4%; Pred. No. 0.55;
 RESULT 1387
 ID ADN95361 standard; protein; 620 AA.
 DE Human BEC/LEC-related protein sequence SeqID284.
 PN WO2003080640-A1.
 PD 02-OCT-2003.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (LICN) LICENTIA LTD.
 Query Match 6.7%; Score 122.5; DB 7; Length 620;
 Best Local Similarity 22.6%; Pred. No. 0.59;
 RESULT 1388
 ID ADP54705 standard; protein; 620 AA.
 DE Human PRO protein sequence SEQ ID NO:681.
 PN WO2004039956-A2.
 PD 13-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 6.7%; Score 122.5; DB 8; Length 620;
 Best Local Similarity 22.6%; Pred. No. 0.59;
 RESULT 1389
 ID ABG20347 standard; protein; 937 AA.
 DE Novel human diagnostic protein #20338.
 PN WO200175067-A2.
 PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 122.5; DB 4; Length 937;
Best Local Similarity 24.5%; Pred. No. 0.96;
RESULT 1390
ID ADN35278 standard; protein; 1028 AA.
DE Helical domain of type III collagen #2.
PN WO2004028404-A2.
PD 08-APR-2004.
PA (FIBR-) FIBROGEN INC.
Query Match 6.7%; Score 122.5; DB 8; Length 1028;
Best Local Similarity 25.3%; Pred. No. 1.1;
RESULT 1391
ID AAR71704 standard; protein; 1078 AA.
DE Collagen alpha 1 (III) chain precursor.
PN WO9508115-A1.
PD 23-MAR-1995.
PA (OSTE-) OSTEOMETER AS.
Query Match 6.7%; Score 122.5; DB 2; Length 1078;
Best Local Similarity 25.3%; Pred. No. 1.1;
RESULT 1392
ID AAY96125 standard; peptide; 1078 AA.
DE Collagen type III alpha-1.
PN US6110689-A.
PD 29-AUG-2000.
PA (OSTE-) OSTEOMETER AS.
Query Match 6.7%; Score 122.5; DB 3; Length 1078;
Best Local Similarity 25.3%; Pred. No. 1.1;
RESULT 1393
ID AAE16478 standard; protein; 1078 AA.
DE Human collagen alphas (III) protein.
PN US6323314-B1.
PD 27-NOV-2001.
PA (OSTE-) OSTEOMETER AS.
Query Match 6.7%; Score 122.5; DB 5; Length 1078;
Best Local Similarity 25.3%; Pred. No. 1.1;
RESULT 1394
ID ABB80736 standard; protein; 1078 AA.
DE Collagen type III-alpha protein.
PN US6355442-B1.
PD 12-MAR-2002.
PA (OSTE-) OSTEOMETER BIOTECH AS.
Query Match 6.7%; Score 122.5; DB 5; Length 1078;
Best Local Similarity 25.3%; Pred. No. 1.1;
RESULT 1395
ID ABB09628 standard; peptide; 1078 AA.
DE Amino acid sequence of human collagen type III alpha1.
PN US6342361-B1.
PD 29-JAN-2002.
PA (OSTE-) OSTEOMETER BIOTECH AS.
Query Match 6.7%; Score 122.5; DB 5; Length 1078;
Best Local Similarity 25.3%; Pred. No. 1.1;
RESULT 1396
ID ADF13078 standard; protein; 1078 AA.
DE Human collagen alpha1(III) chain precursor.
PN US2003119058-A1.
PD 26-JUN-2003.
PA (OSTE-) OSTEOMETER AS.
Query Match 6.7%; Score 122.5; DB 7; Length 1078;
Best Local Similarity 25.3%; Pred. No. 1.1;
RESULT 1397
ID ADN35277 standard; protein; 1313 AA.
DE Helical domain of type III collagen.
PN WO2004028404-A2.
PD 08-APR-2004.
PA (FIBR-) FIBROGEN INC.
Query Match 6.7%; Score 122.5; DB 8; Length 1313;
Best Local Similarity 25.3%; Pred. No. 1.4;
RESULT 1398
ID ADV97860 standard; protein; 1373 AA.
DE Murine protein kinase enzyme Seq 180.
PN WO200500200-A2.
PD 06-JAN-2005.
PA (SUGE-) SUGEN INC.

Query Match 6.7%; Score 122.5; DB 9; Length 1373;
Best Local Similarity 22.7%; Pred. No. 1.5;
RESULT 1399
ID AAE21729 standard; protein; 1413 AA.
DE Human PKIN-24 protein.
PN WO200218557-A2.
PD 07-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.7%; Score 122.5; DB 5; Length 1413;
Best Local Similarity 22.3%; Pred. No. 1.6;
RESULT 1400
ID ADP48530 standard; protein; 1420 AA.
DE Full-length chicken type II collagen.
PN WO2004052910-A1.
PD 24-JUN-2004.
PA (AFPI-) AFFILIATED HOSPITAL ACAD MILITARY SCI PL.
Query Match 6.7%; Score 122.5; DB 8; Length 1420;
Best Local Similarity 23.2%; Pred. No. 1.6;
RESULT 1401
ID ADC59465 standard; protein; 1460 AA.
DE Novel human tyrosine kinase protein.
PN JP2003024075-A.
PD 28-JAN-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 6.7%; Score 122.5; DB 7; Length 1460;
Best Local Similarity 22.3%; Pred. No. 1.6;
RESULT 1402
ID ADU04632 standard; protein; 1460 AA.
DE Human KIAA 1893 polypeptide.
PN WO2004091511-A2.
PD 28-OCT-2004.
PA (GENZ) GENZYME CORP.
Query Match 6.7%; Score 122.5; DB 8; Length 1460;
Best Local Similarity 22.3%; Pred. No. 1.6;
RESULT 1403
ID AEK63749 standard; protein; 1623 AA.
DE Human lemur tyrosine kinase 3 sequence.
PN WO2006099182-A2.
PD 21-SEP-2006.
PA (EXEL-) EXELIXIS INC.
Query Match 6.7%; Score 122.5; DB 10; Length 1623;
Best Local Similarity 22.3%; Pred. No. 1.9;
RESULT 1404
ID ADJ69113 standard; protein; 1644 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID919.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.7%; Score 122.5; DB 7; Length 1644;
Best Local Similarity 21.8%; Pred. No. 1.9;
RESULT 1405
ID ADE47676 standard; protein; 3208 AA.
DE Human NOV14c protein SEQ ID NO:38.
PN WO2003076642-A2.
PD 18-SEP-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.7%; Score 122.5; DB 7; Length 3208;
Best Local Similarity 28.5%; Pred. No. 4.2;
RESULT 1406
ID ADJ78946 standard; protein; 3208 AA.
DE Human NOVX protein Nov14c amino acid sequence.
PN US2004014053-A1.
PD 22-JAN-2004.
PA (ZERR-) ZERRHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (KEKU/) KEKUDA R.
PA (MILL/) MILLER C E.
PA (RIEG/) RIEGER D K.
PA (PEN/) PENA C E A.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (BERG/) BERGHS C.

PA (ZHON/) ZHONG M.
 PA (CASH/) CASHMAN S. J.
 PA (VOSS/) VOSS E. Z.
 PA (BOLD/) BOLDOG F. L.
 PA (PADI/) PADIGARU M.
 PA (SMIT/) SMITHSON G.
 PA (JINW/) JI W.
 PA (GORM/) GORMAN L.
 PA (VERN/) VERNET C. A. M.
 PA (LEIT/) LEITE M. W.
 PA (GUOX/) GUO X. S.
 PA (ANDE/) ANDERSON D. W.
 PA (SPYT/) SPYTEK K. A.
 PA (GERL/) GERLACH V.
 PA (BURG/) BURGESS C. E.
 PA (KHRA/) KHRAMTSOV N. V.
 PA (ORTT/) ORT T.
 PA (ELLE/) ELLERMAN K.
 PA (RAST/) RASTELLI L.
 PA (AGEE/) AGEE M. L.
 PA (CHAU/) CHAUDHURI A.
 PA (CHAN/) CHANT J. S.
 PA (DIPI/) DIPIPO V. A.
 PA (EDIN/) EDINGER S. R.
 PA (EISE/) EISEN A. J.
 PA (GANG/) GANGOLLI E. A.
 PA (GIOT/) GIOT L.
 PA (OOIC/) OOI C. E.
 PA (ROTH/) ROTHENBERG M. E.
 PA (SPAD/) SPADERNA S. K.
 PA (HJAL/) HJALT T.
 PA (LIUX/) LIU X.
 PA (TAUP/) TAUPIER R. J.
 PA (CATT/) CATTERTON E.
 PA (SHEN/) SHENOY S. G.
 Query Match 6.7%; Score 122.5; DB 8; Length 3208;
 Best Local Similarity 28.5%; Pred. No. 4.2;
 RESULT 1407
 ID ABD81094 standard; protein; 482 AA.
 DE Human IRX5 protein, SEQ ID NO:2.
 PN WO2005110464-A2.
 PD 24-NOV-2005.
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 Query Match 6.7%; Score 122; DB 9; Length 482;
 Best Local Similarity 27.4%; Pred. No. 0.48;
 RESULT 1408
 ID ABU05353 standard; protein; 488 AA.
 DE M. tuberculosis and M. leprae marker protein #4.
 PN WO200274903-A2.
 PD 26-SEP-2002.
 PA (INSP-) INST PASTEUR.
 Query Match 6.7%; Score 122; DB 5; Length 488;
 Best Local Similarity 24.8%; Pred. No. 0.48;
 RESULT 1409
 ID AAG67370 standard; protein; 574 AA.
 DE Amino acid sequence of a yeast WASP protein homologue.
 PN WO200144292-A2.
 PD 21-JUN-2001.
 PA (CNRS-) CENT NAT RECH SCI.
 PA (CURI-) INST CURIE.
 Query Match 6.7%; Score 122; DB 4; Length 574;
 Best Local Similarity 24.0%; Pred. No. 0.59;
 RESULT 1410
 ID AAW52322 standard; protein; 574 AA.
 DE WASP homolog protein.
 PN WO200171356-A2.
 PD 27-SEP-2001.
 PA (CNRS-) CENT NAT RECH SCI.
 PA (CURI-) INST CURIE.
 Query Match 6.7%; Score 122; DB 4; Length 574;
 Best Local Similarity 24.0%; Pred. No. 0.59;
 RESULT 1411
 ID ABG95028 standard; protein; 574 AA.

DE Human translocation (17; 19)(q23; p13) protein #1.
 PN WO200269900-A2.
 PD 12-SEP-2002.
 PA (CONF-) CONFORMA THERAPEUTICS CORP.
 Query Match 6.7%; Score 122; DB 5; Length 574;
 Best Local Similarity 24.4%; Pred. No. 0.59;
 RESULT 1412
 ID ADE54724 standard; protein; 575 AA.
 DE Rat Protein AAC33823, SEQ ID NO 529.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO-) GEN HOSPITAL CORP.
 PA (FARB-) BAYER AG.
 Query Match 6.7%; Score 122; DB 7; Length 575;
 Best Local Similarity 26.0%; Pred. No. 0.59;
 RESULT 1413
 ID AEJ09459 standard; protein; 575 AA.
 DE Human EPS-15 interacting protein 1, Epsin 1.
 PN WO2006068768-A2.
 PD 29-JUN-2006.
 PA (SKUB-) SKUBATCH H.
 Query Match 6.7%; Score 122; DB 10; Length 575;
 Best Local Similarity 26.0%; Pred. No. 0.59;
 RESULT 1414
 ID AEA20121 standard; protein; 650 AA.
 DE Novel human polypeptide SEQ ID NO 815.
 PN WO2005049806-A2.
 PD 02-JUN-2005.
 PA (NUVE-) NUVELO INC.
 Query Match 6.7%; Score 122; DB 9; Length 650;
 Best Local Similarity 25.2%; Pred. No. 0.68;
 RESULT 1415
 ID AAB42538 standard; protein; 666 AA.
 DE Human ORFX ORF2302 polypeptide sequence SEQ ID NO:4604.
 PN WO200058473-A2.
 PD 05-OCT-2000.
 PA (CURA-) CURAGEN CORP.
 Query Match 6.7%; Score 122; DB 3; Length 666;
 Best Local Similarity 27.7%; Pred. No. 0.7;
 RESULT 1416
 ID ADZ84991 standard; protein; 668 AA.
 DE Partial PHOS interacting protein, mA044679 (668).
 PN US2005100966-A1.
 PD 12-MAY-2005.
 PA (SAKA-) SAKAMOTO T.
 PA (TAKE-) TAKEDA S.
 Query Match 6.7%; Score 122; DB 9; Length 668;
 Best Local Similarity 25.2%; Pred. No. 0.7;
 RESULT 1417
 ID AEA20120 standard; protein; 725 AA.
 DE Novel human polypeptide SEQ ID NO 814.
 PN WO2005049806-A2.
 PD 02-JUN-2005.
 PA (NUVE-) NUVELO INC.
 Query Match 6.7%; Score 122; DB 9; Length 725;
 Best Local Similarity 25.2%; Pred. No. 0.78;
 RESULT 1418
 ID AAR80327 standard; protein; 762 AA.
 DE Protein polymeric adhesion substrate 1-B.
 PN WO9523611-A1.
 PD 08-SEP-1995.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 6.7%; Score 122; DB 2; Length 762;
 Best Local Similarity 29.6%; Pred. No. 0.82;
 RESULT 1419
 ID AAW57668 standard; peptide; 762 AA.
 DE Collagen-like polymer.
 PN US5773249-A.
 PD 30-JUN-1998.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 6.7%; Score 122; DB 2; Length 762;
 Best Local Similarity 29.6%; Pred. No. 0.82;
 RESULT 1420

ID AAW49715 standard; protein; 762 AA.
DE Protein polymer adhesive substrate PPAS1-B.
PN US5773577-A.
PD 30-JUN-1998.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 6.7%; Score 122; DB 2; Length 762;
Best Local Similarity 29.6%; Pred. No. 0.82;
RESULT 1421
ID AAG42392 standard; protein; 763 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52864.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 122; DB 3; Length 763;
Best Local Similarity 22.4%; Pred. No. 0.82;
RESULT 1422
ID AAG42391 standard; protein; 793 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52863.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 122; DB 3; Length 793;
Best Local Similarity 22.4%; Pred. No. 0.86;
RESULT 1423
ID ABG03569 standard; protein; 819 AA.
DE Novel human diagnostic protein #3560.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 122; DB 4; Length 819;
Best Local Similarity 23.9%; Pred. No. 0.9;
RESULT 1424
ID ADC33029 standard; protein; 819 AA.
DE Human novel contig-encoded polypeptide sequence, SEQ ID NO:3111.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 122; DB 7; Length 819;
Best Local Similarity 23.9%; Pred. No. 0.9;
RESULT 1425
ID ADW99577 standard; protein; 1014 AA.
DE Human gelatin protein - SEQ ID 10.
PN WO2005012356-A2.
PD 10-FEB-2005.
PA (FIBR-) FIBROGEN INC.
Query Match 6.7%; Score 122; DB 9; Length 1014;
Best Local Similarity 25.9%; Pred. No. 1.2;
RESULT 1426
ID ADT55822 standard; protein; 1038 AA.
DE Plant polypeptide, SEQ ID 5899.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 6.7%; Score 122; DB 8; Length 1038;
Best Local Similarity 25.3%; Pred. No. 1.2;
RESULT 1427
ID AAM40399 standard; protein; 1150 AA.
DE Human polypeptide SEQ ID NO 3544.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 122; DB 4; Length 1150;
Best Local Similarity 25.2%; Pred. No. 1.3;
RESULT 1428
ID AQO59439 standard; protein; 1152 AA.
DE Human cancer-associated (CA) protein sequence SEQ ID NO:75.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.7%; Score 122; DB 8; Length 1152;
Best Local Similarity 25.5%; Pred. No. 1.3;
RESULT 1429
ID AD213746 standard; protein; 1152 AA.
DE Murine cancer-associated protein #141.
PN WO2005031001-A2.

PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 6.7%; Score 122; DB 9; Length 1152;
Best Local Similarity 25.5%; Pred. No. 1.3;
RESULT 1430
ID ABR57561 standard; protein; 1259 AA.
DE Human MC25.
PN WO2003029464-A2.
PD 10-APR-2003.
PA (UNIO) UCB SA.
Query Match 6.7%; Score 122; DB 6; Length 1259;
Best Local Similarity 23.6%; Pred. No. 1.5;
RESULT 1431
ID ABW84430 standard; protein; 1476 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4679.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.7%; Score 122; DB 8; Length 1476;
Best Local Similarity 24.0%; Pred. No. 1.8;
RESULT 1432
ID ABB66989 standard; protein; 1537 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 27759.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.7%; Score 122; DB 4; Length 1537;
Best Local Similarity 24.4%; Pred. No. 1.9;
RESULT 1433
ID ABB62819 standard; protein; 1963 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15249.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.7%; Score 122; DB 4; Length 1963;
Best Local Similarity 22.4%; Pred. No. 2.6;
RESULT 1434
ID ABG23029 standard; protein; 3640 AA.
DE Novel human diagnostic protein #23020.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 122; DB 4; Length 3640;
Best Local Similarity 24.1%; Pred. No. 5.3;
RESULT 1435
ID ADW44462 standard; protein; 276 AA.
DE Murine alpha 1 type-IV collagen.
PN WO2005001090-A1.
PD 06-JAN-2005.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 6.7%; Score 121.5; DB 9; Length 276;
Best Local Similarity 25.7%; Pred. No. 0.27;
RESULT 1436
ID AEF19252 standard; protein; 276 AA.
DE Mouse alpha 1 type-IV collagen.
PN WO2006001396-A1.
PD 05-JAN-2006.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 6.7%; Score 121.5; DB 10; Length 276;
Best Local Similarity 25.7%; Pred. No. 0.27;
RESULT 1437
ID ADD45740 standard; protein; 331 AA.
DE Human Protein PIHUB6, SEQ ID NO 11408.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.7%; Score 121.5; DB 7; Length 331;
Best Local Similarity 24.0%; Pred. No. 0.33;
RESULT 1438
ID ADS91507 standard; protein; 625 AA.
DE RGD-enriched human COL5A2 protein.
PN WO2004085473-A2.

PD 07-OCT-2004.
PA (FUJF) FUJI PHOTO FILM BV.
Query Match 6.7%; Score 121.5; DB 8; Length 625;
Best Local Similarity 25.2%; Pred. No. 0.71;
RESULT 1439
ID ADF28121 standard; protein; 717 AA.
DE Adiponectin-like mature protein - SED ID 31.
PN WO2003048326-A2.
PD 12-JUN-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 121.5; DB 7; Length 717;
Best Local Similarity 25.2%; Pred. No. 0.84;
RESULT 1440
ID AAM39127 standard; protein; 744 AA.
DE Human polypeptide SEQ ID NO 2272.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 121.5; DB 4; Length 744;
Best Local Similarity 25.2%; Pred. No. 0.88;
RESULT 1441
ID ADF28118 standard; protein; 744 AA.
DE Adiponectin-like precursor protein - SED ID 28.
PN WO2003048326-A2.
PD 12-JUN-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 121.5; DB 7; Length 744;
Best Local Similarity 25.2%; Pred. No. 0.88;
RESULT 1442
ID ADV86381 standard; protein; 744 AA.
DE Novel C1q domain-containing protein #5.
PN US2004248156-A1.
PD 09-DEC-2004.
PA (HUTT/) HU T.
PA (TANG/) TANG Y T.
PA (GHOS/) GHOSH M J.
PA (WANG/) WANG J.
PA (WANG/) WANG Z.
PA (ZHAO/) ZHAO Q.
PA (XUCC/) XU C.
PA (MULE/) MULERO J.
Query Match 6.7%; Score 121.5; DB 9; Length 744;
Best Local Similarity 25.2%; Pred. No. 0.88;
RESULT 1443
ID ABB62915 standard; protein; 749 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15537.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.7%; Score 121.5; DB 4; Length 749;
Best Local Similarity 24.4%; Pred. No. 0.88;
RESULT 1444
ID ADF28246 standard; protein; 754 AA.
DE Neurological therapy-related protein - SED ID 156.
PN WO2003048326-A2.
PD 12-JUN-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 121.5; DB 7; Length 754;
Best Local Similarity 25.2%; Pred. No. 0.89;
RESULT 1445
ID AAM40913 standard; protein; 755 AA.
DE Human polypeptide SEQ ID NO 5844.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 121.5; DB 4; Length 755;
Best Local Similarity 25.2%; Pred. No. 0.89;
RESULT 1446
ID ADF95261 standard; protein; 1067 AA.
DE Dog procollagen type IIA.
PN WO2005106495-A1.
PD 10-NOV-2005.
PA (PHAA) PHARMACIA & UPJOHN CO LLC.

Query Match 6.7%; Score 121.5; DB 9; Length 1067;
Best Local Similarity 23.1%; Pred. No. 1.3;
RESULT 1447
ID ADD24191 standard; protein; 256 AA.
DE White-tailed deer prion protein amino acid sequence.
PN WO2003059386-A2.
PD 24-JUL-2003.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 6.6%; Score 121; DB 7; Length 256;
Best Local Similarity 36.7%; Pred. No. 0.27;
RESULT 1448
ID ABG22716 standard; protein; 519 AA.
DE Novel human diagnostic protein #22707.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.6%; Score 121; DB 4; Length 519;
Best Local Similarity 22.8%; Pred. No. 0.82;
RESULT 1449
ID ABB11013 standard; peptide; 606 AA.
DE Human membrane-bound protein homologue, SEQ ID NO:1383.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.6%; Score 121; DB 4; Length 606;
Best Local Similarity 23.8%; Pred. No. 0.75;
RESULT 1450
ID AAR13950 standard; protein; 654 AA.
DE E2alpha protein.
PN WO9113172-A.
PD 05-SEP-1991.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 6.6%; Score 121; DB 2; Length 654;
Best Local Similarity 24.4%; Pred. No. 0.82;
RESULT 1451
ID ADE61843 standard; protein; 654 AA.
DE Human Protein P15923, SEQ ID NO 7772.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.6%; Score 121; DB 7; Length 654;
Best Local Similarity 24.4%; Pred. No. 0.82;
RESULT 1452
ID ADE63855 standard; protein; 654 AA.
DE Human Protein XP_047600, SEQ ID NO 9799.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.6%; Score 121; DB 7; Length 654;
Best Local Similarity 24.4%; Pred. No. 0.82;
RESULT 1453
ID AEM81990 standard; protein; 654 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO38496, SEQ:5133.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 121; DB 8; Length 654;
Best Local Similarity 24.4%; Pred. No. 0.82;
RESULT 1454
ID ADX05496 standard; protein; 654 AA.
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 61.
PN WO2005012875-A2.
PD 10-FEB-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 6.6%; Score 121; DB 9; Length 654;
Best Local Similarity 24.4%; Pred. No. 0.82;
RESULT 1455
ID AAR13949 standard; protein; 736 AA.
DE SUP-B27 t(1;19) translocation fusion protein - clone KJ9.
PN WO9113172-A.

PD 05-SEP-1991.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 0.95; Length 736;
 RESULT 1456
 ID AAR15158 standard; protein; 742 AA.
 DE E2A/pr1 fusion protein TYPE II from clone 697-4.
 PN WO9113172-A.
 PD 05-SEP-1991.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 0.96; Length 742;
 RESULT 1457
 ID AAR13948 standard; protein; 819 AA.
 DE SUP-B27 t(1;19) translocation fusion protein.
 PN WO9113172-A.
 PD 05-SEP-1991.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 819;
 RESULT 1458
 ID AAR13951 standard; protein; 825 AA.
 DE E2A/pr1 fusion protein TYPE I from clone 697-4.
 PN WO9113172-A.
 PD 05-SEP-1991.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 825;
 RESULT 1459
 ID AAU86145 standard; protein; 839 AA.
 DE Human PRO7168 polypeptide.
 PN WO200153486-A1.
 PD 26-JUL-2001.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1460
 ID ABG34056 standard; protein; 839 AA.
 DE Human Pro peptide #27.
 PN WO200224888-A2.
 PD 28-MAR-2002.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1461
 ID ADA01322 standard; protein; 839 AA.
 DE Human PRO polypeptide #27.
 PN US2003068779-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1462
 ID ADA43751 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003064474-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1463
 ID ADA43519 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003073196-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1464
 ID ADA43519 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003073196-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1465
 ID ADA01078 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003068780-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1466
 ID ADA43635 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003073190-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1467
 ID ADA06897 standard; protein; 839 AA.
 DE Human PRO polypeptide #27.
 PN US2003068781-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1468
 ID ADA08385 standard; protein; 839 AA.
 DE Novel human secreted and transmembrane protein PRO7168.
 PN US2003068783-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1469
 ID ADB99678 standard; protein; 839 AA.
 DE Human PRO polypeptide SEQ ID 54.
 PN US2003082728-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1470
 ID ADB86961 standard; protein; 839 AA.
 DE Human PRO polypeptide #27.
 PN US2003082726-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1471
 ID ADB66116 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003082729-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1472
 ID ADB99794 standard; protein; 839 AA.
 DE Human PRO polypeptide SEQ ID 54.
 PN US2003073192-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1473
 ID ADB99449 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003073192-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1474
 ID ADB99449 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003073192-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1475
 ID ADB99449 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003073192-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1476
 ID ADB99449 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003073192-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1477
 ID ADB99449 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003073192-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1478
 ID ADB99449 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003073192-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1479
 ID ADB99449 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003073192-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1480
 ID ADB99449 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003073192-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1481
 ID ADB99449 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003073192-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1482
 ID ADB99449 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003073192-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1483
 ID ADB99449 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003073192-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1.1; Length 839;
 RESULT 1484
 ID ADB99449 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003073192-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 1

DE Novel human secreted and transmembrane protein PRO7168.
 PN US2003082731-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.6%; Score 121; DB 7; Length 839;
 Best Local Similarity 24.4%; Pred. No. 1.1;
 RESULT 1474
 ID ADB66000 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003082732-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.6%; Score 121; DB 7; Length 839;
 Best Local Similarity 24.4%; Pred. No. 1.1;
 RESULT 1475
 ID ADC23398 standard; protein; 839 AA.
 DE Human transmembrane PRO polypeptide (SeqID 54).
 PN US2003073193-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.6%; Score 121; DB 7; Length 839;
 Best Local Similarity 24.4%; Pred. No. 1.1;
 RESULT 1476
 ID ADC26091 standard; protein; 839 AA.
 DE Human PRO7168 protein.
 PN US2003073194-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.6%; Score 121; DB 7; Length 839;
 Best Local Similarity 24.4%; Pred. No. 1.1;
 RESULT 1477
 ID ADE04918 standard; protein; 839 AA.
 DE Human PRO polypeptide #27.
 PN US2003068778-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.6%; Score 121; DB 7; Length 839;
 Best Local Similarity 24.4%; Pred. No. 1.1;
 RESULT 1478
 ID ADE11224 standard; protein; 839 AA.
 DE Human PRO polypeptide #27.
 PN US2003073191-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.6%; Score 121; DB 7; Length 839;
 Best Local Similarity 24.4%; Pred. No. 1.1;
 RESULT 1479
 ID ADD88155 standard; protein; 839 AA.
 DE Human PRO polypeptide #27.
 PN US2003082733-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.6%; Score 121; DB 7; Length 839;
 Best Local Similarity 24.4%; Pred. No. 1.1;
 RESULT 1480
 ID ADD95450 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003064473-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.6%; Score 121; DB 7; Length 839;
 Best Local Similarity 24.4%; Pred. No. 1.1;
 RESULT 1481
 ID ADE06380 standard; protein; 839 AA.
 DE Human PRO polypeptide #27.
 PN US2003073195-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.6%; Score 121; DB 7; Length 839;
 Best Local Similarity 24.4%; Pred. No. 1.1;
 RESULT 1482
 ID ADE38155 standard; protein; 839 AA.
 DE Human PRO polypeptide #27.

PN US2003119120-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.6%; Score 121; DB 7; Length 839;
 Best Local Similarity 24.4%; Pred. No. 1.1;
 RESULT 1483
 ID ADD88271 standard; protein; 839 AA.
 DE Human PRO polypeptide #27.
 PN US2003073189-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.6%; Score 121; DB 7; Length 839;
 Best Local Similarity 24.4%; Pred. No. 1.1;
 RESULT 1484
 ID ADD90852 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003073188-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.6%; Score 121; DB 7; Length 839;
 Best Local Similarity 24.4%; Pred. No. 1.1;
 RESULT 1485
 ID ADF99407 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003078401-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.6%; Score 121; DB 7; Length 839;
 Best Local Similarity 24.4%; Pred. No. 1.1;
 RESULT 1486
 ID ADG06500 standard; protein; 839 AA.
 DE Human PRO polypeptide #27.
 PN US2003077742-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.6%; Score 121; DB 7; Length 839;
 Best Local Similarity 24.4%; Pred. No. 1.1;
 RESULT 1487
 ID ADG05451 standard; protein; 839 AA.
 DE Human PRO polypeptide #27.
 PN US2003077741-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.6%; Score 121; DB 7; Length 839;
 Best Local Similarity 24.4%; Pred. No. 1.1;
 RESULT 1488
 ID ADG82452 standard; protein; 839 AA.
 DE Human PRO polypeptide #27.
 PN US2003077744-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.6%; Score 121; DB 7; Length 839;
 Best Local Similarity 24.4%; Pred. No. 1.1;
 RESULT 1489
 ID ADJ37317 standard; protein; 839 AA.
 DE Human tumour therapy associated PRO7168.
 PN US2003211096-A1.
 PD 13-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.6%; Score 121; DB 7; Length 839;
 Best Local Similarity 24.4%; Pred. No. 1.1;
 RESULT 1490
 ID ADE51705 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003104560-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.6%; Score 121; DB 8; Length 839;
 Best Local Similarity 24.4%; Pred. No. 1.1;
 RESULT 1491
 ID ADE51821 standard; protein; 839 AA.
 DE Human secreted/transmembrane polypeptide PRO7168.
 PN US2003104561-A1.

PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 6.6%; Score 121; DB 8; Length 839;
Query Match 24.4%; Pred. No. 1.1;
Best Local Similarity 24.4%; Pred. No. 1.1;
RESULT 1492
ID ADE37679 standard; protein; 839 AA.
DE Human secreted/transmembrane polypeptide PRO7168.
PN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 6.6%; Score 121; DB 8; Length 839;
Query Match 24.4%; Pred. No. 1.1;
Best Local Similarity 24.4%; Pred. No. 1.1;
RESULT 1493
ID ADE37563 standard; protein; 839 AA.
DE Human secreted/transmembrane polypeptide PRO7168.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 6.6%; Score 121; DB 8; Length 839;
Query Match 24.4%; Pred. No. 1.1;
Best Local Similarity 24.4%; Pred. No. 1.1;
RESULT 1494
ID ADD95334 standard; protein; 839 AA.
DE Human secreted/transmembrane polypeptide PRO7168.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC. 6.6%; Score 121; DB 8; Length 839;
Query Match 24.4%; Pred. No. 1.1;
Best Local Similarity 24.4%; Pred. No. 1.1;
RESULT 1495
ID ADE38034 standard; protein; 839 AA.
DE Human PRO polypeptide #27.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 6.6%; Score 121; DB 8; Length 839;
Query Match 24.4%; Pred. No. 1.1;
Best Local Similarity 24.4%; Pred. No. 1.1;
RESULT 1496
ID ADE76123 standard; protein; 839 AA.
DE Human PRO polypeptide #27.
PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC. 6.6%; Score 121; DB 8; Length 839;
Query Match 24.4%; Pred. No. 1.1;
Best Local Similarity 24.4%; Pred. No. 1.1;
RESULT 1497
ID ADE39446 standard; protein; 839 AA.
DE Human PRO polypeptide #27.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC. 6.6%; Score 121; DB 8; Length 839;
Query Match 24.4%; Pred. No. 1.1;
Best Local Similarity 24.4%; Pred. No. 1.1;
RESULT 1498
ID ADE04250 standard; protein; 839 AA.
DE Human PRO polypeptide #27.
PN US2003096364-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC. 6.6%; Score 121; DB 8; Length 839;
Query Match 24.4%; Pred. No. 1.1;
Best Local Similarity 24.4%; Pred. No. 1.1;
RESULT 1499
ID ADE39847 standard; protein; 839 AA.
DE Human PRO polypeptide #27.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC. 6.6%; Score 121; DB 8; Length 839;
Query Match 24.4%; Pred. No. 1.1;
Best Local Similarity 24.4%; Pred. No. 1.1;
RESULT 1500
ID ADE19712 standard; protein; 839 AA.
DE Human PRO polypeptide #27.
PN US2003138903-A1.
PD 24-JUL-2003.

PA (GETH) GENENTECH INC. 6.6%; Score 121; DB 8; Length 839;
Query Match 24.4%; Pred. No. 1.1;
Best Local Similarity 24.4%; Pred. No. 1.1;